B. bronchiseptica
Human ORFX ORF2085
Novel human diagno
Novel human diagno
Human polypeptide
Human polypeptide

Human polypeptide
Human polypeptide
Human polypeptide
Peptide 683 derive
Peptide BBO5 deriv
Drosophila melanog
Sequence of a bioa
Sugar beet chitina
Drosophila melanog
Ser-Pro-Pro-Pro ge
Novel human diagno

Minimum DB seq Maximum DB seq

Database

Perfect score:

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Sequence:

Scoring table:

Searched:

Arabidopsis thalia Bloadhesive precur Ser-Pro-Pro-Pro Novel human dlagno Herbicidally activ

Human polypeptide Human low density Ser-Pro-Pro gene 1 Prod. of DNA of pl Complete form of 1

us-09-855-754b-19.rag

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    B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                          AAO04412
AAO02076
AAO020124
AAO02134
AAO02036
AAR11739
AAR11739
AAR28150
AAB7302
AAB7302
AAB77250
AAB77250
AAB77250
AAB9333
AAB9332
AAB9332
AAB105332
AAR063338
                                                                                                 AAE17146
AAE16203
AAB42321
ABG09876
ABG09877
             AAE16201
AAE16193
AAE16199
                                                       AAE16200
AAE16202
AAE16184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP |) INST PASTEUR.
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B. bronchiseptica
Bordetella paraper
Bordetella paraper
Pertactin antigen
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
Pertactin antigen
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Bordetella bronchi
                                                                                           7, 2003, 16:31:28 ; Search time 30.1363 Seconds (without alignments) 256.453 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1: /SIDS2/gcgdata/geneseqy-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseqy-emb1/AA1981.DAT:*
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335
1 Garappapkpapgpgpgp.....QRQPEapapgppagrelsaa
       GenCore version 5.1:4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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AAE16185
AAR14321
AAE16195
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AAR14320
AAR16330
AAR26503
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Gapop 10.0 , Gapext 0.5
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Score

Result Š 335 335 320 314 303 303 284 284 284

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                                         (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the mantigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                    Gaps
                              present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                            35..643
/label= P70
260..262
/note= "motif associated with cell-cell adhesion"
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/note= "motif associated with cell-cell adhesion"
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                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPPGPPQPPQPPQPPQPPQPPQRQPPQRQPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whooping cough; P70 antigen; P95 precursor protein; vaccination.
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                                                                                                                                                                                                                                                                    100.0%; Score 335; DB 23;
100.0%; Pred. No. 3.9e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               AAR25578 standard; Protein; 922 AA.
Claim 26; Fig 1c; 47pp; English.
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                                                                                                                                                                                                                                                                                               58; Conservative
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575.61
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Best Local Similarity
                                                                                                                                                                                                                                      58 AA;
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
            A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloining of 40-50kb fragments into the BamHI site of cosmid pH679. The cosmids were screened with a 1.8kb clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (*P95*) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                       Length 922;
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                                                                                                                                                                                                                                                                                                    Score 335; DB 13;
Pred. No. 2.7e-17;
Mismatches 0;
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/note= "Pertactin region I"
564..621
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                                                                                                                                                                                                                                                                 922 AA;
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used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative or guantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                  Gaps
                                                                                                                                           1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRPQPPQRPAGRELSAA
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                                                                                                Length 922;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                  Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                            100.0%; Score 335; DB 23;
100.0%; Pred. No. 2.7e-17;
.1ve 0; Mismatches 0;
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/label= re
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ses 58; Conservative
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                                                                                                                                                                                                                                                 Pertactin antigen P.70.
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                                                                               922 AA;
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                                                                                                                                                                             RESULT 4
AAR14321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                     pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448 (1989).
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQREAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                              The 46 Xs represent amino acids missing in the specification.
                                                                                                                                                                                                                                                                                                                                     Length 922;
                                                                                                                                                        microorganisms are transformed for the expression of
                                                                 Pichia micro'rganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                 95.5%; Score 320; DB 12;
96.6%; Pred. No. 3.4e-16;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
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                                                                                                                   Disclosure; Fig 1C; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16195 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
             WPI; 1991-325214/44.
N-PSDB; AAQ14320.
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                 922 AA;
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                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16195;
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                      Matches
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52 AA.

AAE16194 standard; peptide;

RESULT 7

(first entry)

26-MAR-2002

AAE16194;

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    B. bronchiseptica strain II-5 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                            Gaps
                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQP-PQP-PQP-PQPPQPPQPPQPPQRDEAPAPQPPAGRELSAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                          Length 60;
                                                                                                        Score 314; DB 23;
Pred. No. 1.3e-16;
                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                       AAE16197 standard; peptide; 56
                                                                                                        93.7%;
96.7%;
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica.
                                                                                                                                          Conservative
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                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                       58;
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                                                                       Sequence
                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                          AAE16197;
                                                                                                                                       Matches
                                                                                                                                                                                                                                                                            AAE1619.
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B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin; Pichia; B. pertussis; B. parapertussis.
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89.7%; Pred. No. 1.9e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14320 standard; Protein; 911 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                            Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.7
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                       WO200190143-A2.
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Gaps

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Length 56; Indels

Score 303; DB 23; Pred. No. 8.1e-16; 0; Mismatches 1;

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90.4%; 94.8%;

Local Similarity nes 55; Conserv

Best Loca Matches

à g

Query Match

1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPPARAPPQPPAGRELSAA 58

Peptide

Pept1de Peptide Peptide Pept1de Peptide Peptide

Peptide Peptide

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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against arrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 284; DB 13;
Pred. No. 1.4e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
254..299
/note= "Pertactin region I"
                                                                                                                                  260..262
/label= RGD_tripeptide
701..703
/label= RGD_tripeptide
                                                                                           /label= Repeat_region
                                                                                                                        Repeat_region
                                       Location/Qualifiers
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                                                     35..632
/label= P.68
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ilarity 89.7%;
Conservative
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                                                                                                                                                                                                                                                           92WO-GB00561
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/label= هم
رود
          Bordetalla bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 AA;
                                                                                                                                                                                                                                                           27-MAR-1992;
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                                                                                                                                                                                                                                 15-0CT-1992.
                                                                                                                                                                                                                                                                                                                                             Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                    Protein
                                                                                                                                     Peptide
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Region
                                                                                                         Region
                                                                              Region
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ID AAE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
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89.7%; Pred. No. 1.4e-13;
11ve 0; Mismatches 0;
                                    Location/Qualifiers
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'label - repeat
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                                                                                                                                                                                                                                                                                                                                                                     91WO-GB00487
        Bordetella bronchiseptica.
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                                                                                                                                                          578..580
/label- re
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/label- re
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                                                                            . 275
                                                                                                                                  ..576
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                                                                                                                                                                                                                   . 586
                                                                                                                                               /label=
578..580
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ14319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prn proteins.
                                                                                                                                                                                                                                                                                                                                                                     28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                               32-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1993
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Gaps

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Sequence

Query Match

Best Loca Matches

559

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AAR26503;

RESULT 9

Length 911; Indels 28

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Boursaux-eude

Guiso-maclouf N,

WPI; 2002-097639/13.

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Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                          present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%; Score 284; DB 23; Length 911;
89.7%; Pred. No. 1.4e-13;
ive 0; Mismatches 0; Indels
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 28; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                     Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE16196 standard; peptide; 53
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                                                                                                                                                                     (INSP ) INST PASTEUR
                                                                                                                                                                                                                                 WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 AA;
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                                             WO200190143-A2
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Best Local Simi
Matches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAE16196
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.3%; Score 282.5; DB 2
89.7%; Pred. No. 2.4e-14;
ive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boursaux-eude
                                                                                                                                                               Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE16201 standard; peptide; 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloopsical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRPQRPQRPAPAPAPAPAGRELSAA 58
                                                                                                                                                                                                                                                                                                                                                                                                  Length 54;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                         Score 265; DB 23; Pred. No. 4.6e-13; O; Mismatches 5;
                                                                                                                                                                                                                                                                                         79.1%;
84.5%;
                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                     54 AA;
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                           Query Match
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 B. bronchiseptica strain II-1 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. AAE16193 standard; peptide; 49 23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P (first entry) Bordetella bronchiseptica. (INSP) INST PASTEUR WO200190143-A2 26-MAR-2002 AAE16193; RESULT 13 AAE16193

Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica for The present invention relates to Bordetella bronchiseptica pertactin Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

49 AA; Sequence

pertactin outer membrane protein region ii.

AAE16200 standard; peptide; 52

RESULT 15

AAE16200 ID AAE1

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                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQRPQRPAPQPPAGRELSAA
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                                     Length
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                              DB 23;
                              Score 263.5; DB 23;
Pred. No. 5.5e-13;
0; Mismatches 0;
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Query Match
Best Local Similarity 84...
Action 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin;
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                                                                                                                                                                                                                                                                                                                          RESULT 14
AAE16199
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                                                                                                                                                                                                                                                                                                                                                                                                                     NAME OF COLOR OF STATES OF
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AAE16200;
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26-MAR-2002 (first entry)

B. bronchiseptica strain II-8 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica,

WO200190143-A2

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin artibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burlfying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

52 AA; Sequence

Gaps . 9 Score 256; DB 23; Length 52; Pred. No. 2e-12; 0; Mismatches 3; Indels 76.48; 84.58; Best Local Similarity 84.5 Matches 49; Conservative Query Match

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28 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPPAPAPQPPAGRELSAA ŏ g

Search completed: May 7, 2003, 16:47:08 Job time : 31.1363 secs

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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: May 7, 2003, 16:53:34 ; Search time 16.7905 Seconds

(without alignments)
306.927 Million cell updates/sec

Ferfect score: 322
Sequence: 1 GARAPPAPRPAPQPGPQPFP......QRQPEAPAPQPPAGRELSAA 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: 349150
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

349150 seqs, 92025710 residues

Searched:

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PUS06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 43, P. Sequence 47, Ap. Sequence 47, Ap. Sequence 47, Ap. Sequence 22, Sequence 23, Sequence 5, Sequence 5, Sequence 24, Sequence 44, Sequence 18 Description Sequence Sequence Sequence Sequence Sequence Sequence US-09-855-754-18 US-09-855-754-19 US-09-855-754-16 US-09-855-754-15 US-09-855-754-17 US-09-855-754-17 US-09-855-754-17 US-09-855-754-17 US-09-855-754-20 US-09-855-754-20 US-09-855-754-21 US-09-855-754-22 US-09-855-754-22 US-09-855-754-22 US-09-855-754-22 US-09-855-754-22 US-10-023-529-47 US-09-976-740-47 SUMMARIES Query Match Length DB 91.5 888.5 888.5 887.6 882.1 79.8 79.8 79.8 79.5 65.2 65.2 65.2 Score 285 282 264.5 133 132.5 132.5 Result

Sequence 47, Appl	Sequence 3, Appli	Sequence 2, Appl1	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appl1	Sequence 1002, Ap	Sequence 1002, Ap	Sequence 7, Appli	Sequence 4, Appl1	.0	Sequence 1, Appli		Sequence 34988, A	Sequence 36844, A	Sequence 967, App	Sequence 62, Appl	Sequence 2, Appli	Sequence 5, Appl1	Sequence 4, Appl1	Sequence 61, Appl	Sequence 1, Appli	Sequence 60, Appl	Sequence 4, Appli	6	17,	
12 US-10-023-523-47	9 US-10-171-384-3	10 US-09-823-240-2	12 US-10-042-417-32	9 US-10-020-215-2	9 US-09-959-987-2	9 US-09-925-299-1002	10 US-09-925-299-1002	10 US-09-904-987-7	10 US-09-850-887-4	10 US-09-765-272-160	9 US-10-171-384-1	10 US-09-791-171-70	10 US-09-864-761-34988	10 US-09-864-761-36844	10 US-09-764-864-967	9 US-09-298-523B-62	9 US-09-298-523B-2	9 US-10-067-457-5	9 US-10-077-584-4	9 US-09-298-523B-61	9 US-09-298-523B-1	9 US-09-298-523B-60	9 US-09-824-574-4	9 US-10-077-584-9	9 US-09-820-843A-17	
550	827	802	197	1274	641	647	647	1543	274	641	824	999	171	171	316	701	707	863	171	069	691	929	1647	68	274	
41.1	39.9	39.4	38.0	38.0	37.7	37.7	37.7	37.7	37.6	37.4	37.4	37.0	36.6	36.6	36.6	36.5	36.5	36.2	36.0	35.9	35.9	35.9	35.7	35.6	32.6	
132.5	128.5	127	122.5	122.5	121.5	121.5	121.5	121.5	121	120.5	120.5	119	118	118	118	117.5	117.5	116.5	116	115.5	115.5	115.5	115	114.5	114.5	
20	21	22	23	54	52	56	27	28	53	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45	
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ALIGNMENTS

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTION IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGEBRICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGEBRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US,09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHILN VOI. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 322; DB 9; Best Local Similarity 100.0%; Pred. No. 1.3e-15; Matches 56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
Sequence 18, Application US/09855754
Sequence 18, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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US-09-855-754-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-855-754-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 18
LENGTH: 56
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                               US-09-855-754-16
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US-09-855-754-4
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Best Local 9
                                                                                                                                                                                       TYPE: PRT
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Publication No. US20020192237A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND SORDETELLA
TITLE OF INVENTION: IMMUNCANIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GUISO-MACIOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI NO BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR PILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
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TITLE OF INVENTION: BRONGTELLA PRAAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNCERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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Pred. No. 2.3e-13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 303; DB 9;
Pred. No. 2.4e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
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; Sequence 6, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
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94.88;
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94.8%;
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SOFTWARE: Patentin Ver. 2.1
FO TH NO. 5
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Best Local Similarity
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Best Local Similarity
Matches 55; Conserv
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LENGTH: 922
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GENERAL INFORMATION

APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPITIES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERRUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPITICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPITICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PELING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTING DATE: 2000-05-25
SOFTWARE: PATENTING VOICE-25
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TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE
TITLE OF INVENTION: MUNDRERIES US/09/855,754
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                           Score 294.5; DB 9;
Pred. No. 8.9e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.5%; Score 285; DB 9; 92.9%; Pred. No. 3.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Bordetella bronchiseptica US-09-855-754-15
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                         ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-855-754-15; Sequence 15, Application US/09855754; Publication No. US20020192237A1
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1 Similarity 91.7%;
55; Conservative
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Matches 52; Conservative
                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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Gaps

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J US-09-855-754-14

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: PEGIPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PRATACTIN IN BORDETELLA PRIVISSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSETWARE: PATENTIN VET. 2.1
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Publication No. US2020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENE. COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
                                                                                                                                                                                                                                                GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                 Length 49;
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                                                                          Score 264.5; DB 9;
Pred. No. 7.4e-12;
0; Mismatches 0;
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Best Local Similarity 86.0%; Pred. No. 2.4e-11;
Matches 49; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 258; DB 9
Pred. No. 2e-11;
0; Mismatches
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
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US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-855-754-20
Sequence: 20, Application US/09855754
Publication No. US20020192237A1
PUBLICATION BOURDATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,
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illarity 85.7%;
Conservative
                                                                             82.18;
ilarity 87.58;
Conservative
                                                                          Ouery Match
Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 48; Conserv
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US-09-855-754-21
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LENGTH: 48
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTORINI IN BORDETELLA
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOUTHWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                            Length 911;
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                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                     Score 285; DB 9;
Pred. No. 3.5e-12;
0; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 282; DB 9;
Pred. No. 5.4e-13;
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                                                                                                  ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
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Publication No. US20020192237A1
AGENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                 88.5%;
ilarity 92.9%;
Conservative
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1 Similarity 91.1%;
51; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 4
LENGTH: 911
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Best Local Simi
Matches 52;
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US-09-855-754-17
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LENGTH: 52
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Matches 38; Conserv
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RESULT 13
US-09-855-754-5
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FILE REPERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARRAPERTUSSIS, AND BORDETELLA PARRAPERTUSSIS, ATTLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA
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Pred. No. 2.9e-11;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 42;
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Pred. No. 2.6e-08;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/0985554 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                            Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.2%;
Best Local Similarity 73.2%;
Matches 41; Conservative
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Best Local Similarity 87.5%;
Matches 49; Conservative
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; ORGANISM: BO:
US-09-855-754-23
                                                                                                                                        US-09-855-754-22
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LENGTH: 54
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Publication No. US20020192237A1

GENERAL INFORMATION:

APPLICANT: BOURSAUX EUDE, CAROLINE

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPE

TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS,

TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS

FILE REFERENCE: 03455-0206-00000

CURRENT FILING DATE: 2001-09-10
                                                                                                                APPLICANT: GUISO-WACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND JITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PAPLICATION NUMBER: 60,206,969
PRIOR PAPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
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BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.2%; Score 210; DB 9;
Best Local Similarity 73.2%; Pred. No. 3.2e-07;
Matches 41; Conservative 0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
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Sequence 5, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Bordetella pertussis
US-09-855-754-5
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 39
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Romon W.

APPLICANT: Alona, Anibal A.

TITLE OF INVENTION: APPRENCE LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: 08/616,289

PRIOR APPLICATION NUMBER: 08/6031,930

PRIOR PELING DATE: 1997-11-27

PRIOR PELING DATE: 1997-66-33

PRIOR FILING DATE: 1997-66-33

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 43

SEQ ID NO 43

LENGTH: 538

TYPE: FRT

OUGHY WACCh

A1.3%: SCOTE 133; DB 9; Length 538;

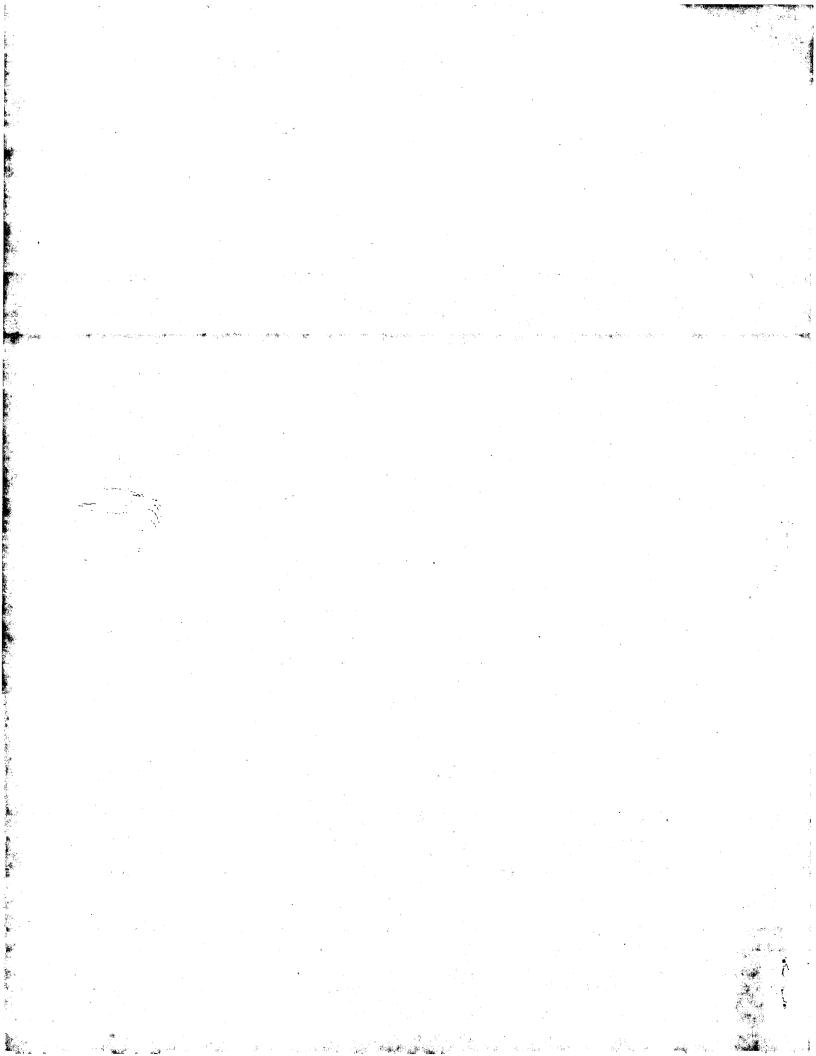
QUETY MACCh

Best Local Similarity 47.4%: Pred. No. 0.026;

MATCHES 27; CONSELVATIVE 2; MISMMATCHES 18; Indels 10; Gaps 2;

AARAPPARAPRAPARPARPREPRAPPRAVAREPPLEPPROPRAPPOQORPPROPORP 234
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Search completed: May 7, 2003, 17:30:52 Job time : 16.7905 secs



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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

Мау Run on:

7, 2003, 16:41:02 ; Search time 10.494 Seconds (without alignments) 513.008 Million cell updates/sec

US-09-855-754B-18

Title: Perfect score:

322 1 Gakappapkpapgpgpgpgp..........grqpeapapgppagrelsaa 56 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-	Description	pertactin - Bordet	68K outer membrane	outer membrane pro	hypothetical 47.8K	pherophorin-S - Vo	proline-rich prote	UL36 protein - hum	hypothetical proli	sulfated surface q	ö	T20H2.9 protein -	hypothetical prote	nuclear protein EB	cysteine-rich exte	chitinase (EC 3.2.		hypothetical prote		protein-tyrosine-p	hypothetical prote	proline-rich prote	proline-rich prote	extensin - Volvox	hypothetical prote			hypothetical prote	03	hydroxyproline-ric
COLUMNIC	ID	S15204	A47675	A32560	JC2301	T10798	S16748	WMBEH6	A34043	A33647	S21961	A86335	T48814	S42442	A48232	S51939	B48232	н83619	S47538	T14355	AE2295	T17547	T17531	S22697	T10340	T31611	T17737	T24470	JQ1696	T07907
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	Match Length	922	911	910	430	599	449	3164	141	485	534	1137	1952	487	209	439	196	270	431	1494	383	544	412	464	875	1585	288	165	426	446
* Query	Match	94.1	88.5	65.2	51.1	46.3	45.8	45.5	45.3	45.3	•	44.3	44.3	43.9	43.5	43.5	43.3	43.0	43.0	43.0	41.9	41.8	41.6	41.6	41.5	41.5	41.3	41.1	41.1	41.1
	Score	303	282	210	164.5	149	147.5	146.5	146	146	144	142.5	142.5	141.5	140	140	139.5	138.5	138.5	138.5	135	134.5	134	134	133.5	133.5	133	132.5	132.5	132.5
Result	No.	н	~	m	4	S	9	7	&	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

proline/lysine-ric hypothetical prote	proline-rich prote extensin-like prot	proline-rich prote immediate-early pr	extensin-like prot procyclin homolog	lysine/proline-ric extensin homolog T	pisti extensin-ii hypothetical prote	ORF2 protein - sai procyclic acidic r	proline-rich prote
T17908 B96534 T17815	T17636 JQ1686	T17525 EDBEIF	T10741 T17557	T1/88/ T06291	S75138	B34770 A26036	B24264
000	ก่อ	77	200	900	10	~ ~	7
496 494 225	339	549 1460	309	760	1749	102 129	240
41.1	40.5	4.04 4.04 4.1	30.00	9 9 9	39.4	39.3	39.3
132.5	130.5	130	127.5	127.5	127	126.5	126.5
30 31	333	36.5	38	y 4 4 y 0 -	12	4 4 2 4	45

ALIGNMENTS

RESULT 1 -815204
pertactin ⊨ Bordétella parapertussis N;Alternate names: outer membrane protein P70
C; Species: Bordetella parapertussis
c;Date: 0/ Apr 1394 *Sequence_revision 0/ Apr 1994 *text_cnange U8-Oct-1999 C;Accession: S15204; S14659
R;Li, L.J.; Dougan, G.; Novotny, P.; Charles, I.G.
A.Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A: Reference number: \$15204; MUID:91251771; PMID:2041476
A;Molecule type: DNA
A; Residues: 1-922 <lil></lil>
A; Cross-references: EMBL: X54547; NID: 939761; PIDN: CAA38419.1; PID: 939762
C;Genetics:
A;Gene: prn C;Keywords: membrane protein
Query Match 94.1%; Score 303; DB 2; Length 922;
0
OY 1 GAKAPPAPKPAPOPGPOPGPOPPOPPOPPOPPOPPOPPAPAPOPPAGRELSAA 56
DD 564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQPPQPPAPAPAPA

68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica C;Species: Bordetella bronchiseptica C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A47675 R;Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J. Gen. Microbiol: 138, 1697-1705, 1992 A:Title: Cloning, nucleotide sequence and heterologous expression of the protective of A;Reference number: A47675; MuID:92407514; PMID:1527510 RESULT 2

A; Accession: A47675

A;Status: preliminary
Myolecule type: nucleic acid
A;Residues: 1-911, LLII.>
A;Residues: 1-911, LLII.>
A;Cross-references: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397
A;Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

Gaps 4 h 88.5%; Score 285; DB 2; Length 911; Simijarity 92.9%; Pred. No. 6.6e-12; Conservative 0; Mismatches 0; Indels Query Match Best Local Simi Matches 52;

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GAKAPPAÅKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 56

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Gaps

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proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S16748
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991
A;Description: Cloning and characterization of a proline-rich gene expressed specific A;Recession: S16748
A;Accession: S16748
A;Residues: 1-449 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: human herpesvirus 1
C; Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C; Accession: 130085
R; McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
              A;Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK.10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The complete DNA sequence of the long unique region in the genome of herpes A; Reference number: A30083; MUID:88274327; PMID:2839594
A; Accession: 130085
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-3164 <MCG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KPQPKPPPRPQPKPQPKPPPRPQPKPPPRPPRPSPCPPQPPKPQPKPPPRPGP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PPQPPQRQPE---APAP 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147.5; DB 2; Length 449;
Pred. No. 0.0026;
3; Mismatches 16; Indels 17
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                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQP-PQRQPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                   5 PPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                             Score 149; DB 2;
Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 146.5; DB Pred. No. 0.014; 2; Mismatches
                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UL36 protein - human herpesvirus 1 (strain 17)
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Best Local Similarity 67.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.6%;
Matches 29; Conservative
                                                                                                                                                                Query Match
Best Local Similarity 54.5%;
Matches 24; Conservative
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Best Local Similarity
A; Residues: 1-599 <GOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 QPPAG 50
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C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
D;NA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A;Reference number: JC2299; MUID:96031989; PMID:8535973
A;Accession: JC2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P
                                                                                                                                                                                                                                                 R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6 A;Reference number: A32560; MUID:89264462; PMID:2542937
A;Accession: A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pueropublication various carterial cypecies: Volvox carterial cypecies: Volvox carterial cypecies: Volvox carterial cypecies: Volvox carterial cypecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 cyaccession: T10798 #sequence_revision 16-Jul-1999 #sequence_revision 16-Jul-1999 #sequence_revision No.; Wenzl, S.; Sumper, M. A; Fitle: Differential targetting of closely related ECM-glycoproteins: The pherophorin A; Recession: T10798 #sequence revision T10798 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-430 <WAD>
A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                            C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: DNA
A Residues: 1-910 cCHA>
A Cross-references: GB:304560; NID:9144053; PIDN:AAA22980.1; PID:9144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
C: Keywords: membrane protein
F; H-34/Domain: signal sequence #status predicted <SIG>
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAKAPPAPKPA----PQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPQPQROPEAPAPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQ--RQPEA-----
                                                                                                                                            outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 2;
Pred. No. 4.4e-07;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical 47.8K protein - Pneumocystis carinii
N:Alternate names: ORF-3
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Best Local Similarity 73.2%;
Matches 41; Conservative (
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Matches 32; Conservative
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PEPQPP 318
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Indels

Length 3164;

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Ritheologis, A.; Scker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maith, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Authors: Geytence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48814
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
Stbmitted to the protein Sequence Database, April 2000
A;Reference numbe;: 224541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1137 <STO>
A;Cross-references: GB:AE005172; NID:g8778985; PIDN:AAF79900.1; GSPDB:GN00141
                                                                                                                                                                                                                               T20H2.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
                                                                    A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 15E6.220 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 142.5; DB 2;
Pred. No. 0.011;
4; Mismatches 13;
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C;Species: human herpesvirus 4, Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 142.5; DB
Pred. No. 0.017;
3; Mismatches
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1)arity 54.5%;
Conservative
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Best Local Similarity 59.28
Matches 29; Conservative
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A; Molecule type: bNA
A; Residues: 1-1952 <SCH>
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                C; Accession: A86335
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A; Introns: 281/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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                                                                                                                                                                            RESULT 11
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7. Cell Blol. 1007, 3439-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A;Reference number: A33647; MUID:90094551; PMID:2689458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S21961
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
A;Boscription: Cloning and characterization of a proline-rich gene expressed specificall
A;Reference number: S16748
hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment) (Species: Owenia fusiformis C;Species: Owenia fusiformis C;Date: Oy-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000 C;Accession: A34043 B34043 R;Bakalara, N; Collet, J.; Planells, R; Thouveny, Y.; Fontes, M. Biochem. Blophys. Res. Commun. 166, 66-73, 1990 A;Fitle: Presence in invertebrate genomes of sequences characterized by the repetition A;Reference number: A90159; MUID:90147742; PMID:2105723
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNĀ
A; Residues: 1-485 <ERT>
A; Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C; Keywords: glycoprotein
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9
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Pred. No. 0.0013;
0; Mismatches 22; Indels
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Pred. No. 0.0035;
3; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 РРАРКРАРОРСРОРСРОРСРОРОРОРРОРРОРОВЕЛЬНИЕ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X60377; NID:g22598; PID:g22599 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
44.7%; Score 144; DB 2;
Best Local Similarity 54.9%; Pred. No. 0.0051;
Matches 28; Conservative 3; Mismatches 14;
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A;Introns: 256/1; 299/3; 387/3; 470/1
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ilarity 53.2%;
Conservative
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Best Local Similarity 52.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
                                                                                                                                                                                                                                                                             A;Residues: 1-141 <BAK>
A;Cross-references: GB:M32217
A;Accession: B34043
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Matches 25; Conserv
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A; Residues: 1-534 <ROB>
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Indels

Length 1137;

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16; DB 2;

Length 1952;

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chiffnase (EC 3.2.1.14) precursor - beet
C.Species: Beta vulgaris (beet)
C.Date: 28-Oct-1996 #sequence.vision 07-Feb-1997 #text_change 10-Jul-1998
C.Accession: S51939; S72315; S4505
R.Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.Plant Mol. Biol. 27, 211-216, 1995
A.Jitle: A proline-rich chitinase from Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X79301; NID:9488730; PID:9488731
A;Note: the authors translated the codon TGC for residue 416 as Gly
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46.2%; Pred. No. 0.0079;
iive 5; Mismatches 19
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C; Superfamily: plant chitinase homology
C; Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted <S
F;26-439/Product: chitinase #status predicted <WAT>
F;183-423/Domain: plant chitinase homology <PCH>
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A; Molecule type: mRNA
A; Residues: 191-397 <BER2>
C; Genetics:
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Matches 24; Conserv
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A; Molecule type: DNA
A; Residues: 1-439 <BER>
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ne : 11.494 secs
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A; Residues: 1-487 c.FRA.
A; Residues: 1-487 c.FRA.
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
B; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
B; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
A; Tather and School Scho
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A:Reference number: PQ0474; MUID:93005740; PMID:1392607
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Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1991
Pritle: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MID:93342083; PMID:8341705
                                                                                                                                                                                     nuclear proteins: a
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A; Residues: 39-209 <GGL>
A; Cross-references: EMBL:214020; NID:g19918; PID:g19919
A; Experimental source: EMBL:214020; Strain Petit Havana SR1
C; Superfamily: glutelin
C; Reywords: cell wall; extracellular matrix; fertilization; glycoprotein
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-209/Product: cysteline-rich extensin-like protein 1 #status experimental <MAT>
F; 146/Binding site: carbohydrate (Asn) (covalent) #status predicted
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48232; PQ0475; S24617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-f8, 'PPP', 89-487 <DAM>
A; Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C; Superfamily: hydroxyproline-rich glycoprotein
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Pred. No. 0.0068;
1; Mismatches 19;
                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1.487 <SAM>
R; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Reference number: S32973
A; Accession: S32988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:L13439; NID:g310922;
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illarity 52.1%;
Conservative
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Best Local Similarity
Matches 25; Conserv
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A; Residues: 1-209 <WUA>
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85 PPRPRPCPSPPPPRPCPSPPPPQP--RPRPSPPPSPPPA 127

Gaps

Length 439;

GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 7, 2003, 16:31:49; Search time 5.43782 Seconds (without alignments) 427.133 Million cell updates/sec

Title: Perfect score:

US-09-855-754B-18 322 I GAKAPPAPKPAPQPGPPQPGP......QRQPEAPAPQPPAGRELSAA Sequence:

56

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P24328 bordetella	Q03035 bordetella	P14283 bordetella	P40603 brassica na	P10220 herpes simp	P21260 owenia fusi	volvox		P12978 epstein-bar	_	P48038 oryctolagus	_	•		P25050 herpesvirus	-	P22576 herpesvirus	_	_	PO5143 mus musculu	Q24120 drosophila	Q64467 mus musculu	Q05859 mus musculu	Q05860 mus musculu	P08469 trypanosoma		P78621 emericella	_	P23093 plasmodium	P51111 rattus norv	P04726 triticum ae	P70315 mus musculu	P22670 homo sapien
SUMMARIES	ΙD	PERT_BORPA	PERT_BORBR	PERT_BORPE	APG_BRANA	TEGU_HSV11	YPRO_OWEFU	SSGP_VOLCA	APG_ARATH	EBN2_EBV	MOZ_HUMAN	ACRO_RABIT	GP1_CHLRE	Y066_NPVOP	EXLP_TOBAC	COLL_HSVS7	MOT8_MOUSE	COLL_HSVSC	PARB_TRYBB	PRP2_MOUSE	PRP3_MOUSE	CAPU_DROME	G3PT_MOUSE	FM14_MOUSE	FMN1_MOUSE	PAR1_TRYBB	PARC_TRYBB	SEPA_EMENI	CSP_PLABE	CSP_PLABA	HD_RAT	3DA6_WHEAT	WASP_MOUSE	RFX1_HUMAN
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367 3184 3184 415 4415 1048 1362 172 172 1139 206		ANDAR	. 21, Creat . 21, Last ; . 41, Last ; sor (Outer ;	rtussis acteria	PubMed Novc	"; :409-41 LUTINOG HE R-G- ESION,	MEK. OCATION CONTRIB : SYNTH S.	ntry is ntry is s Insti nformat it ins statem a lice	38419.1; 01454.1; 01454.1; 09; Pertact, 99; pertact,	9991; periocia Pertactin; 1. PERTACTIN; Signal; Virul 34 922 647 922
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120.0.5 120.0.		r 1 30RPA PERT_BORPA 24328;	01-MAR-1992 (Rel. 2. 01-MAR-1992 (Rel. 2. 15-JUN-2002 (Rel. 4. Pertactin precursor	PRN. Bordetella parapertussis. Bacteria; Proteobacteria; Bordetella. NCBI_TaxID=519;	[1] SEQUENCE FRO STRAIN-CN259 MEDLINE-9129 Li L.J., Dou "P.70 pertace	Sscherichia (ol. Microb 1- FUNCTION MEDIATEN BACTERN	- SUBURIT - SUBCELLA - 1 - DISEASE - 1 - MISCELLA - CONCENTI	this MISS-1 between the between the lise by not nodified and notities reconstities reconstities and	EMBL; X54547; CAA38419.1; EMBL; A26124; CAA01786.1; EMBL; A19182; CAA01454.1; PIR; S12204; S15204; PIR; S14659; S14659; InterPro; IPR004899; Pertac	interPro; irrord InterPro; irrord Pfam; PF03213; P PRINTS; PR01404; Outer membrahe; SIGNAL ICHAIN ICHAIN ISCHAIN ISCHA
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                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Outer membrane.
-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+) CONCENTRATIONS.
                                                                                   (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                      26
               LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Gen. Microbiol, 138:1697-1705(1992).

-i- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLIS; A PROC MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella bronchiseptica.";
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRPQREAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.94.
PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
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                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                            Length 922;
                                                                                                                                                                                                                                                                                                                                                                               Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                         1; Indels
                                                                                                                                           ; DB 1;
6.4e-12;
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Last annotation update)
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                                                                                                                                               Score 303;
                                                                                                                                                             Pred. No.
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InterPro: IPR004899; Pertact_sup.
InterPro: IPR003992; pertactin.
InterPro: IPR003991; pertactin_vir.
Pfam: PF03212; Pertactin_1.
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PRINTS; PR01484; PRTACTNFAMLY.
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nilarity 94.8%;
Conservative
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(Rel. 26, I
(Rel. 41, I
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                                                                                                                                                                                                                                                                                                      PERT_BORBR
Q03035;
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MEDLINE-96196517; PubMed-8609998;
Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;
"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.; "Molecular coloning and characterization of protective outer membrane protein P.69 from Bordella pertussis."; Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                             Gaps
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-i- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                ELL ATTACHMENT SITE (POTENTIAL).
X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                             -I- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC
MEDIATED BY THE R-G-D SEQUENCE, PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                             4
                                                                                                                                                                         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                             01-7EB-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRINGROWN PRINGROWN (P. 1993).
                                                                                                                                                                                                           0; Indels
                                                                                                    (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                       Score 285; DB 1;
Pred. No. 7.2e-11;
0; Mismatches 0;
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J. Gen. Microbiol. 138:1697-1705(1992).
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92.9%;
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P14283;
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana gene.";
Plant J. 3:111-120(1993).
-!- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT, HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-94004980; Pubmed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                            LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
APG OR CEX.
                                                                                                                                                                                                                                                  CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oraper J., Scott R.; Gametophytic expression of an anther-specific
                                                                                                                                                                                                                                                                                                                                                                                                                5 (APPROXIMATE).
5 X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 1;
Pred. No. 1.9e-06;
0; Mismatches 1;
                                                                                                                                                                                                        PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                   (APPROXIMATE).
                                                                                                                                               Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                  POTENTIAL.
                 InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam. PF03212; Pertactin; 1.
PRINYS; PR01482; PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.2%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                    910
711
910
262
PIR; A32560; A32560.
                                                                                                                                                                                                                                                                                                                                                                           276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APG_BRANA
P40603;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                        CHAIN
PROPEP
SITE
                                                                                                                                                                                                                                                                                                             DOMAIN
REPEAT
REPEAT
                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                        HAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
APG_BRANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                          3 KAPPAPKPAPQPGPQPGPQPPQPPQPPQ------PPQPPQRQPE---APAP 45
                                                                                                                                                                                                                                                                              MEDLINE-88274327; PubMed-2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNabl D., Peiry L.J., Soctit J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1.",
herpes simplex virus type 1.",
i- FUNCTION: TEGUMENT PROTEIN.
i- FUNCTION: TEGUMENT PROTEIN.
i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                  Match 45.8%; Score 147.5; DB 1; Length 449; Local Similarity 44.6%; Pred. No. 0.0053; Loss 29; Conservative 3; Mismatches 16; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQP-PQRQPEAPAPQPPAG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146.5; DB 1; Length
Pred. No. 0.025;
2; Mismatches 9; Indels
                                428 428 POTENTIAL.
449 AA; 48779 MW; 9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 3164 AA.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; 130085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03585; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10299;
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141

PRT;

STANDARD;

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Gaps

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48

Length 485; 18; Indels

45.3%; Score 146; DB 1; 52.3%; Pred. No. 0.0069; iive 3; Mismatches 18

A52216400A031421 CRC64;

POLY - PRO

50436 MW;

485 AA;

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5 рраркрарорсрорсрорсрорроррорроррорропредрагарарорр
Glycoprotein; Sulfation; Hydroxylation
                                                                                                                        23; Conservative
                                                                                      Query Match
Best Local Similarity
                                   DOMAIN
SEQUENCE
                                                                                                                          Matches
                                                                                                                                                                                                                                                                      APG_ARATH
 W I I S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INIVIDIAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
ATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-90147742; PubMed-2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bakalara n., Collet J., Planells R., Thouveny Y., Fontes M.;
Pressnce in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Biochem. Biophys. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nagariensis / HKIO;
MEDLINE-90094551; PubMed-2689458;
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri; molecular structure of
                                                                                                Bukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 1; Length 141;
Pred. No. 0.0028;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 РРАРКРАРОРСРОРСРОРОРОРОРОРРОРРОРОВРОВЕАРАРОРРАСЯ 51
                                                                                                                                                                                                                                                                                                                                                                                                                    15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              H-T-H MOTIF (POTENTIAL).
                  01-NOV-1995 (Rel. 18, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) Hypothetical proline-rich protein (Fragment). Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 AA
                                                                                                                                                                                                                                                                                                                                                               POLY-PRO
                                                                                                                                                                                                                                                                                                                       Hypothetical protein; DNA-binding.
NON_TER 1 1
DOMAIN 9 58 POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
01-NOV-1995 (Rel. 32, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
01-OCT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 45.3%;
Local Similarity 53.2%;
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                                                  141 AA;
                                                                                                                                           NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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SEQUENCE FROM N.A.

STRATN=C.** Columbia;

A Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Con L., Conway A.B., Conway A.R., Ergin C.Y.,

Conway A.B., Conway A.B., Conwar A.B., Full C.Y.,

Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

A Langin-Hooper S., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Lee J.M., Nerman W.C., Osborne B.I.,

A Langin-Hooper S., Lee J.M., Nauven M., Narman W.C., Osborne B.I.,

A Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Suh H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C. M., Verter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                       15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
APG OR ATICO130 OR T20H2.9.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                   Draper J., Scott R.; "Gametophytic expression of an anther-specific "Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene."; Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                          eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                   P40602; 093214; 09LNT8;
01-FBB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
534 AA
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=94004980; PubMed=8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 408:816-820(2000).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATURATION
  APG_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thaliana.
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InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U47742; AAC50662.1;
Genew; | HGNC:13013; ZNF220.
                                                                                                                                                                                                                                                         Best Local Similarity 52.1
Matches 25; Conservative
                           -1- PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                                      437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
              SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                 MOZ_HUMAN
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                     MOZ_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-84270667; PubMed-6087149;
MEDLINE-84270667; PubMed-6087149;
Baer R. V., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.,
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                           ANTER-SPECIFIC PROLINE-RICH PROTEIN APG.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90266473; PubMed-2161150;
Pettl L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen J.I., Wang F., Kieff E.; "Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                             Score 142.5; DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                       3 KAPPAPKPAPQPGPQPGPQPPGPPQPPQPPQPPQRQPE-APAPQP-PA 49
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.012;
4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                               S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 AA
                                                                                                                                                                                                                                                        BY SIMILARITY POTENTIAL.
                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                           Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                            EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AY058847; AAL24235.1;
                                                                                                                                                                  PIR; $21961; $21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91202599; Pubmed-1850028;
                                                                                                                                                                                                                                                                                                                    58007 MW;
                                                                                                                                                                                                                                                                                                                                           44.3%;
                                                                                                                                   EMBL; X60377; CAA42925.1; -.
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 59.2
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                    534 AA;
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ACT_SITE
CONFLICT
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CONFLICT
SEQUENCE
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P12978;
                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                     Signal.
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MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968; PubMed-8782817;
MACDIAGORIA N. Starton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,
A Graganti R.S. Jr., Civin C.I., Disteche C., Dube I., Frischauf A.M.,
A Chaganti R.S. Jr., Civin C.I., Volinia S., Watmore A.E., Housman D.E.;
The translocation t(8;16) (pll.pl3) of acute myeloid leukaemia fuses
The translocation t(8;16) (pll.pl3) of acute myeloid leukaemia fuses
The translocation: MR ERREESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
THOUSING MACAGATION: NUCLear.
TOWNICATION: MAY REPRESSIN A T(8;16) (Pl1;Pl3) CHROMOSOMAL
TRANSLOCATION THAT PRODUCES A MOX-CBP CHIMAERA OBSERVED IN THE
MYMS SUBTYPE OF ACUTE MYELDID LEUKEMIA.

C -- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
C -- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T01618; -.
Transcription regulation; Activator; Nuclear protein; DNA-binding;
Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 6 X 2 AA TANDEM REPEATS OF 52544 MW; DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRE
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                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBÇNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE-Testis;
STRAIN=New Zealand white; TISSUE-Testis;
Richardson R.T., O'Rand M.G.;
Bloching and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";
Blochim. Biophys. Acta 1219:215-218(1994).
IF IS A SERINE PROFESSE OF TRYPSIN-LIKE CLEAVAGE SPECIFCITY, IT IS SYMPHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                               BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                       translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                Score 140; DB 1; Length 2004;
Pred. No. 0.043;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                         9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPAPKPAPQPGPQPGPQPPQPPQP-PQPPQPPQRQPEAPAPQPP 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 AA
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GLU-RICH.
GLU-RICH.
POLY-GLU.
POLY-SER.
GLN/PRO-RICH.
                                                                                                                PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
C2HC-TYPE.
                                                                                                                                                                       POLY-GLU.
POLY-GLU.
POLY-ARG.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                              MOZ-CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence)
15-JUN-2002 (Rel. 41, Last annotata)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_2; 2.
Proto-oncogene; Chromosomal tr
                                                                                                                                                                                                                                                                                                                                                                                     43.5%;
                                                                                                                                                                                                                                                                                                                                                            2004 AA; 225054
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.00
Local 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                      1026
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1242
1302
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                                                                                                         Nuclear protein
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P48038;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                  ZN_FING
DOMAIN
ZN_FING
DOMAIN
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"Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Biochemistry 40:2978-2987(2001).
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Adair W.S., Apt K.E.;
"cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-; FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                         MENORS: 2014427.

INTERPTO: IPR001314; Chymotrypsin.
INTERPTO: IPR001254; Ser_protease_Try.
Ffan; PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00130; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LBS; 1.
PROSITE; PS00135; TRYPSIN_LSS; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
SIGNAL.

1 16
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ACROSIN LIGHT CHAIN (BY SIMILARITY)
ACROSIN HEAVY CHAIN (BY SIMILARITY)
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.0%; Score 138.5; DB 1;
47.3%; Pred. No. 0.017;
tive 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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or send an email to license@lsb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                              ACROSIN
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MEDLINE=21159092; PubMed=11258910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46422 MW;
                                                        EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 AA;
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                                                                                                              MEROPS; S01.223;
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us-09-855-754b-18.rsp

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STANDARD;
                                                                                                                                                                                                                                                          Hypothetical protein
DOMAIN 86
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REPEAT
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILTRE-97271300; PubMed-9126251;
AALPERS C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
"The Orgyla pseudotsugata multinucleocapsid nuclear
Ppolyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95343549; PubMed-7618274;
Marens C.H., Carlson C., Rohrmann G.F.;
Aldentification, sequence, and transcriptional analysis of lef-3,
gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyla
                                                                                                                                                                                                                                                                                                                                                                                                 VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>.</del>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIOTOGY 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 APPAPK-PAPQPGPQPGPQPGPQPPQP---PQPPQPPQRQPEAPAPQPP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 136; DB 1
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y066_NPVOP STANDARD; PRT; 875 AA. 083949; Q65364; O10323; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 98.6 kDa protein (ORF71).

    -!- SUBUNIT: Associates with GP2 and GP3.
    -!- PTM: N-glycosylated and O-glycosylated.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                   EMBL; M58496; AAA69706.1; ALT_SEQ. GlycosuiteDB; O9FP06; -.
InterPro: IPRO02965; P.Ich_extensn.
INITERPRO: IPRO03882; PIStll_extensn.
PRINTS; PRO1211; PRICHEXTENSN.
PRINTS; PRO1218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; Pubmed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .udosugata.";
Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54219 MW;
                                                                                                                                                                                                                  EMBL; AF309494; AAG45420.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 806-875 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               555
339
279
399
455
493
                                                                                                                                                                                                                                                                                                                                                            Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   259
399
455
455
55 AA;
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                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pseudosugata.
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                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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SO THE THE THE TENT OF THE TEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).

Nicotiana tabacum (Common tobacco).

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                                         F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPAPKPAPQPGPQPGPQPP-QPPQPPQRPQRQPEAPAPQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JQ1696; JQ1696.
InterPro; IPR000419; Pollen_Ole_e_I.
Pfam; PPF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 41.5%; Score 133.5; DB 1; Best Local Similarity 56.8%; Pred. No. 0.057; Matches 25; Conservative 2; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. Petit Havana; TISSUE-Pistil;
MEDLINE-93005740; PubMed-1392607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         875 AA; 98603 MW;
                                                                                                                                                                                                                                EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; IFOS.
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ved. Usage by and for commercial
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or send an email to license@lsb-sib.ch).
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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90279084; PubMed=2161952;
Geck P., Whitaker S.A., Medveczky M.M., Medveczky P.G.;
"Expression of collagenlike sequences by a tumor virus, herpesvirus sainiri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92046383; PubMed-1658399;
Geck P., Whitaker S.A., Medveczky M.M., Medveczky P.G.;
"Expression of collagenlike sequences by a tumor virus, herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQ--PGPQ--PGPQ--PGPQPPQPPQPPQPPQRQPEAPAPGPPAG 50
   4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 51A495CC94017812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                ŝ
                                                                                                                                                                      165 AKQPPQPPPAKQPSPPPPPVKAPSPSPAKQPPPPPPVKAPSPSPATQPP 216
                                                                        41.1%; Score 132.5; DB 1; Length 426; 50.0%; Pred. No. 0.039; 1ve 3; Mismatches 18; Indels 5.
                                                                                                                                                   48
                                                                                                                                                2 AKAPPAPKPAPQPGPQPGP----QPGPQPPQPPQPPQPPQRQPE-APAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN-LIKE.
EF3DF0FE0FB446F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Herpesvirus saimiri (strain 484-77).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131.5; DB 1;
Pred. No. 0.016;
2; Mismatches 17;
                                                                                                                                                                                                                                                                                                         (Rel. 34, Last sequence update)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                           105 AA
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.8%; Scc
Best Local Similarity 53.6%; Pre
Matches 30; Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A36770; CGBEHS.
InterPro; IrRO00087; Collagen.
Pfam; PF01391; Collagen; 1.
Collagen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 70 C
105 AA; 10260 MW;
                                         44278 MW;
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                                                                     Query Match
Best Local Similarity 50.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 Collagen-like protein.
                                       426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ICBI_TaxID=10382
                                                                                                                                                                                                                                                                      COLL_HSVS7
P25050;
                                                                                                                                                                                                                                                                                                           01-MAY-1992
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
REPEAT
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
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                                                                                                                                                                                                                                        RESULT 15
COLL_HSVS7
   FFS
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homo sapien

pneumocysti pneumocysti pneumocysti bordetella

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Q991e9 rattus norv
Q9cx9 streptomyce
O13305 pneumocysti
Q69023 human herpe
P9797 volvox cart
Q88777 cryza sativ
Q96v11 pneumocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE_20359389; PubMed=10899896;

MEDLINE_20359389; C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250087; CAB76441.1; -.

InterPro; IPR004899; Pertact.sup.

InterPro; IPR002965; P.Ich_extensn.

Pfam; PF03112; Pertactin; I.

PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 76
0.09k5g4
0.09k5g1
0.09k1g7
0.09k1g7
0.09k1g8
0.09k1g8
0.09k1g8
0.09k1g8
0.09k1g8
0.09k1g8
0.09k1g8
0.01k23
0.01k23
0.01k23
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0.01k23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus). Bacteria; broteobacteria; beta subdivision; Alcaligenaceae; Bordetella. NCBI_TaxID-518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA; 11416 MW; 5140669692808F8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.168) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA.
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Q9JLE9
Q9JCX9
O13305
Q69023
P93797
Q8S7Y7
                                                                 PRT;
                  Q9K5G1
Q9ALP3
Q9ALP7
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493
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STRAIN-BBCH
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189.5
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SEQUENCE
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Matches
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Q9K5G9
 SO DR RET THE SO
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                                                                                                          May 7, 2003, 16:38:52 ; Search time 28.6201 Seconds (without alignments) 403.166 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bordetell
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                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09aiq2
09k5h3
09k5h1
09a1q4
09a1q4
09ak5h1
09ak5h9
09k5h9
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09kjy0 |
09ahp0 |
09k5g5 |
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              GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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09KJX9
09KJX2
09K5H2
09K5H1
09K5H1
09K5H2
09K1P9
09K1P8
09K1P8
09K7V0
09KJY1
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_nammal:*
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sp_vertebrate:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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Match Length
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264.5 264.5 264.5 264.5 264.5 258

303 291.5 291.5 285 285 285 285

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09KJX9

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STRAIN-335;
WEDLINE-20359389; PubMed=10899896;
BOUTSAUX-Edde C. Guisco N.;
BOUTSAUX-Edde C. Guisco N.;
BOUTSAUX-SIGHE C. Guisco N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
RMBL; AJZ50083; CAB76437.1;
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002956; P.rich_extensn.
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Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL; AJ250089; CAB76443.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Princh_extensn.
PF03212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQRQPPARPAPQPPAGRELSAA 56
                       170 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 225
1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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                                                                                                                                                                           115 AA
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MEDLINE-20359389; PubMed-10899896;
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                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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NON_TER
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Q9K5G7
                                                                                                                           RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                      Keil D.J., Ferwick B.; "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 GAKAPPAPKPAPQPGPQPGPQPPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 97
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                   Pertactin (Fragment).
sordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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EMBL; AROO7265; AAG34441...
InterPro; IPR0013992; pertactin.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1; -.
InterPro: IPR004899; Pertact_sup.
InterPro: IPR02965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXIENSN.
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26107 MW; 368C142508D77057 CRC64;
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122 AA; 12395 MW; BED00966A40FF994 CRC64;
                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                            122 AA
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MEDLINE-21117018; PubMed-11179374;
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PRINTS; PRO1217; PRICHEXTENSN.
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                            PRELIMINARY;
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252 AA;
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Best Local S
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Indels

Length 215;

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09K5H1 **09K5H1**;

RESULT 6

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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1; ...
Interpro: IPR004899; Pertact.sup.
Interpro: IPR002965; Prich_extensn.
PF03212; Pertactin; I
                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQRPBAPAPAGRELSAA 56
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                    215 215
215 AA; 22327 MW; 5C21D45CF784B4AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
                                                                                                                                               Score 291.5; DB 2;
Pred. No. 1.8e-17;
0; Mismatches 0;
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STRAIN-KM22;
MEDLINE-21117018; Pubmed-11179374;
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MEDLINE-20359389; PubMed-10899896;
  Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                 90.5%;
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Matches 52; Conservative
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Best Local Simi
Matches 53;
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Q9ALP9
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Q9K5H5
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Boursaux-Eude C., Gurso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

EMBL; AJ250085; CAB76439.1;

InterPro; IRR004899; Pertact.sup.
Pfam; PF03212; Pertactin; 1.

NON_TER 109 109
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                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                             Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMEL, ANOTOZ63; AAG38439.1; -. InterPro; IPR0013992; Pertactin.
InterPro; IPR0013992; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
                                       Query Match 94.1%; Score 303; DB 2; Length 11
Best Local Similarity 94.8%; Pred. No. 1.2e-18;
Matches 55; Conservative 0; Mismatches 1; Indels
9B67012D3B9AEECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%; Score 291.5; DB 2
94.6%; Pred. No. 1.1e-17;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                         109 AA
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                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CVGEO;
MEDLINE-20359389; PubMed-10899896;
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
  11453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                         PRELIMINARY;
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  111 AA;
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SEQUENCE
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es 49; Conserv
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                                SEQUENCE FROM N.A.
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          NCBI_TaxID=518;
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Bordetella
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SEQUENCE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K., Mooi F.R.;
"Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 GAKAPPAPKPA----PQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                   4;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceaė;
                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 911;
                                                                                                                                                           Score 285; DB 2; Length 200;
Pred. No. 5.9e-17;
0; Mismatches 0; Indels
Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                           200
20826 MW; 9F3AC6E4128942E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                           01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.5%; Score 285; DB 2; 92.9%; Pred. No. 2e-16; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ24597; CAB82515.1; ...
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertact.
Fam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACNREAMLY.
                   Infect. Immun. 69:1917-1921(2001).
EMBL, AX007271; AAG38447.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_ich_extensn.
Pfam; PF03212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                      PRT;
                                                                                       / Match 88.5%;
Local Similarity 92.9%;
hes 52; Conservative
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            bronchiseptica Pertactin.
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                                                                                                                                                                                                                                                                                                                                                                                         Bordetella,
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Matches
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Q9L4E2
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Q9K5H9
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Boursaux Ende C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL. AJ250079; CAB76433.1; -.
InterPro; IPR004899; Pertact_sup.
                                                                               pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250077; CAB76431.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQPPQPPAPAPQPPAGRELSAA 69
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                                                                                                                                                                                                                                                                                                                                           Length 104;
                             Boursaux-Eude C., Guiso N.; "Polymorphism of Repeated Regions of Pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2002 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Bertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTS-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                      Score 264.5; DB 2;
Pred. No. 1.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.1%; Score 264.5; DB 2;
ilarity 87.5%; Pred. No. 1.7e-15;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         82.1%; Scur.
87.5%; Pred. No. 1...
0; Mismatches
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MEDLINE=20359389; PubMed=10899896;
MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                                  InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                Pfam; PF03212; Pertactin; 1.
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Best Local Similarity 87.5
Matches 49; Conservative
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                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                   STRAIN-MBORDE 31
                                                                                                NCBI_TaxID=518;
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                                                                                                                                                   Keil D.J., Fenwick B., Wariability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-B;

**STRAIN-B;

**STRAIN-B;

**Variability in the pertactin genes of Bordetella bronchiseptica

**STRAIN-BROWN STRAIN-BROWN STR
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF156771; AAF82395.1; -InterPro: IPR004899; Pertact_sup. InterPro: IRR002965; P. rich_extensn. PF03212; PertactIn: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR156772; ARF82396.1; -1
InterPro; IRR04899; Pertact_sup.
Pfam: PF03212; Pertactln; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA; 11693 MW; FA3A76596F7097EB CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-07N-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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Pred. No. 1.9e-15;
0; Mismatches 0;
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1larity 87.5%; Pred. No. 1.9e-15;
Conservative 0; Mismatches 0;
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(TrEMBLrel. 21, Last anno
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115 AA; 11705 MW;
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1 Similarity 87.5%;
49; Conservative
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PRN.
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                                                                                                                                                                                                                                                          amino acid repeats.
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                                                                                                SEQUENCE FROM N.A.
Bordetella.
NCBI_TaxID=518;
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01-JUN-2002 (
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 198;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                               Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AA; 20575 MW; AC940EC331A725AF CRC64;
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82.1%; Score 264.5; DB 2;
Best Local Similarity 87.5%; Pred. No. 2.9e-15;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       Infect. Immut. 69:1917-1921(2001).
BMBL; Ar298590; AAK16691.1;
Interpro: IPR003992; pertact.in.
Interpro: IPR004899; Pertact.sup.
Interpro: IPR002965; P_rich_extensn.
                                                                                                                                                                                                                   MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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7, 2003, 16:31:28 ; Search time 25.46 Seconds (without alignments) 256.453 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAY:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAY:* 'geneseq/genesegp-embl/AA1989.DAT /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAI
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAI
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAI
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/SIDSZ/gcgdata/geneseqgp-embl/AA1986.DAI
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/SIDSZ/gcgdata/geneseqgp-embl/AA1986.DAI
/SIDSZ/gcgdata/geneseqgp-embl/AA1989.DAI
/SIDSZ/gcgdata/geneseqgp-embl/AA1989.DAI /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1990 'gcgdata/geneseq/geneseqp-embl/AA1995. /gcgdata/geneseq/genesegp-embl/AA1996 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998. /gcgdata/geneseq/geneseqp-embl/AA1992 /gcgdata/geneseq/geneseqp-embl/AA1993 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997 1/AA1993 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991 A_Geneseq_101002: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Bordetella paraper	ັຫ	B. bronchiseptica	B. bronchiseptica		B. bronchiseptica	Bordetella pertuss		B. bronchiseptica	Peptide 683 derive	Peptide BBO5 deriv	Synthetic Bordetel	Human ORFX ORF2085	Novel human diagno	Novel human diagno	Drosophila melanog	Novel human diagno	Ser-Pro-Pro ge		Human polypeptide	Novel human dlagno	Novel human diagno	Herbicidally activ	Human low density	Rabbit low density	beet	Np70 protein carbo	Human Npw38BP1 tra	Np70 protein seque	Human RNA metaboli	NpwBP. Homo sapie				
AAE16185	AAE1619	-	AAE16200	AAE16201		-	AAE1714	AAE16203	AAR11737	_	-	AAB42321	ABG09876	ABG09877	ABB70063	ABG27250	ABB78537	AA002036	AAO02124	AA004412	AA002076	AA004929	AAO04573	ABG21919	ABG04360	ABB93838	AAB82806	AAB82807	AAR28150	AAY67470	AAY82327		AAY72165	AAB47514
23	23	23	23	23								21	22	22	22	22	23	22	22	22	22	22	22	22	22	23	22	22	13	21	21	21	22	22
922	9	48	25	54	42	910	910	39	31	31	24	006	1217	1239	446	406	9.	82	88		66	44	82	325	356	350	538	550	439	250	641	641		641
94.8	94.4	94.1	82.8	···	76.8	ಌ	76.8	4.69	56.3	55.9						45.5	45.0	44.2	4.1.2	43.9	43.9			٠				41.9		41.4	4.1.4	4.1.4	4.1.4	41.4
263.5	262.5	261.5	238.5	237.5	213.5	213.5	213.5	193	156.5	155.5	128.5	128	128	128		126.5	125	123	123	122	122	121.5	121	119.5	119.5	118.5	116.5	116.5	115.5	115	115	115	115	115
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AAE16193 standard; peptide; 49 AA.

AAE16193;

B. bronchiseptica strain II-1 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II. Guiso-maclouf N, Boursaux-eude C; 23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P. 26-MAR-2002 (first entry) Bordetella bronchiseptica. (INSP) INST PASTEUR. WPI; 2002-097639/13. WO200190143-A2. 29-NOV-2001.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

1;

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Gaps
                               ;
      Length 49;
                               Indels
100.0%; Score 278; DB 23;
100.0%; Pred. No. 3.5e-15;
:Ive 0; Mismatches 0;
                           49; Conservative
               Local Similarity
  Query Match
                          Matches
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49 g ò

AAE16194 standard; peptide; 52 AA. (first entry) 26-MAR-2002 AAE16194; AAE16194 RESULT

B. bronchiseptica strain II-2 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as veccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                        Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\tt II.}
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                                                     Length 52;
                                                                                           49
                                                                                                            52
                                                                                     1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                   Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                    Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                      ö
                                                  Score 266.5; DB 2
Pred. No. 2.8e-14;
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                         AAR14320 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1B; 38pp; English.
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/label=_repeat
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ilarity 94.2%;
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/label= re
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/label= r
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                                                           Best Local Similarity
Matches 49; Conserv
                              52 AA;
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                                                                                                                                                                                                20-JAN-1992
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                              Sequence
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Matches
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AAE16183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                              B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                             Length 911;
                                                                                                    49
                                                                                      1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                    Indels
                                             DB 12;
                                           Score 266.5; DB 12;
Pred. No. 2.3e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              260..262
/label- RGD_tripeptide
701..703
/label- RGD_tripeptide
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/label= P.68
266..279
/label= Repeat_region
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/label- Repeat_region
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                                           Query Match 95.9%;
Best Local Similarity 94.2%;
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                              Bordetalla bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-366258/44.
N-PSDB; AAQ34566.
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Best Local Similarity
                     911 AA;
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                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                          610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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                           POPPOPPOROPEAPAPOPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                   AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 28; 47pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guiso-maclouf'N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.9%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P.
1 GAKAPPAPKPAPOPGPOPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY 2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-097539/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD26440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when tweed in affinity antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fulds, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                             B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 266; DB 23; Length 53;
Pred. No. 3.1e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pertactin outer membrane protein region il
                                        AAE16196 standard; peptide; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE16197 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1c; 47pp; English.
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ilarity 92.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2000; 2000US-206969P
                                                                                                                (first entry)
                                                                                                                                                                                                                                    Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AA;
                                                                                                                                                                                                                                                                   WO200190143-A2.
                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                      29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                           AAE16196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Matches
                    AAE16196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16197
       RESULT
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

(INSP) INST PASTEUR.

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQRQPEAPAQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels.
                                                                                                                                                                                                                                                                                                                                                                                         Score 264.5; DB 23;
Pred. No. 4.2e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16198 standard; peptide; 58 AA.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           95.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                              56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin;
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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us-09-855-754b-14.rag

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pertactin antigens. DNA sequence used are represented in AA014319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575..612
/note= "contains 9 direct repeats of Pro-Gln-Pro"
712..714
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260..262
/note= "motif associated with cell-cell adhesion"
266..285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 263.5; DB 12; Length 922; Liarity 84.5%; Pred. No. 3.9e-13; Conservative 0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia microòrganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pärapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR25578 standard; Protein; 922
  /label= repeat
610..612
/label= repeat
                                                                                                                                                                                                                                                                                                                (WELL ) WELLCOME FOUNDATION LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35..643
                                                                                                                                                                                                             91WO-GB00487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                    Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AA014320
                                                                                                                                                                                                             28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding-site
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                                                                                                                                                                                                                                                                 02-APR-1990;
                                                                                                        W09115571-A
                                                                                                                                                            17-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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     S X C C C C C C C X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X 
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                                                                                                Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQRPQREAPAPQPPAGRELSAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 263.5; DB 23;
84.5%; Pred. No. 5.2e-14;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR14321 standard; Protein; 922 AA
Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
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/label- repeat
271..275
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/label- repeat
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598..600
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/label- re
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/label- re
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/label- r
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les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 AA;
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AAR1432 RESULT

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Gaps

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Boursaux-eude C;

us-09-855-754b-14.rag

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Guiso-maclouf N,
                              N-PSDB; AAD26442
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                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                    A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the prn. gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                          Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella parapertussis pertactin outer membrane protein, p.70.
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                                                                                                                                                                                                                                                                                                                                       DB 13; Length 922;
                                                                                                                                                                                                                                                                                                                                     Score 263.5; DB 13;
Pred. No. 3.9e-13;
0; Mismatches 0;
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254..304
/note= "Pertactin region I"
764..621
/note= "Pertactin region II"
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                                                                                                                                                    Claim 1; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                     94.8%;
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91WO-GB02302
                    90GB-0027901
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                                      (WELL ) WELLCOME FOUND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                             WPI; 1992-250033/30.
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                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                  922 AA;
                                                                                         N-PSDB; AAQ26509
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23-DEC-1991;
                   21-DEC-1990;
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                                                          Charles IG;
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                                                                                                                                                                                                                                                                                                                  Sequence
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Region
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
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                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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84.5%; Pred. No. 3.9e-13;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                            Disclosure; Page 34; 47pp; English.
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2002-097639/13.
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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodsical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                  bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                           -----PQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                       DB 23; Length 60;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                          Score 262.5; DB 2.
Pred. No. 6.3e-14;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                             AAE16199 standard; peptide; 48 AA
                                                                                                                                                                                                ;
0
                                                                                                                                                                          94.4%;
ilarity 81.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica
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                                                                                                                                                              Query Match
Best Local Similarity (
                                                                                                                                                   60 AA;
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                                                                                                                                                    Seguence
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Guiso-maclouf N, Boursaux-eude C; Claim 26; Fig 1c; 47pp; English. (INSP) INST PASTEUR WPI; 2002-097639/13.

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P

29-NOV-2001.

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48 AA;
Seguence
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AAE16201 standard; peptide; 54 AA.

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                                                                                                                                                                                                                                                            8. bronchisertica strain II-8 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                          Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                       Gaps
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       DB 23; Length 48;
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                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
       Score 261.5; DB 23;
Pred. No. 6.4e-14;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 238.5; DB
Pred. No. 4e-12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guiso-maclouf N, Boursaux-eude
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                                                                                                                                                                    AAE16200 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.8%;
ilarity 86.8%;
conservative
    94.18;
llarity 98.08;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-097639/13.
Query Matich
Best Local Similarity
Matches 48; Conserv
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Best Local Similarity
Matches 46; conserv
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                                                                                                                                                                                                   AAE16200;
                                                                                                                                       RESULT 14
AAE16200
ID AAE16
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AAE16201
ID AAE16
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    B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

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                                                                 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                  Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                           Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                        23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                          25-MAY-2000; 2000US-206969P
                          26-MAR-2002 (first entry)
                                                                                               Bordetella bronchiseptica
                                                                                                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                    WPI; 2002-097639/13.
                                                                                                                  WO200190143-A2
                                                                                                                                     29-NOV-2001.
         AAE16201;
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, alycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiqens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. The present invention relates to Bordetella bronchiseptica pertactin

54 AA; Sequence

Gaps 7; 85.4%; Score 237.5; DB 23; Length 54; 83.6%; Pred. No. 5e-12; 1ve 0; Mismatches 2; Indels 7; 2; Indels Query Match
Best Local Similarity 83.69
Matches 46; Conservative

; ;

1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP-----PQRQPEAPPQPPAGRELSAA 49 ó g

7, 2003, 16:47:04 Search completed: May Job time : 26.46 secs

Sednence Sed

Sequence 87, Sequence 87, Sequence 6, A Sequence 21, Sequence 21,

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APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOMFUTER: LAD ONTA: COOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: 13,067
REFERENE/DOCKET NUMBER: POPOV-2
TELECHONE: (703) 243-6410
INFORMATION FOR SECIED NO: 4:
SEQUENCE CHARACTERISTICS:
ILENGTH: 911 amino acids
LENGTH: 911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.9%; Score 266.5; DB 4; Best Local Similarity 94.2%; Pred. No. 1.6e-16; Matches 49; Conservative 0; Mismatches 0;
                         US-09-056-556-230
US-09-072-596-225
US-09-072-596-225
US-09-072-596-226
US-08-471-780C-44
US-08-466-710C-44
US-08-466-710C-44
US-08-466-710C-44
US-08-466-710C-44
US-08-411-780C-87
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US-08-466-710C-87
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US-08-860-635A-21
US-09-281-476-21
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
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Sequence 11
Sequence 11
Sequence 11
Sequence 16
Sequence 14
Sequence 28
Sequence 29
Sequence 29
Sequence 29
Sequence 29
Sequence 29
Sequence 20
Sequenc
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1 GAKAPPAPRPAPQPGPGP......QRQPEAPAPQPPAGRELSAA
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US-08-27-716-11

US-08-250-6-11

US-08-265-16

US-09-314-265-16

US-09-314-265-14

US-09-227-420-4

US-09-227-420-4

US-09-227-420-4

US-09-041-886-29

US-09-041-886-30

US-09-041-886-31

US-09-041-886-30

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US-08-556-419-21
US-09-041-886-15
US-08-457-273B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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Match Length
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Maximum DB seq
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131.5
128.5
121.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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Gaps

3;

Length 911; Indels

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APPLICATION NUMBER: US/08/460,269C
                                                       NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                           ; INFORMATION FOR SEQ ID NO: 2; SEQUENCE CHARACTERISTICS; SEQUENCE CHARACTERISTICS; LENGTH: 910 amino acids; TYPE: amino acid ; DODLOGY: linear; MOLECULE TYPE; protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 911253.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE FINYENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08237716
Patent No. 5589384
GENERAL INFORMATION:
                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.8
Best Local Similarity 83.7
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-616-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 NO. CITY: Arlington STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-237-716-11
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Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                       ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 922;
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 263.5; DB 4;
Pred. No. 3e-16;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/460,269C
ATORILING DATE: 02-Jun-1995
ATORILING DATE: 02-Jun-1995
ATORILING DATE: 02-Jun-1995
NAME: Lebovitz, Richard M.
REFERENCE/DOCKET NUMBER: 37,067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Inhear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 243-6333
                                 Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 243-6
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
               US-08-460-269C-6
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Gaps
  Length 910;
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                                                                                               1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Nixon & Vanderhye, P.C.
1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATE: US/08/237,716 FILING DATE: 02-MAY-1994
  DB 4;
76.8%; Score 213.5; DB 4
83.7%; Pred. No. 7.3e-12;
Live 0; Mismatches 1
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Gaps
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Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: MacDonald, Marcy E.
APPLICANT: Juyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                        ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 23;
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: PALINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.7%; Score 121.5; DB 4;
88.0%; Pred. No. 3.3e-05;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,269C
FILIAGO DATE: 02-Un-1995
ATTORNEY, AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11near
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                     Sequence 8, Application US/08460269C
Patent No. 6197348
GENERALINFORMATION:
GENERALINFORMATION: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 POPGPOPPOPPOROPEAPAPOP 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER REACABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: 'IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-246-982A-16
                                                                      RESULT 6
US-08-460-269C-8
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Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: Chong, Pele
APPLICANT: Lein, Michel H
TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                      /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-FEB-1997
ATTORNEY/AGREEM: 42**
NANCELLANCE NAME AND ASSETT OF A TORNEY/AGREEM: A NANCE A TORNEY A T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-06;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.3%; Score 131.5; DB 1; Best Local Similarity 74.2%; Pred. No. 6e-06; Matches 23; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Sim & McBurney STREET: 6th Floor, 330 University Avenue CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
46.2%; Score 128.5;
Best Local Similarity 88.5%; Pred. No. 8.2e
Matches 23; Conservative '0; Mismatches
                                                                  /label= LTB sequence
                                                                                                                                                                                           /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PAPQPGPQPGPQPPQPPQRQPEAPAPQP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PGPEIAPQPGPQPPQPPQP---QPEAPAPEP 32
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NAME: Stewart, Michael I
REGISTRATION UNBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
PELEBONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                    NAME/KEY: Region
LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: Region LOCATION: 1..2 OTHER INFORMATION:
                                                                                                                           NAME/KEY: Region
LOCATION: 4 7
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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US-08-750-624-11
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Gaps

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GENERAL INFORMATION:
APPLICANT: DOORDAY, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIROSS
FILE REFERENCE: 3789/80902
CURRENT APPLICATION NUMBER: US/09/314,268
EARLIER APPLICATION NUMBER: 09/314,268
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PLICATION OF: 2.1
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                                                                                                  9 KPAPQPGPQPGPQPPQ-PPQRQPEAPAPQPPA-----GRELSA 48
                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TERA; FILPULA, DAVID ITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           í, is; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAP-KPA-PQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 APPAP-----KPA-PQPGPQPGPQPPQPPQPPQRPBAPPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.3%; Score 112; DB 4; Best Local Similarity 48.9%; Pred. No. 0.00064; Matches 23; Conservative 6; Mismatches 16
                  Best Local Similarity 50.0%; Pred. No. 0.012; Matches 25; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.0027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.1%; Score 111.5;
Best Local Similarity 48.9%; Pred. No. 0.0
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Human papillomavirus type 49
US-09-314-268-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-11990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
                                                                                                                                                                                                                 Sequence 149, Application US/09314268 Patent No. 6346377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09026587
Patent No. 5912128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5202236
                                                                                                                                                                                            US-09-314-268-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-026-587-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5202236-3
                                                                                                          QQ .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KPAPQPGPQPGPQPPQPPQ-PPQRQPEAPAPQPPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Score 114;
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08453265
Patent No. 5693/57
GENERAL INFORMATION:
GEPLICANT: MacDonald, Marcy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      CLASSIFICATION: MAY 20, 1994
ATTORNEY AGENT INFORMATION:
NAME: GOLGSTEIN, JORGE, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                  TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LUDWIG, Steven R.
REGISTRATION NUMBER: 36, 203
REFERENCE/DOCKET NUMBER: 06C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 311-2600
                                                                                                                                                                                                                                                                                                                                                                                                           41.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 50.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             US-08-246-982A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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5

Gaps

GENERAL INFORMATION:

DB 1;

41.0%; Score 114;

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POLYNUCLEOTIDE VACCINE PROTECTIVE
AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR
DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110; DB 2; Length 380;
Pred. No. 0.0042;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GPPAPPAGGPPPPPGPPPPGPPPPGLPPSGVPAAAHGAGGGPPPAPP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEA-----PAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
               FastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Naval Medical Res. 6 Dev. Cmd. STREET: Bldg. 1, T-12 8901 Wisconsin Ave.
                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0471 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-885-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,587
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-155-888-2
; Sequence,2, Application US/08155888
; Patent No. 6066633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, Martha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICAȚION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SPEVACK, A. DAVId
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sedegah, Martha
TITLE OF INVENTION: POLYNUCLE
TITLE OF INVENTION: ACAINST P
TITLE OF INVENTION: DELIVERIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical Re
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3£0 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: GenB:
; CLONE: 624964
US-09-227-420-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QC
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Pred. No. 0.0042;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPP-QPPQRQPEA-----PAPQPP 41
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Cal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,587
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09227420
Patent No. 5990087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: B1111049, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.6%;
49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.09
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
CLONE: 624964
                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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STATE: CA.
                                                                                                                                                                               CITY:
STATE:
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Search completed: May
Job time: 11.188 secs
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9
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                                                                                                                                         Length 478;
                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                             329 GPGAPQGPGAPQGPPQQPPQQPPQQPPQQPPQQPPQQPRPQP 374
                                                                                                                                                                                                              1 GAKAPPAP----KPAPQPGPQPGPQPPQ--PPQPPQRQPEAPAPQP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TILLE OF INVENTION: Proapoptotic Peptides, Dependence
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bredesen, Dale E.
APPLICANT: Rablzadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
PORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores Lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                Score 108; DB 3;
Pred. No. 0.0077;
3; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 KPAPQPGPQPGPQPP---QP--PQRQPEAPAPQPPAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION UNDHER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE GHARACTERISTICS:
LENGTH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09041886
Patent No. 6235872
                                                                                                                            Query Match 38.8%;
Best Local Similarity 50.0%;
Matches 23; Conservative
: LENGTH: 478 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECCLE TYPE: protein

US-08-155-888-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California : United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UR
                                                                                                                                                                                                                                                                                                                                         US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                      g
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7, 2003, 16:57:01

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   Polypeptides and Methods of Use
             NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                         SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KPAPQPGPQPPQPP---QP--PQRQPEAPAPQPPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107.5; DB Pred. No. 0.0093; 2; Mismatches 1:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.7%;
ilarity 45.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 530 amino acids
amino acid
                                                                                           CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-29
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                    92122
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein 7, 2003, 16:53:34; Search time 14.6917 Seconds (without alignments) 306.927 Million cell updates/sec Run on:

US-09-855-754B-14 Title:

Perfect score:

278 1 GAKAPPAPKPAPQPGPGP......QRQPEAPAPQPPAGRELSAA 49 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

349150 segs, 92025710 residues Searched:

Total number of hits satisfying chosen parameters:

349150

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	0	Query	Query	6	f	
2	30016	ייים רכוו	reng cu	9 :	OT .	Describtion
7	278	100.0	4	6	US-09-855-754-14	Sequence 14. Appl
7	266.5	95.9	52	σ	US-09-855-754-15	15.
m	266.5	95.9	911	6	US-09-855-754-4	4.
4	264.5	95.1	26	σ	US-09-855-754-18	Sequence 18, Appl
ις.	263.5	94.8	58	6	US-09-855-754-19	Sequence 19. Appl
9	263.5	94.8	922	0	US-09-855-754-6	, A
7	261.5	94.1	48	σ	US-09-855-754-20	20
80	250.5	90.1	52	6	US-09-855-754-17	17
6	247	88.8	59	6	US-09-855-754-16	16,
10	238.5	85.8	52	σ	US-09-855-754-21	21,
11	237.5	85.4	54	6	US-09-855-754-22	Sequence 22, Appl
12	213.5	76.8	42	6	US-09-855-754-23	23,
13	213.5	76.8	910	6	US-09-855-754-5	
14	193	69.4	39	6	US-09-855-754-24	24
15	117	42.1	827	6	US-10-171-384-3	3,
16	116.5	41.9	538	0	US-09-976-740-43	43
17	116.5	41.9	538	12	US-10-023-529-43	43
18	116.5	41.9	538	12	US-10-023-523-43	43,
19	116.5	41.9	550	6	US-09-976-740-47	47. 4

Sequence 47, Appl	Sequence 47, Appl	Sequence 2, Appli	Sequence 1002, Ap	Sequence 1002, Ap	Sequence 1, Appli	Sequence 2, Appl1	Sequence 10, Appl	Sequence 125, App	Sequence 4, Appli	Sequence 282, App	Sequence 2, Appli	Sequence 7, Appli	٠.	Sequence 4, Appli	Sequence 34988, A	Sequence 36844, A	Sequence 62, Appl		Sequence 5, Appl1	_	'n		Ä	Sequence 14, Appl	m
2 US-10-023-529-47	2 US-10-023-523-47	US-09-959-987:2	US-09-925-299-1002	0 US-09-925-299-1002	US-10-171-384-1	0 US-09-823-240-2	0 US-09-823-240-10	US-10-072-036-125	0 US-09-850-887-4	US-10-043-487-282	US-10-020-215-2	0 US-09-904-987-7	US-10-077-584-9	US-10-077-584-4	0 US-09-864-761-34988	0 US-09-864-761-36844	US-09-298-523B-62	US-09-298-523B-2	US-10-067-457-5	US-10-067-457-1	0 US-09-770-689A-5	US-09-548-933-15	0 US-09-910-087-21	US-09-922-199A-14	0 US-09-800-729-138
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116.5	116.5	115	115	115	112.5	112	110	110	108	107.5	107.5	107.5	104.5	104.5	103.5	103.5	103	103	103	103	102.5	102.5	101.5	101	101
20	21	22	23	24	22	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
APPLICANT: GUISO-MACLOUE, NICOLE
APPLICANT: GUISO-MACLOUE, NICOLE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPLICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: 10495-0206-00000
CURRENT APPLICATION NUMBER: 12006-09000
CURRENT FILLING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOUNSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 278; DB 9;
100.0%; Pred. No. 2e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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  US/09855754
                        US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 49; Conservative
Sequence 14, Application Publication No. US2002019
                                      GENERAL INFORMATION:
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US-09-855-754-19
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                                                                                                                                             SEQ ID NO 18
LENGIH: 56
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 266.5; DB 9;
Pred. No. 1.3e-12;
0; Mismatches 0;
                                     TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN:
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 266.5;
Pred. No. 1.46
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                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; Sequence 18, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity 94.2%;
19; Conservative
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Best Local Similarity 94.28;
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LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 4
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                       Score 264.5; DB 9
Pred. No. 1.9e-12;
0; Mismatches 0
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Pred. No. 2.2e-12;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 03495-70206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                    TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT CORGANISM: Bordetella bronchiseptica US-09-855-754-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX EUDE, CAROLINE
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-09-1
                                                                                                                                                                                                                                                    Query Match 95.1%;
Best Local Similarity 87.5%;
Matches 49; Conservative
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84.5%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Matches 49; Conservative
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PRIOR FILING DATE: 2000-0
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Gaps

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DB 9; Length 52;

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PARACENT IN BORDETELLA PERRUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR PAPLICATION NUMBER: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALCHLIN VOT. 2.1
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APPLICANT: GUISO-MACLOUP, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/4655,754
                                                                                                                                                            1 GAKAPPAPKPA----PQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                         Score 250.5; DB 9;
Pred. No. 1.6e-11;
0; Mismatches 0;
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86.8%; Pred. No. 1.1e-10;
tive 0; Mismatches 2;
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Pred. No. 3.1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica
US-09-855-7,54-16
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US-09-855-754-21
                                                                                                                                                                                                                                                                                                     US-09-855-754-16
Sequence 16, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                       Query Match
Best Local Similarity 90.6%;
Matches 48; Conservative
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80.0%;
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 80.0
Matches 48; Conservative
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Matches 46; Conservative
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PRIOR FILING DATE: 2000-05
       US-09-855-754-17
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LENGTH: 59
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LENGTH: 52
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TITLE OF INVENTION: PELIFORE CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONGTELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: USO/9/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSOFTWARE: PALENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS
FILE REPERENCE: 034995-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
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                                                                                                                                                                              Length 922;
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Pred. No. 2.6e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                 2.3e-11;
                                                                                                                                                                                 DB 9;
                                                                                                                                                                              Score 263.5; I
Pred. No. 2.3e-
0; Mismatches
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Sequence 20, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                               ) ORGANISM: Bordetella parapertussis
US-09-855-754-6
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Publication No. US20020192237A1
GENERAL INFORMATION:
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1 Similarity 98.0%;
48; Conservative
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ilarity 84.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 17
LENGTH: 52
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Best Local Similarity
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Matches 49; Conserv
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                                                                            TYPE: PRT
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 39
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Best Local Similarity
Matches 41; Conserv
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LENGTH: 910
                                         US-09-855-754-5
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US-10-171-384-3
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
PRICA APPLICATION NUMBER: 60/206,969
PRICA PLOATION NUMBER: 60/206,969
PRICA PLOATION NUMBER: 60/206,969
PRICA PLOATION NUMBER: 2011-09-10
PRICA PLANTING NUMBER: 2011-
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUS, THEIR USE IN DIAGNOSTICS, AND IN FILLE OF INVENTION: BRONCHISEPTICA, THEIR US DATE: 2000-000
CURRENT PILLING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR PILLING DATE: 2000-05-25
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                                         DB 9; Length 42;
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       -- POROPEAPAPOPPAGRELSAA
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; Pred. No. 4.7e-
0; Mismatches
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Pred. No. 1.36
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US-09-855-754-23
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GAKAPPAPKPAPQPGPQPGPQPPQP
                                                                                                                                                                                                                                               Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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APPLICANT: BOURSAUX-BUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                  CAROLINE
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Best Local Similarity 83.6%;
Matches 46; Conservative
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Best Local Similarity 83.7%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
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LENGIH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHIELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHIERPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                     TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPICA, THEIR USE IN DIAGNOSTICS, AND ITILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.4%; Score 193; DB 9; Best Local Similarity 77.6%; Pred. No. 1.1e-07; Matches 38; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 213.5; DB 9
Pred. No. 6.2e-08;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
Sequence 5, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EDDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10171384 Publication No. US20030031680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella pertussis
US-09-855-754-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 76.8%;
1 Similarity 83.7%;
41; Conservative (
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GENERAL INFORMATION:

APPLICANT: The Brigham & Women's Hospital, Inc.

APPLICANT: The Brigham & Women's Hospital, Inc.

APPLICANT: Belex, David

APPLICANT: Herron, Bruce

APPLICANT: Rao, Cherie

TILE OF ENVENTION: P53 Binding Protein-Related Protein in Cardiomyopathy

TILE OF ENVENTION: P53 Binding Protein-Related Protein in Cardiomyopathy

TILE OF ENVENT APPLICATION NUMBER: US/10/171,384

CURRENT APPLICATION NUMBER: US/10/171,384

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 3

LENGTH: 877

TYPE: PRT

ORANISM: Homo sapiens

US-10-171-384-3
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Search completed: May 7, 2003, 17:30:50 Job time: 15.6917 secs

4; Gaps

Query Match 42.1%; Score 117; DB 9; Length 827; Best Local Similarity 56.1%; Pred. No. 0.25; Matches 23; Conservative 3; Mismatches 11; Indels

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Мау Run on:

7, 2003, 16:41:02 ; Search time 9.18228 Seconds (without alignments) 513.008 Million cell updates/sec

US-09-855-754B-14 278 1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 49 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	68K outer membrane		Ω	proline-rich prote	hypothetical 47.8K	U,	nuclear protein EB	hypothetical prote	hypothetical prote	sulfated surface q	hypothetical prolí		cysteine-rich exte	hypothetical prote		hypothetical prote	hydroxyproline-ric	proline-rich prote	T20H2.9 protein -	glyceraldehyde-3-p	protein-tyrosine-p	hypothetical prote	hypothetical prote	proline-rich prote	pistil extensin-li	nase (EC 3.2.	hypothetical prote	cysteine-rich exte	acrosin (EC 3.4.21
	Sesc	58K	berta	oute	orol	odyr	her	nclo	.od At	odkt	sūlfa	odyr	rol	syste	γpo	JL36	ypo	ydr	rol	120H	1 Jyc	prote	poyr	ypo	rol	ist	shit	odyt	yst	cro
SUMMARIES		A47675	S15204				110798																		T17531 F				232	
	a	A4	S1	A3	S1	ဌ	TI	S4	60	T0	A3	A3	TI	A4	T 4	3	H8					-								A34
	DB											~		~	~	-	~											2		-
	Query Match Length	911	922	910	449	430	599	487	929	1684	485	141	544	209	1952	3164	270			_	440	1494	383	875	412	426		165		415
dР	Query	95.9	94.8	76.8	47.5	~	46.0	45.0	44.8	44.8	44.6	43.9	43.9	43.7	43.7	43.5	43.3	43.2	43.0	42.4	42.3	42.3	42.1	42.1	41.9	41.7	41.5	41.4	41.4	41.4
	Score	266.5	263.5	213.5	132	131	128	125		124.5	124	122	. 122	121.5	121.5	121	120.5	120	119.5	118	117.5	117.5	117	117	116.5	116	115.5	115	115	115
	Result No.	1	7	e	4		9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27.	28	53

Perfectin - Bordetella parapertussis

Nalternate names outer membrane protein P70

S. Speciaes: Bordetella parapertussis

C. Speciaes: Bordetella parapertussis

C. Speciaes: Bordetella parapertussis

C. Speciaes: Bordetella parapertussis

C. Date: 07-Apr-1954 # sequence_revision 07-Apr-1994 #text_change 08-Oct-1999

C. Accession: S15264; S14659

Mol. Microbiol. 5, 409-417, 1991

A;Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A;Reference number: S15204; MUID:91251771; PMID:2041476

A;Recession: S15204

A;Residues: 11-922 <LIII>
A;Residues: 11-922 <LIII>
A;Residues: 12-22 <LIII>
A;Residues: 12-22 <LIII>
A;Gene: prn

C;Genetics:

A;Gene: prn

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Gaps

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Length 922; Indels

Score 263.5; DB 2; Pred. No. 2.2e-11; 0; Mismatches 0;

Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative (

1 GAKAPPAPKPAPQPGPQPG-

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----POPPOPPORQPEAPAPOPPAGRELSAA 49

extensin - Volvox	hypothetical prote	hypothetical prote	proline/lysine-ric	pistil extensin-li	proline-rich prote	proline-rich prote	protein F2401.6 [1	acrosin (EC 3.4.21	extensin homolog I	circumsporozoite p	proline-rich prote	circumsporozoite p	OmpA family protei	protein kinase C (extensin class I (
S22697	T31611	B96534	T17908	PQ0476	T17737	T17815	A96650	S47538	T06291	OZZŐMB	T17636	OZZOBK	D87682	S61918	S14970	
N	~	7	~	~	7	~	~	7	~	-	~	-	~	-	7	
464	1585	494	496	154	288	225	70	431	760	332	339	348	449	1139	132	
41.4	41.4	40.6	40.6	40.5	40.5	40.3	10.1	40.1	40.1	39.9	39.9	39.9	39.9	39.9	39.7	
115	115	113	113	112.5	112.5	112	111.5	111.5	111.5	111	111	111	111	111	110.5	
30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 A47675 A68 Outer membrane protein P.68 pertactin - Bordetella bronchiseptica C;Species: Bordetella bronchiseptica C;Species: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A47679 J. Gen. Microbiol: 138, 1697-1705, 1992 J. Gen. Microbiol: 138, 1697-1705, 1992 A;Title: Cloning, uncleotide sequence and heterologous expression of the protective A;Reference number: A47675; MUD:92407514; PMID:1527510 A;Reference number: A47675 A;Reference number: A47675 A;Retus: preliminary A;Reference number: A47675 A;Status: preliminary A;Cross-references: GB:54815; GB:546416; NID:939396; PIDN:CAA38584.1; PID:939397 A;Status: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319) Query Match Best Local Similarity 94.2%; Pred. No. 1.4e-11; Matches 49; Conservative 0; Mismatches 0; Indels 3; Gaps 1; Active conservative 0; Mismatches 0; Indels 3; Gaps 1; Active conservative 0; Mismatches 0; Indels 3; Gaps 1; Active conservation conservation of the protective conservation of the protective conservation of the protective conservation of the protective conservative 0; Mismatches 0; Indels 3; Gaps 1; Active conservation of the protective conservation of the conservation of the protective conservation of the c
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C; Species: Volvox carteri
C;Date: 16-U1-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T1079B
R;Godl, K; Hallman, A; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophori
A;Reference number: Z17154; MUID:97162277; PMID:9009264
A;Accession: T10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rossidues: 1-599 <GOD>
A;Crossreferences: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Crossreferences: EMBL:Y07752; NID:g1655698; PiDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Risample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A; Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins:
A; Reference number: $42440; MUID:86259739; PMID:3460083
A; Accession: $42442
A; Molecule type: mRNA
A; Residues: 1487 <SAM>
A; Residues: 1487 
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R;Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen
A;Reference number: S42447; MUID:85063846; PMID:6209719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear protein EBNA2 - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S42442; S32988; S42447
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A; Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                              Gaps
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Pred. No. 0.034;
1; Mismatches 1
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1; Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 128;
3;
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1 Similarity 51.2%;
21; Conservative 1
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28; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          313 PEPQPP 318
                                                                                                                                                                                                                     36 PAPQPP 41
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Best Local S
Matches 21
   Matches
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                                                                                                                                                                                                                     C; Species: Bordetella pertussis
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Accession: A32560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.6
A; Reference number: A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        딥
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R. Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
Bubmitted to the EMBL Bata Library, August 1991
A; Reference number: S16748
A; Accession: S16748
A; Molecule type: mRNA
A; Residues: 1-449 < ROB>
A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
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A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Cross-references: GB:304560; NID:9144053; PIDN:AAA22980.1; PID:9144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
C; Keywords: membrane protein
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6:9 #status predicted <MAT>
564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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Pred. No. 0.011;
3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                   outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 213.5; DB 2;
Pred. No. 5.4e-08;
0; Mismatches 1;
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Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQP 40
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    Pneumocystis carinii

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83.7%;
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Best Local Similarity 55.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC2301
A; Molecule type: DNA
A; Residues: 1-430 <WAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names:
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hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C; Species: Owenia fusiformis
C; Species: Ovenia fusiformis
C; Date: 07-Jun-1990 #text_change 01-Dec-2000
C; Accession; A.44043; B34043
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A; Title: Presence in invertebrate genomes of sequences characterized by the repetitio
A; Title: Presence number: A90159; MUID:90147742; PMID:2103723
A; Accession; A.4043
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross:references: GB:M32217
                                                                                                                                                      structure of the cellu
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000 C;Accession: A33647
R;Ertl, H; Mengele, T; Wenzl, S; Engel, J.; Sumper, M.
J. Cell Biol. 100, 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of A;Reference number; A33647; MUD: 90094551; PMID: 2689458
A;Accession: A33647
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 CERT>
A;Residues: 1-485 CERT>
C;Keywords: 91ycoprotein
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 0.059;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 141;
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A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: A57R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124; DB 2
Pred. No. 0.039;
1; Mismatches
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R; Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A; Reference number: Z18806
A; Accession: T17547
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.98;
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1)arity 59.0%;
Conservative
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A Residues: 59-136 <BA2>
A Cross-references: GB:M32217
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Best Local Similarity
Matches 23, Conserv
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                              Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; LJ, J.H.; LI, Y.; Liu, X.; Liu, Z.X.; Luros, J.S.; Maiti, E.; Kim, C.C.A.; LJ, J.H.; LI, Y.; Liu, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE005173; NID: 95080823; PIDN: AAD39332.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Sate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C; Accession: 105632
R; Bemis, G; Rohlfing, T.; Morris, M.
R; Berence number: 214682
A; Reference number: 214682
A; Status; Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1684 < DBM>A; Residue
                                                                                                                                                                                                                         hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AKAPPAPK-PAPQPGPQPGPQP----PQPPQPPQRQPEAPAPQPPAGRE 45
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A;Note: WUGSC:H_DJ1186C01.1
                                          Score 124.5; DB 2;
Pred. No. 0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DJ1186C01.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 124.5; DB Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sulfated surface glycoprotein 185 - Volvox carteri
C;Species: Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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51.0%;
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60.5%;
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Best Local Similarity
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A; Residues: 1-929 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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Gaps

4

Length 3164; 8; Indels

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C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: 130085
R;Accession: 130085
A;Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Reference number: A30085
A30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-3164 cMCS>
A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2943 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPG 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQRQPEAPAPQPPAG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.5%; Score 121; DB 1;
65.9%; Pred. No. 0.28;
ive 2; Mismatches 8;
                                                                                    human herpesvirus 1 (strain 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7, 2003, 16:55:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.5
Best Local Similarity 65.9
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 7
Job time: 12.1823 secs
                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                      cysteine-rich extensin-like protein 1 precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence: poly 1994 #sequence: 26-May-1994 #sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Developmental expression of tobacco pistil specific genes encoding novel extens
A:Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T4884
C;Accession: Jagn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923 Ride S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C. Plant Cell 4, 104-1051, 1992 A:Title: Developmental expression of tobacco pistil-specific genes encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: profilminary
A;Molecule type: DNA
A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 39-209 <GOL>
A,Ecsidues: 39-209 <GOL>
A,Experimental source: EMBL:214020; NID:g19918; PID:g19919
C,Superfamily: glutelin
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DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 РРАРКРАРОРСРОРБОРРОРРОРОВЕАРАРОРР 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121.5; DE
Pred. No. 0.03;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 121.5; DB
Pred. No. 0.17;
%; Mismatches
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Best Local Similarity 56.8%;
Matches 21; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-209 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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A;Map position: 2
A;Introns: 281/3
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RESULT 15

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:

May 7, 2003, 16:31:49; Search time 4.75809 Seconds (without alignments) 427.133 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-855-754B-14 278 1 Garappapkpapgpgpgpgp......Qropeapapgppagrelsaa 49

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	003035 bordetella	P24328 bordetella	P14283 bordetella	P40603 brassica na	P12978 epstein-bar	•	P21260 owenia fusi	Q92794 homo sapien	P10220 herpes simp	P40602 arabidopsis	-	_			-	P08001 sus scrofa		-	_	P23093 plasmodium	_		_	_	P51111 rattus norv	_	P06914 plasmodium		008816 rattus norv	Q95107 bos taurus	рошо	8 homo sapi	P93329 medicago tr
SUMMARIES	ID	PERT BORBR	PERT_BORPA	PERT_BORPE	APG_BRANA	EBN2_EBV	SSGP_VOLCA	YPRO_OWEFU	MOZ_HUMAN	TEGU_HSV11	APG_ARATH	G3PT_MOUSE	Y066_NPVOP	EXLP_TOBAC	HXA3_MOUSE	GP1_CHLRE	ACRO_PIG	BRD4_HUMAN	ACRO_RABIT	CSP_PLABE	CSP_PLABA	MOT8_MOUSE	KPC1_TRIRE	SEPA_EMENI	VASP_HUMAN	HD_RAT	CIKF_HUMAN	CSP_PLAYO	Y066_NPVAC	WASL_RAT	WASL_BOVIN	WASL_HUMAN	HD_HUMAN	NO20_MEDTR
	DB	-	-	-	-		Н	-	Н	-		-	-		-	-	-	-	-	-		-	-		н,	-	-	Н	-		-	⊣ .	⊣,	-
	Query Match Length	911	922	910	449	487	485	141	2004	3164	534	440	875	426	443	552	415	1362	431	339	347	265	1139	1790	380	3110	757	367	808	501	505	505	4 (268
đ	Query Match	95.9	94.8	76.8	47.5	45.0	44.6	43.9	43.5	43.5	42.4	42.3	42.1	41.7	41.7	41.7	41.4	40.5	40.1	39.9	•	٠		39.9	39.6	39.6	39.4	38.8	38.8	38.7	38.7	38.7	38.7	38.5
	Score	266.5	263.5	213.5	132	125	124	122	121	121	118	117.5	117	116	116	116	115	112.5	111.5	111	111	111	111	111	110		109.5	108	2	107.5	107.5	107.5	107.5	101
	Result No.	1	7	ო	4	S	9	7	80	6	10	H	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50	30	31	33	33

	Q9umn6 homo sapien P58840 homo sapien					
EXTN_MAIZE MEFD_MOUSE	TRX2_HUMAN ACRL_HUMAN	PRP2_MOUSE PRP3_MOUSE	MB11_ARATH RFX1_HUMAN	FM14_MOUSE FMN1_MOUSE	HD_MOUSE VGLD_PRVRI	•
						
267	2715 232	261 296	642 979	1206 1468	3119	
8 8 8 8	88.3	6. 6. 6. 6.	38.1	38.1	38.1 37.9	
106.5	106.5 106	106 106	106	106	105.5	
34 35	36	38	41	42	44	

ALIGNMENTS

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DOMAIN
REPEAT
                                       REPEAT
REPEAT
                                REPEAT
                                                       DOMAIN
                                                                                                                                                              PERT_BORPE
                                                                                                Matches
                                                                                         Best
                                                                                                                                                      RESULT
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                                                                                                                                                                               SEEEEEEES
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBLO utstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                               ;
                                                                                                                                                                                                                                                                          Gaps
CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ATTACHMENT SITE (INVOLVED IN
                                                                               3;
                                                                                             DB 1; Length 911;
                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                               Indels
                              3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                               Score 266.5; DB 1;
Pred. No. 1.6e-10;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERTACTIN (P.70). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, S14659; S14659.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR00392; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                              STRAIN-CN2591;
MEDLINE-91251771; PubMed-2041476;
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNEAMLY
                                                93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03212; Pertactin; 1.
                                                              Query Match 95.9%;
Best Local Similarity 94.2%;
Matches 49; Conservative (
                                                                                                                                                                                                              Bordetella parapertussis
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647
922
262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S15204; S15204.
PIR; S14659; S14659.
                                                911 AA;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane;
                                                                                                                                                                                                                                      NCBI_TaxID=519;
                                                                                                                                                      PERT_BORPA
P24328:
                                                SEQUENCE
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                                                                                                                                                PERT_BORPA
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"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novchny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterizathon of protective outer membrane protein P.69 from Bordetella pertusais.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                   X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPQPQPAPPAPGPPAGRELSAA 49
                              LINES).
1 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1 J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                   ٠<u>.</u>
                                                                                                                                                                                                                                                                                      DB 1; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                                                                                                                       Score 263.5; DB 1;
Pred. No. 2.4e-10;
                                                                                                                                                               4 (APPROXIMATE)
9 X 3 AA APPROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 264 AND 332.
MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J04560; AAA22980.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96196517; PubMed-8609998
                                                                                                                                                                                                                                     Ψ.
                                                                                                                                                                                                                                                                                            94.88;
                                                                                                                                                                                                                                  95178
                                                                                                                                                                                                                                                                                                                                                      49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                       290
275
275
280
285
603
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                                                                                                                                                                                                                                  922 AA;
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID-3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
--- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
--- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDILINE-94004980; MEDILINE-94004980; PubMed-8401599; Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; "Gametophytic and sporophytic expression of an anther-specific
                                                                                                                                                                      X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                   CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                            (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                        76.8%; Score 213.5; DB 1; Length 910;
83.7%; Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                               PERTACTIN (P.69)
                                                                                                                                                                                                                  (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                     449 AA.
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                            Signal; Virulence; Repeat
                                                                                                                          POTENTIAL
          InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_v1r.
                                                                                                                                                             LINES)
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
                                        Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                   93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape).
PIR; A32560; A32560.
                                                                                                                                                                                                    276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                               Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATURATION.
                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR CEX.
                                                                                                                                                                                                                                                                                                                                                                                                   APG_BRANA
P40603;
                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
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                                                                                        SIGNAL
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MEDLINES-8427(667; PubMed-6087149;

MEDLINES-8427(667; PubMed-6087149;

Back R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,

Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,

Tuffnell P.S., Barrell B.G.,

"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";

Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen J.I., Wang F., Kieff E.,
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SÜBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90266473; PubMed-2161150;
Pettl L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins";
Virology 176;563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; V01555; CAA24877.1; ALT_INIT.
TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
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                                                                                                                                                                                              47.5%; Score 132; DB 1; Length 449; 55.3%; Pred. No. 0.02; tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X 2 AA TANDEM REPEATS OF
DEF40D7F8ED61D1A CRC64;
                                                                                                                    POTENTIAL.
9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                               3 KAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                         BY SIMILARITY.
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91202599; PubMed-1850028;
                                                                                   132 132 B
428 428 P
449 AA; 48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52544 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1- PÎM: PHOSPHORYLATED.
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA;
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                                                                                                                                                                                                       Local Sim-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF LMP-1
                                                        NON_TER
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBN2_EBV
P12978;
                                                                                                                                                                                                 Query Match
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DB 1; Length 487;

45.0%; Score 125;

Query Match

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Gaps

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SSGP_VOLCA

RESULT 6

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-!- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
                                                                                                                                 MEDLINE-90147742; PubMed-2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; B34043; B34043.
PIP; B34043; B34043.
PIP DIAPPOTHETING TO THE TRIPLET OF THE TRIPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Nuclear.
-i- DISEABE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL
TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE MYELOID LEDEMENIA.
-i- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
-i- SIMILARITY: BELONGS TO THE MYST (SAS/MO2) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%; Score 122; DB 1; Length 14 llarity 52.5%; Pred. No. 0.035; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM, 601408; -.
InterPro, IPR001386; Histone_H1/H5.
InterPro, IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-96376968; PubMed-8782817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:13013; ZNF220.
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Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma.
Local Sim.
21;
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Q92794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                         RRY RRY REPRING THE REPRING TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. SUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC DERECURES OR THIS SUBSTRUCTURE (C3Z STRUCTURE). THE COVALENT CROSS-LIKKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
I. PIM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNATION OF A PARTICULAR OF THE PROPERTY OF A PARTICULAR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
NCBI_TaxID=6347;
                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 0.065;
1; Mismatches 16; Indels
Pred, No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 POLY-PRO.
50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                              PPAPKPAPQPGPGPGPPQPPQPPQRGPEAPAPQPPAGRE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT: 485 AA. P2197; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01-307; 01
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothatical proline-rich protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
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                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfation; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.
                                       51.2%;
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ilarity 54.1%;
Conservative
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                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Volvocaceae; Volvox.
NCBL_TaxID=3067;
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                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A33647; A33647
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Best Local Similarity
Matches 20; Conserv
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                                       Best Local
Matches 2
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DOMAIN

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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-88374327; Pubmed-2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
McGab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BREAKPOINT FOR TRANSLOCATION TO FORM
                        translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                   Score 121; DB 1; Length 2004;
Pred. No. 0.28;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                             9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                   1659 PQPPPPQPQPAPQPPPPQQQPQQPQPQPQPQPPPPP 1695
                                                                                                                                                                                                                                                                                                                                    5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
10-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                           3164 AA
                                                                                                                                                                                                              GLN/PRO-RICH
                                                 PHD-TYPE 1.
PHD-TYPE 2.
                                                                                      C2HC-TYPE
                                                                                                                      POLY-ARG
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
POLY-GLU.
                                                                          POLY - SER
                                                                                                   POLY-GLU
                                                                                                              POLY-GLU
                                                                                                                                                                                                                                                 MOZ-CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; 130085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
9; ZF_PHD_1; 1
6; ZF_PHD_2; 2
Chromosomal t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                    43.5%;
56.8%;
                                                                                                                                                                                                                                                             2004 AA; 225054
                                                                                                                                                                                                                                                                                   Query Match 43.5
Best Local Similarity 56.8
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                          302
                                                                                                                                                                                               597
PS01359;
PS50016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10299;
          PROSITE; PS50016
Proto-oncogene;
                                                                                                                                                                                               1593
1643
1897
1546
                                   Nuclear protein
ZN_FING 206
ZN_FING 259
                                                                                                                                                                                                                                                                                                                                                                                                           TEGU_HSV11
ID TEGU_HSV11
AC P10220;
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01-MAR-1989
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SEQUENCE
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RX MEDINE-21016719; PubMed-11130712;

RX Theologias A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologias A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RM White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Corway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Corway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter, J.L., Johnkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Leiz C.B., Li J.H., Li Y.-P.,

RA Hiltscher J., Miranda M., Nguyen M., Ngorone B.I.,

RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vasperg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                ACCARATH STANDARD; PRT; 534 AA.
B40602; 093114; 09LNTB;
B40602; 093114; 09LNTB;
B40602; 093114; 09LNTB;
B5-JUN-2002 (Rel. 41, Last sequence update)
B5-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudioctyledons; core eudicots; Rosidae; eurosigis II; All assicales; Brassicaceae; Arabidopsis.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the STRIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP coinsortium (Salk/Stenford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!-TISSUE SPRCIFCITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-!-DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar Draper J., Scott R.;
Gametophytic and sporophytic expression of an anther-specific Arabidopsis thallana gene.";
Plant J. 3:111-120(1993).
                                                                4.
                  DB 1; Length 3164;
                                                            Indels
                                                                                                                            2943 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQNG 2982
                                                                                                   6 PAPKPAPQEGPQPGPQP-PQP-PQP-PQRQPEAPAPQPPAG 43
                                                            8;
Score 121; DB 1
                                                            2; Mismatches
                43.5%;
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                                  Best Local Similarity 65.9
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:816-820(2000).
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                  Query Match
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                         POTENTIAL.
ANTER SPECIFIC PROLINE-RICH PROTEIN APG.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ICR Swiss; TISSUB-Testis;
MEDLINE-95254745; PubMed=7736666;
Melch J.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-meiotic spermatogenic
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
SPERMIGGENESIS AND IN THE SPERMATOZOON.
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
NAD(+) = 3-phospho-D-glyceroy1 phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: HOMOTETRAMEN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYLOPISAMIC (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYLOPISAMIC (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CD-1, TISSUE=Testis;
MEDLINE=9227372; PubMed=1375514;
Welch J.E., Schatte E.C., O'Enten D.A., Eddy E.M.;
Expression of a glyceraldehyde 3-phosphate dehydrogenase gene specific to mouse spermatogenic cells.";
                                                                                                                                                                                                                                                                                                              DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 G3PP_MOUSE STANDARD; PRT; 440 AA.
064467; Q60550;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-Gaperandehyde 3-phosphate dehydrogenase, testis-specific (EC 1.2.1.12) (GAPDH).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                             0.16;
ohes 11; Indels
                                                                                                                                                                                                                                                                                                                                                          3 KAPPAPKPAPQPGPQPGPQPPQ-----PPQPPQRQPE-APAPQP-PA 42
                                                                                                                                                                                                                                              S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                          Pred. No. 0.16
4; Mismatches
                                                                                                                                                                                                                                                                                                            Score 118;
                                                                            EMBL; X60377; CAA42925.1; -
EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AX058847; AAL24235.1; -
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                 58007 MW;
                                                                                                                                                                                                                                                                                                            42.4%;
52.1%;
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                                                                                                                                                                                                                                                                                                                   Local Similarior
hes 25; Conservative
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325
334 AA;
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ACT_SITE
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          083949; 065364; 010323; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 98.6 kDa protein (ORF71). Orgyla pseudotsugata multicapsid polyhedrosis virus (OPMNPV). Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO.
GLYCERALDEHYDE 3-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97271300; PubMed-9126251;
Ahrens C.B., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;
                                  SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PPAPK-----EAPAPQPGPQPPQPPQPPQRPQP----EAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DI STAILMANTII).
MISSING (IN REF. 2).
L -> V (IN REF. 2).
05FF0A093D1ABD9C CRC64;
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1; Mismatches
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GERM CELLS. LEVELS INCREASE UNTIL DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%; Score 117.5;
46.2%; Pred. No. 0.1!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                               HSSP, P56649; IDSS.
MGD; MGI:95653; Gapds.
InterPro: IPRO00173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh, C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=96201426; Pubmed=8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 806-875 FROM N.A. MEDLINE-95343549; PubMed=7618274;
                                                                                                                                                                                                                                                                                                                                                                                                Glycolysis; Oxidoreductase; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 AA; 47657 MW;
                                                                                                                                                                                                                                   EMBL; M60978; AAA53033.1; -.
                                                                                                                                                                                                                                                      EMBL; U09964; AAA80276.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  73
100
256
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NCBI_TaxID=164623;
                    DURING MATURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
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CONFLICT
SEQUENCE
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Best Local Simil
Matches 24; (
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CARBOHYD
SEQUENCE
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REPEAT
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                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; eusaterida I; Solanales; Solanaceae; Nicotiana.
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, gene essential for Orgyia pseudotsugata baculovirus DNA replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 117; DB 1; Length 875;
Pred. No. 0.27;
3; Mismatches 13; Indels
                                                                                                                                  VITOLOGY 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPY AND LDMNPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpris; IPR000419; Pollen_Ole_e_I.
Pfam: PF01190; Pollen_Ole_e_I; I.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 PQQPPQQPPQQPPQQPPQQPPQPPQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 РРАРКРАРОРСРОРСРОРРОРРОРОВОРОВАРАРОР 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 075930; AAC59070.1; -. ERMBL; 039145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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Q03211;
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"The homeo domain of a murine protein binds 5' to its own homeo box."; Proc. Natl. Acad. Sci. U.S.A. 83:9532-9536(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryogenesis.";
Dev. Biol. 124:125-133(1987).
-!- FUNCTION; SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
                                                                                                                                                                                             Gaps
        PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 185-258 FROM N.A.
MEDLINE-85024859; PubMed-6091896;
McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.;
Molecular cloning and chromosome mapping of a mouse DNA sequence homologous to homeotic genes of Drosophila.";
cell 38:675-680(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
51A495CC94017812 CRC64;
                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ICR Swiss;
MEDLINE-96323206; Pubwed-8710855;
Tan D.; Shao X., Pu L., Guo V., Nirenberg M.;
"Sequence and expression of the murine Hoxd-3 homeobox gene.";
Proc. Natl. Acad. Sci. U.S.A. 93:8247-8252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fainsod A., Bogarad L.D., Ruusala T., Lubin M., Crothers D.M., Ruddle F.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruddle F.H., Hart C.P., McGinnis W.;
"Structural and functional aspects of the mammalian homeo-box
sequences.";
                                                                                                                                                                                                                                                       165 AKQPPQPPPAKQPSPPPPPPPVKAPSPSPAKQPPPPPVKAPSPSPATQPP 216
                                                                                                                                                                                                                          41
                                                                                                                                                        DB 1; Length 426;
                                                                                                                                                                                                                        2 AKAPPAPKPAPQPGPQPGPQP-----PQPPQPPQRQPE-APAPQPP
                                                                                                                                                                                         14; Indels
                        X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88030407; PubMed-2444477;
Fainsod A., Awgulewitsch A., Ruddle F.H.;
"Expression of the murine homeo box gene Hox 1.5 during
                                                                                                                                                                                                                                                                                                                                    HXA3_MOUSE STANDARD; PRT; 443 AA. P02831; 061197; 1.75-17UL;1986 (Rel. 01, Created) 01-NOV'1997 (Rel. 35, Last sequence update). 15-JUN-2002 (Rel. 41, Last annotation update) HOXA3 OR HOXA-3 (HOX-1.5) (MO-10).
                                                                                                                                                       Score 116; DB :
Pred. No. 0.19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87092283; PubMed-2879282;
                                                                                                                        44278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 185-258 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rends Genet. 1:48-51(1985).
                                                                                                                                                       41.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 54-280 FROM N.A.
                                                                                                                                                                        46.28;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/c;
Hofmann M., Boehm T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
DEVELOPMENTAL STAGE
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
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4 APPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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Local S...
20;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                    plant
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  ï
                                          SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: EXPRESSED IN A SPATIALLY RESTRICTED MANNER EMBRYOS 8.5 DAYS P.C., EXPRESSION IS LIMITED TO THE CNS WITH AN ANTERIOR BOUNDARY IN THE HINDBRAIN AND EXTENDING POSTERIORLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
    SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS BINDS 5' TO ITS OWN HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                  THROUGH CAUDAL REGIONS OF THE SPINAL CORD. THE SAME SPATIAL EXPRESSION IS SEEN IN EMBRYOS 9.5 TO 12.5 DAYS P.C. SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21159092; Pubmed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S -> G (IN REF. 3 AND 4).
A -> G (IN REF. 3 AND 4).
SA -> PG (IN REF. 3 AND 4).
C -> M (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND 4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTP-TYPE HEXAPEPTIDE. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.7%; Score 116; DB 1
54.3%; Pred. No. 0.19;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:96175; Hoxa3.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00025; ANTENNAPEDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y11717; CAA72404:1; -.
EMBL; U56399; AAC52778:1; -.
EMBL; K02591; AAA37822:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A03315; A03315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 AA;
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185
195
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Q9FPQ6; Q03927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ranscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSFAC;
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DNA_BIND
CONFLICT
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Matches 2
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GP1_CHLRE
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'Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins.";
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGETATIVE CELL WALL PROTEIN GP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINKED (GLCNAC. .) (POSA584890465502F5 CRC64;
                                                                                                                                                                                                                                                                   -!- SUBUNIT: Associates with GP2 and GP3.
-!- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 116; DB Fred. No. 0.22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M58496; AAA69706.1; ALT_SEQ. GlycoSulteDB; Q9FPQ6; -InterPro; IPR002965; P_Itch_extensn. InterPro; IPR003882; Pistil_extensin. PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54219 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF309494; AAG45420.1;
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Search completed: May 7, 2003, 16:48:06 Job time : 6,75809 secs

09k5q4 bordetella 09k5q4 bordetella 09alq0 bordetella 09alx6 bordetella 09alx8 bordetella 09sim9 bordetella 09sim9 bordetella 09sim0 bordetella 09sim1 bordetella 09sim1 bordetella 08sim1 bordetella 08sim2 bordetella 09sim3 bordetella 09sim3 bordetella 09sim4 pneumocysti 09tv4 pneumocysti 09sim1 volvox cart 09fv1 pneumocysti 09sim1 volvox cart 09fv1 pneumocysti 09sim1 volvox cart

088143 Q93L98 069257 Q8RSU0

09K5G1 09ALQ0 09ALP5 09AIX8 09SEM9

0959M8 0956N0 0956N1

069259

Q9UVD1 Q96V14 Q8W158 Q93L97 Q9P944

Q96VJ1 Q9JLE9 P93797 Q9SBM1 Q01823

09ull5 homo sapien 08sz47 drosophila 09vzc2 drosophila

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Thu May
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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL, AJ250077, CAB76431.1; -...
Interpro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=9.73H+;
MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella.
NCBI_TaxID=518;
                                                    228.5
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SEQUENCE
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Q9K5H9
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 49
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09ahp0
09k5h5
09alp9
09l4e2
09k5h1
09a5q4
09k5y9
    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                               671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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sp_virus:*
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ALIGNMENTS

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Gaps

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Length 104;

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Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
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                                                                                                                                                                                     Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL, AF298590; AAK166911.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002865; P.rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AR156772; AR782396.1; -. InterPro; IR904899; Pertact_sup. Pfam; PF03212; Pertactin; 1. NON_TER 1 115 115 SEQUENCE 115 AA; 11705 MW; EIABD4D347D20652 CRC64;
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                                                                              09KJY0;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CT-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                           115 AA.
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MEDLINE=21117018; PubMed~11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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                                                           PRELIMINARY;
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198 AA;
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ses 49; Conserv
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SEQUENCE
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O9AHP0:
                                                        Q9KJY0
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                             Q9KJY0
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                                                                                                                                                                                                                                                                                                                                                                               Moursaux Eude C., Guiso N.;

Boursaux Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

Portusais, Bordetella parapertussis, and Bordetella bronchiseptica.";

Infect. Immun. 68.4815.4817(2000).

EMBL; AJ250079; CAB76433.11;

InterPro; IPR004899; Pertact.sup.

Pfam; PF03212; Pertactin; 1.

NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 278; DB 2; Length 105; llarity 100.0%; Pred. No. 2.8e-17; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
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                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  105 AA
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InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
  PRT;
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100.0%;
                                                                                                                               Pertactin (P.68) (Fragment)
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Matches 49; Conservative
  PRELIMINARY;
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les 49; Conserv
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                                                                                                                                                                                                                                     Bordetella.
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Q9K5H5 Q9K5H5;

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RESULT 6

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09K5H5

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STRAIN-CVGEO;
MEDLINE-20359389; PubMed=10899896;
MEDLINE-20359389; C., Gulso N., Gulso
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EMBL, AJ24527; CAB82215.; -
InterPro: IPR003992; pertactin.
InterPro: IPR003992; pertactin.
InterPro: IPR004899; Pertactin_vir.
PF03212; Pertactin; 1.
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Mooi F.R.;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Prcteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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PRINTS; PRO1484; PRIACTNFAMLY.
PRINTS; PRO1484; PRIACTNFAMLY.
PRINTS; PRO1484; PRIACTNFAMLY.
      200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                             Score 266.5; DB 2;
Pred. No. 4.5e-16;
0; Mismatches 0;
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Pred. No. 1.6e-15;
0; Mismatches 0;
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                                                          Query Match
Best Local Similarity 94.2%;
Matches 49; Conservative
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Best Local Similarity 94.2%;
Matches 49; Conservative
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         SEQUENCE
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Q9L4E2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1;
InterPro; IPR004899; Pertact_sup.
InterPro: IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
127 GAKAPPAPKPAPAPGPGPGPGPGPPQPPQPPQPPGRAPAPQPPAGRELSAA 175
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107 AA; 11036 MW; 1AC13209D0238107 CRC64;
                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 266.5; DB 2;
Pred. No. 2.7e-16;
0; Mismatches 0;
                                                                                                                                                                           107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Infect. Immun. 69:1917-1921(2001).
EMBL: AY007211, AAG3447.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003995; Pertactin.
InterPro; IPR002965; P. rich_extensn.
Pfam: Pf03212; Pertactin; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20359389; PubMed=10899896;
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PRINTS; PRO1217; PRICHEXTENSN.
NON TER 1
NON_TER 200 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=518;
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NON_TER
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pertussis, Bordetella parapertussis, and Bordetella pertussis, Infect. Immun. 68:4815-4817(2000).

EMBL. AJ550087, CABF6441.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_interpro.
PRINTS; PR02121; Pertactli; 1.
PRINTS; PR03121; PRICHEXTENSN.
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"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPGPPQPPQPPQPPQRPPGRPAPAPAPAPGRELSAA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 264.5; DB 2; Length 111;
Pred. No. 4.1e-16;
0; Mismatches 0; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 122;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).

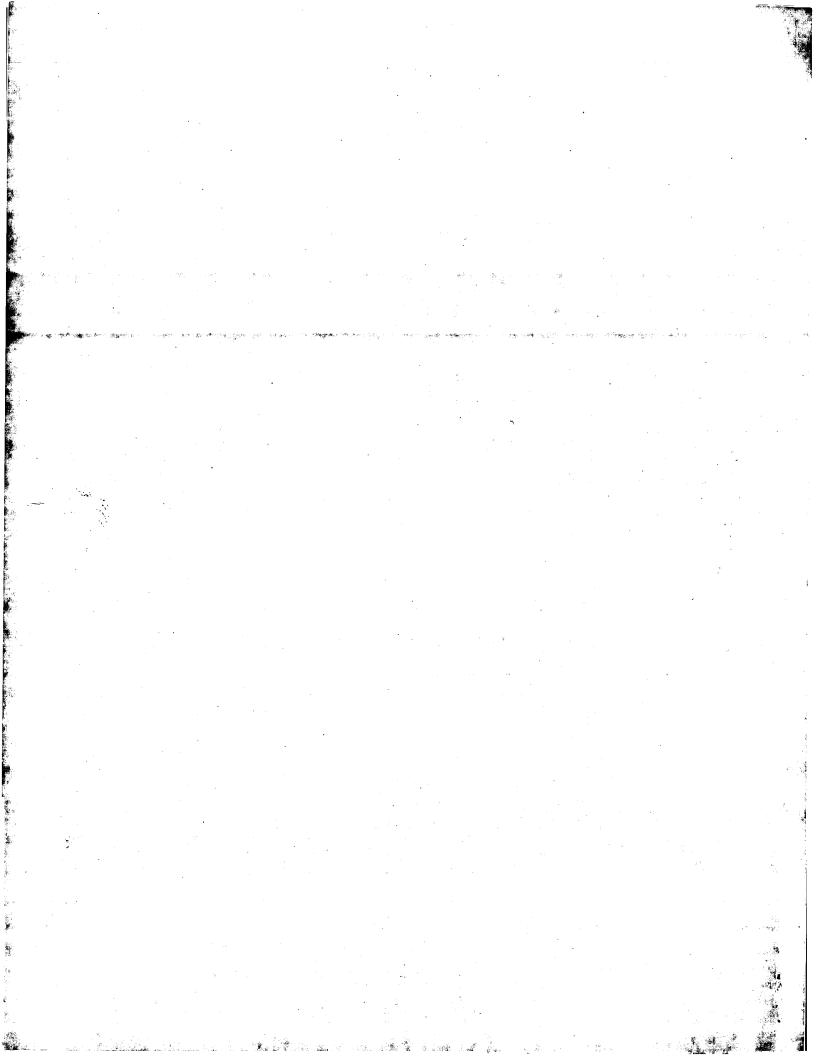
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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122 AA; 12395 MW; BED00966A40FF994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                11416 MW; 5140669692808F8E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 4.4e-16;
0; Mismatches 0;
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InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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87.58;
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Best Local Similarity 87.5%;
Matches 49; Conservative
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Best Local Similarity 87.5:
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NON_TER 111 1
SEQUENCE 111 AA;
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Q9KJX9
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                                                                                                                                                                                                                                                                                                                                                                22 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPPQPPQPPAPAPPQPPAGRELSAA 74
                                                                                                                                                                                        ch 95.7%; Score 266; DB 2; Length 109; I Similarity 92.5%; Pred. No. 3e-16; 49; Conservative 0; Mismatches 0; Indels
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                              109 109
109 AA; 11192 MW; 85EBEF7483665DD3 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Infect. Immun. 69:1917-1921(2001).
EMBL, AY007263; AAG38439.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03312; Pertactin; 1.
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MEDLINE-21117018; PubMed-11179374;
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Boursaux-Eude C., Guiso N.;
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PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 1 215
SEQUENCE 215 AA; 22327 AW;
                              Pertactin (P.68) (Fragment).
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Best Local Similarity
Matches 49; Conserv
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPGPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.8%; Score 263.5; DB 2; Length 111; Best Local Similarity 84.5%; Pred. No. 5e-16; Matches 49; Conservative 0; Mismatches 0; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 95.1%; Score 264.5; DB 2; Length 252; Local Similarity 87.5%; Pred. No. 8.1e-16; les 49; Conservative 0; Mismatches 0; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                             "Novel Genetic and Phenotypic Heterogeneity in Bordetella Bornofilsaphica Partaciln.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AX007265; AAG38441.1;
InterPro; IPR003995; pertacitn.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                252 252
252 AA; 26107 MW; 368C142508D77057 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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01-00T-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
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InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                     STRAIN=ATCC19395;
MEDLINE=21117018; PubMed=11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DEL;
MEDLINE-20359389; Pubmed-10899896;
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                            Pfam; PF03212; Pertactin; 1.
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Q9K5H3;
01-OCT-2000 (TEMBLEEL 15,
01-OCT-2000 (TEMBLEEL 15,
01-JUN-2002 (TEMBLEEL 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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09K5H3
1D 09K5H:
AC 09K5H:
DT 01-OC:
DT 01-OC:
DT 01-OC:
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RRY RRY RAY READER READER READER READER DEADER DEADER DEADER DEADER DEADER DEADER READER READ
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Tr. "Polymorphism|of Repeated Regions of Pertactin in Bordetella
Tr. "Polymorphism|of Repeated Regions of Pertactin in Bordetella
Tr. "Polymorphism|of Repeated Regions of Pertactin in Bordetella
Tr. Infect. Immun, 68:4815-4817(2000).
DR EMBL; AJ250083; CABF6431.1; -
DR Interpro; IPR004899; Pertact_sup.
DR Interpro; IPR004899; Pertact_sup.
DR PRINTS; PR01212; Pertactin; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
FT NON_TER 115 115
TON_TER 115 115
TON_TER 115 AA: 117.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115;
                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.7%; Pred. No. 6.2e-16;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 7, 2003, 16:53:12
Job time: 27.0426 secs
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPG-
                                                                                                                                                                                     SEQUENCE FROM : N.A.
                                                                                                                             NCBI_TaxID=518;
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GenCore version 5.1.4_p5_4578
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7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec Мау Run on:

1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA 52 US-09-855-754B-15 297 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 908470 segs, 133250620 residues Searched:

908470

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002:* Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp·embl/AA1992.DAT:* /SIDS2/gcgdata/geneseq/geneseqp·embl/AA1993.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqg-embl/AA1987.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1997.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

									·	
Description	B. bronchiseptica	Pertactin antiqen	prn proteins. Bor	Bordetella bronchi	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Pertactin antiqen	Bordetella paraper	Bordetella paraper
ŒΙ	AAE16194	AAR14320	AAR26503	AAE16183	AAE16196	AAE16197	AAE16198	AAR14321	AAR25578	AAE16185
DB	23	12	13	23	23	23	23	12	13	23
% Query Match Length DB ID	52	911	911	911	53	26	28	922	922	922
% Query Match	100.0	100.0	100.0	100.0	96.5	0.96	92.6	92.6	92.6	92.6
Score	297	297	297	297	286.5	285	284	284	284	284
Result No.	п	7	ю	4	5	9	7	80	6	10

B. bronchiseptica	Bordetella pertuss	Bordetella pertuss	B. bronchiseptica	Peptide 683 derive	Peptide BBO5 deriv	_			Human polypeptide	Human polypeptide		Novel human diagno	Drosophila melanog	Human polypeptide	Human polypeptide	Sugar beet chitina	Novel human diagno	Ser-Pro-Pro ge	Human polypeptide	Arabidopsis thalla	Synthetic Bordetel	Ser-Pro-Pro-Pro	Bloadhesive precur	Herbicidally activ	Human low density	Novel human diagno	dopsis							
3 AAE16195	m	_	m	m	3 AAE1618		m		.2 AAR11739	_	n	-		~	~	22 ABG27250									7 AAR8764	m	9 AAP82971	3 ABB9383	2 AAB82806	12 ABG04360	11 AAG36453	11 AAG36452	1 AAG36451	
09	48	~		~	0		5	31				1239	80	•		406	•	44	88	439	325	76	82	470			334				1222	1257	1275	
95.3	87.5	87.2	86.9	7.1.4	7.1.4	7.1.4	64.5	52.2	51.9	48.0	43.0	48.0	45.5	45.5	45.1		4.1.8		43.8	43.8	43.4	43.3	43.3	42.9	42.8	42.3	42.1	42.1	4.1.4				41.2	
283 266.5	260	259	258	212	212	212	191.5	155	154		•	142.5	135	135	134	134	133	131	130	130	129	128.5		127.5	127	125.5	125	125	123	122.5	122.5	122.5	122.5	
11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

AAE16194 standard; peptide; 52 AA. 26-MAR-2002 (first entry) AAE16194; RESULT 1

B. bronchiseptica strain II-2 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

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Bordetella pertactin antigens for whooping cough vaccines
                                      microorganism transformants - for production of
                                                                     Disclosure; Fig. 1B; 38pp; English.
     WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1991;
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                                                                                                                                                                    Sequence
                                     Pichia
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                     Courter membrane protein or their fragments. Pertactin (purer membrane protein) or their fragments. Pertactin (PRN) is used as and used to detect antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity cromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                   52;
                   present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                          ch 100.0%; Score 297; DB 23; 1 Similarity 100.0%; Pred. No. 2.8e-16; 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                              AAR14320 standard; Protein; 911 AA.
Claim 26; Fig 1c; 47pp; English.
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/label- repeat
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica.
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/label= re
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'label= re
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/label- re
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/label- re
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label= re
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/label- r
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                                                                                                                                                                                                                                                                                                                                                                              Pertactin antigen P.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clare JJ, Romanos MA;
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                        52 AA;
                                                                                                                                                                                                                                                                                                                                                         20-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1991;
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                                                                                                                                                                        Sequence
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                                                                                                                                                                                             Query Match
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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                         610
                                                                                                                                               Length 911;
                                                                                                                                                                                                    100.0%; Score 297; DB 12;
100.0%; Pred. No. 2.3e-15;
1ve 0; Mismatches 0;
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/label= RGD_tripeptide
701..703
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/label- RGD_tripeptide
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/label= Repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 28pp; English.
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/label- P.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91GB-0006568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetalla bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WELL ) WELLCOME FOUND LID
                                                                                                                            Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                             911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         prn proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; Bordetella infection;
The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQRPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 297; DB 13; Best Local Similarity 100.0%; Pred. No. 2.3e-15; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254..299
/note- "Pertactin region I"
559..610
/note- "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; v
therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16183 standard; Protein; 911 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INSP ) INST PASTEUR.
                                                                                                                                                                                              entire P.94 sequence
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N-PSDB; AAD26440.
                                                                                                                                                                                                                                                              911 AA;
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                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16183;
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques to in infinity chromatographic columns. Pertactin is useful as antiques an infinity chromatographic columns. Pertactin is useful as antiques and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                          B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                           Pertactin; P_{RN}; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
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Pred. No. 1.8e-15;
                                                                              100.0%; Score 297; DB 23;
100.0%; Pred. No. 2.3e-15;
.ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                           AAE16196 standard; peptide; 53
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2001; 2001WO-EP06457
                                                                           Query Match
Best Local Similarity 100.0
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 52; Conserv
                                                 911 AA;
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                                                 Sequence
                                                                                                                                                                                                                                                                                           AAE16196;
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for

RESULT 6 **AAE1619**7

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                         25-MAY-2000; 2000US-206969P
                  Bordetella bronchiseptica.
                                                                                                                                                                                                                (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                         WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 AA;
                                                        WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1992
                                                                                               29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fulids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                             B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
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                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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Pred. No. 2.4e-15;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guiso-maclouf N, Boursaux-eude C;
                                            AAE16197 standard; peptide; 56 AA.
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000; 2000US-206969P.
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                          Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-097639/13.
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                                                                                                                                                                                                      Pertactin; PRN;
                                                                                                                                                                                                                                                                                               WO200190143-A2.
                                                                                                                         26-MAR-2002
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                                                                                    AAE16197;
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Matches
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                            The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as veccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                   Length 58;
                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                              Score 284; DB 23
Pred. No. 3e-15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14321 standard; Protein; 922 AA.
Claim 26; Fig 1c; 47pp; English.
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/label- repeat
575..577
/label- repeat
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                                                                                                                                                                                                                                                                                                                            95.68;
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.7
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin antigen P.70.
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RESULT 7 **AAE16198**

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recombinant cosmids prepared by partial digestion of B.parapertusis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb claif fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (*P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 6kbD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids pro577 to Profil or Ala574 to Profil2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A cosmid library was constructed by transforming E.coli HB101 with
                                               /note="contains 5 direct, tandem repeats" 575..612
575..612
/note="contains 9 direct repeats of Pro-Gln-Pro" 712..714
/note= "motif associated with cell-cell adhesion"
260..262
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                    Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella parapertussis pertactin outer membrane protein, p.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 922;
             /note= "motil www. 266..285

^note= "contains 5 direct, tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 284; DB 13;
Pred. No. 2.2e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
254..304
/note= "Pertactin region I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE16185 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.6%;
                                                                                                                                                                                                             91WO-GB02302
                                                                                                                                                                                                                                                                          (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.6
Best Local Similarity 89.7
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parapertussis
                                                                                                                                                                                                                                                                                                                                       WPI; 1992-250033/30.
N-PSDB; AAQ26509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 AA;
   Binding-site
                                                                                                Binding-site
                                                                                                                                                                                                             23-DEC+1991;
                                                                                                                                                                                                                                            21-DEC-1990;
                                                                                                                                             W09211292-A.
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                                                                                                                                                                             09-JUL-1992
                                                                                                                                                                                                                                                                                                        Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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Region
                                                                Region
                                   Region
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                                   Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.59 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPQP-----PQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 284; DB 12; Length 9 Pred. No. 2.2e-14; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
35..643
/label- P70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR25578 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1C; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   WELL ) WELLCOME FOUNDATION LTD
                  repeat
                                               'label- repeat
                                                                                repeat
                                                                                                               repeat
                                                                                                                                           'label- repeat
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89.7%;
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                                                                                                                                                    7...597
/label-
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                                                           ວၓ6..588
/label- re
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                                                                                                                           ..594
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                              583..585
                                                                                            589..591
                                                                                                          label-
                                                                                                                                                                                                        label-
                                                                                                                                                                                                                                                                                                                                                                                                                                     Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ14320
                                                                                                                                                                                                                                                                                                                                     28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                     02-APR-1990;
                                                                                                                                                                                                                                                                     409115571-A.
                                                                                                                                                                                                                                                                                                     17-OCT-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Clare JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Protein
Pept1de
                                Peptide
                                                              Peptide
                                                                                            Peptide
                                                                                                                            Pept1de
                                                                                                                                                           Peptide
                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                         Pept1de
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Boursaux-eude C;

Guiso-maclouf N,

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
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                                                                                                                                                                                                                                                                           Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 284; DB 23;
Pred. No. 2.2e-14;
); Mismatches 0;
564..621
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
                                                                                                          23-MAY-2001; 2001WO-EP06457
                                                                                                                                     25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                              WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922 AA;
                                             WO200190143-A2
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                                                                          29-NOV-2001
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AAE16195
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B, bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordeteila infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 95.3%; Score 283; DB 23;
Best Local Similarity 86.7%; Pred. No. 3.6e-15;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16193 standard; peptide; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000; 2000US-206969P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AA;
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Gaps

4

Length 48;

Score 260; DB 23; Pred. No. 1.7e-13;); Mismatches 0;

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Conservative

Query Match Best Local Similarity Matches 48; Conserv

87.5%; 92.3%;

AAE16200 standard; peptide; 52

AAE16200

26-MAR-2002 (first entry)

AAE16200;

1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA

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us-09-855-754b-15.rag

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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. bronchiseptica strain II-7 pertactin outer membrane protein region ii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRPQRPAPAPAPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 266.5; DB 23; Length
Pred. No. 5.6e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE16199 standard; peptide; 48 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3ordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 94.2
49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200190143-A2
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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B. bronchiseptica strain II-8 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica.

40200190143-A2. 29-NOV-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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Pred. No. 2.2e-13;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                           Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16201 standard; peptide; 54
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                                                                                                                                                                                                                                              23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-097639/13.
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Best Local Similarity
Matches 49; Conserv
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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the sordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

48 AA;

Sequence

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

The present invention relates to Bordetella bronchiseptica pertactin

claim 26; Fig 1c; 47pp; English.

AAE16201;

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                        B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                        25-MAY-2000; 2000US-206969P
                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                     Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-097639/13.
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Search completed: May 7, 2003, 16:47:05 Job time: 28.0187 secs

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ä

4; Gaps

Query Match 86.9%; Score 258; DB 23; Length 54; Best Local Similarity 89.1%; Pred. No. 2.7e-13; Matches 49; Conservative 0; Mismatches 2; Indels

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Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 11, Appli
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(cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/laa/6B_COMB.pep:*
(cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-460-269C-6
US-08-460-269C-2
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US-08-750-624-11
US-08-750-624-11
US-08-760-28-16
US-08-460-269C-8
US-09-041-886-29
US-09-041-886-29
US-09-041-886-31
US-08-451-886-31
US-08-451-886-31
US-08-451-886-31
US-08-451-886-31
US-08-451-886-31
US-08-451-886-15
US-08-451-886-15
US-08-451-273B-42
US-08-451-28-134
US-08-451-28-134
US-08-451-28-32
US-08-451-253-32
US-08-451-253-32
US-08-451-253-32
US-08-451-253-32
US-08-451-253-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                US-09-855-754B-15
297
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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65, Appl 66, Appl 4, Appl 621, Appl 1149, Appl 53525, App 525, App 525, Appl 525, Appl 621, Appl 622, Appl 623, Appl			Gaps 0;	
Sequence		gan, P.C.	Length 911; Indels 0;	RELSAA 52 RELSAA 610
4 US-08-478-029A-65 4 US-09-026-4 2 US-09-027-4 2 US-09-227-420-4 4 US-09-227-420-4 4 US-09-281-476-21 4 US-09-314-268-149 6 5352575-5 6 US-09-056-556-230 4 US-09-056-556-231 4 US-09-056-556-231 4 US-09-072-596-225 4 US-09-072-596-226 5 US-09-073-838-216 6 5470718-4 0 US-09-535-008-61	ALIGNMENTS	EY J. HAEL A. RESSION OF HETEROLOGOUS ST White, Zelano & Braniga ndon Blvd., Sulte 1400 ompatible PC-DOS/MS-DOS Release #1.0, Version # A US/08/460,269C n-1995 n-1995 n-1995 n-1995 st 37,067 MYDER: POPOV-2 MYDER: POPOV-2 MYDER: POPOV-2 MYDER: POPOV-2 ST acids ecids	Score 297; DB 4; L Pred. No. 8.4e-19; D; Mismatches 0;	GARAPPAKRAPOPGPOPGPOPPOPPOPPOPPOROPEAPAPOPPARELSAA
37.2 408 37.0 3810 37.0 380 37.0 380 37.0 509 36.0 402 36.0 1113 35.9 1118 35.9 1118 35.9 490 35.7 366 35.5 543		Here 1. 18-460-269C-4 guence 4, Application US/08460269C tent No. 6197548 GENERAL INFORMATION: APPLICANT: CLARE, JEFFREY J. ROMANOS, MICHAEL A. TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: Millen, White, STREET: 2200 (larendon Bl. CLTY: ARLINGTON STATE: VA CONFORT: USA CONFORT: USA CONFORT: USA CONFORT: USA CONFORT: USA COMPTER READABLE FORM: MEDIUM TYPE: FILOPPY disk COMPTER: TBM PC COMPATION OPERATING SYSTEM: PC-DOS/OS CONFORT: TREADABLE FORM: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 37,0 REGISTRATION NUMBER: 37,0 REGISTR	th similarity 100.0%; Similarity 100.0%; 52; Conservative	arkpapopgpopgi
 110.5 110 110 110 110 110 107.5 106.5 106.5 106.5 106.5 106.5 106.5	Ŧ -	269C 4, 6, 6 10, 10, 10, 10, 10, 10, 10, 10, 10, 10,	atc Sal	1 2
288 339 332 332 335 344 443 453 453 453 453 453 453 453		RESULT 1 US-08-460-2 Sequence Patent N GENERAL M AL	Query Ma Best Loo Matches	Qy

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                                                                               APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 922;
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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COMPUTER: IBM-PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 284; DB 4; I
Pred. No. 1.1e-17;
0; Mismatches 0;
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APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Inhear ;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                   Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 922 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.6%;
Best Local Similarity 89.7%;
Matches 52; Conservative
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US-08-460-269C-6
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                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             71.4%; Score 212; DB 4;
78.8%; Pred. No. 1.9e-11;
tive 0; Mismatches 1
             NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOOKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 910 amino acids
TYPE: amino acids
                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECLLE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1991
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRMEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08237716
Patent No. 5589384
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22201
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Region

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Gaps
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Sequence 16, Application US/08246982A

Patent No. 5686288

APPLICANT: NacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Gusella, James F.

TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100

CITY: Washington

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                      APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 APPAPKPAPQPG-----PQPGPQ-PPQPPQPPQRQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: WAY 20, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.1%; Score 125; DB 6;
53.2%; Pred. No. 0.00025;
tive 0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3119 amino acids
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.24
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-246-982A-16
                                                                                                                                                                                         NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amiro acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20005
                                                                                       Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:3
                                                                                                                                                                    PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: James, Olive A
APPLICANT: Genes, Olive A
APPLICANT: Klein, Michel H
TITLE OF INVENTION: ALJUVANT COMPOSITIONS COMPRISING A
TITLE OF INVENTION: ALJUVANT COMPOSITIONS COMPRISING A
UNDBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                      /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 127; DB 4; Length 24;
Pred. No. 1.6e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION WHERE: US/08/750,624
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                     Score 130; DB 1;
Pred. No. 1.2e-05;
2; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney
6th Floor, 330 University Avenue
                                          /label- LTB sequence
                                                                                                                                                                                                                                                                                                                                                                  10 PAPQPGPQPPQPPQPPQPPQRQPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                           5 PGPEIAPQPGPPQPPQP-----QPEAPAPEP 32
                                                                                                                       /label= hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REERENCE/DOCKET NUMBER: 1038-660
TELEPHONE: (416,595-1165
FELEPHONE: (416,595-1165
FILERAX: (416,595-1165
FILERAX: (416,595-1165
FILERAX: (416,595-1165
FILERAX: (416,595-1165
FILERAXI ON FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 РОРСРОРРОРРОРРОРОЯОРЕАРАРОРР 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.88;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.6%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 79.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & MCBUS STREET: 6th Floor, 336 CITY: Toronto STATE: Ontario COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                               NAME/KEY: Region
LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
                                  OTHER INFORMATION:
                                                                                                  LOCATION: 4..7
OTHER INFORMATION:
                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: M5G 1R7
NAME/KEY:
LOCATION:
                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-750-624-11
                                                                                                                                                                                                                                              US-08-237-716-11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 120; DB 4;
Pred. No. 6.4e-05;
); Mismatches 0
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 PQPGPQPPQPPQPPQRQPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PQPGPQPPQPPQP-----OPEAPAPQP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
                                                                                                                                                                                                                                                            NAME: Lebovitz, Richard M.
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28, Application US/09041886
5, 6235872
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 933,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.4%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 51.1%;
Matches 24; Conservative
                                                                     ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 82,4
FILING DATE: 07-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5202236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-460-269C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-041-886-28
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5202236-37
;Patent No.
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                                                      Gaps
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                                                      11;
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Pred. No. 0.0045;
2; Mismatches 13; Indels 11;
               Length 3119;
                                                                                                                                                                                                                                                                                                             APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                        51
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
               Score 120.5; DB 1;
Pred. No. 0.0045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 KPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA----
                                                                                        9 KPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA----
                                                                                                                                                                                                                                                                                                                                                                                                         Kessler, Goldstein & Fox
                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0609,3880003
                                                                                                                                                                                                                      Sequence 16, Application US/08453265
Patent No. 5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                                            MacDonald, Marcy E. Ambrose, Christine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                           1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET UNBER: 06(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.6%;
               Query Match
Best Local Similarity 50.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17
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Best Local Similarity 50.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIOM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                               APPLICANT:
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Length 23;

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9
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     DAVID M.; STRAUSBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 APPAPAFAPAPALAPAPUNPNPSSPSSPSSPPTPPPTPPSPSPSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 APPAPKPAPQPG-----PQPG-PQPPQPPQPPQRQPEAPAPQPP
APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUS
SUSAN L.; MCCANDLISS; RUSS; WEI, TENA; FILPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 120; DB 6;
Pred. No. 0.00068;
0; Mismatches 17
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5

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Score 116; DB 4; Length 530;
Pred. No. 0.0023;
2; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KPAPQPGFQPGPQPPQPPQP--PQRQPEAPAPQPPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

39.1%; Score 116; DB 4;
Best Local Similarity 45.6%; Pred. No. 0.0024;
Matches 26; Conservative 2; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                        P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-041-886-30
; Sequence 30, Application US/09041886
Patent No. 6735872
; GENERAL INFORMATION:
                                                                                REGISTRATION NUMBER: 31,815
REFERENCE/DOCKER NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEC ID NO: 29:
SEQUENCE CHAMACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        39.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-849
INFORMATION FOR SEO ID NO: 30
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          LENGTH: 530 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 552 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide US-09-041-886-30
                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 45/CTTY: San Diego
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92122
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                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KPAPQPGPQPGPQPPQPPQPPQP--PQRQPEAPAPQPPAG------RELSA
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 513; 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:

PAPLICANT: Bredesen, Dale E.

APPLICANT: Ralizadeh, Sharroz

TITLE OF INVENTION: Polypeptides and Methods of Use

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STAFE: 4770 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 116; DB
; Pred. No. 0.002
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORKEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/OCKET NUMBER: P-I
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.1%;
Best Local Similarity 45.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTR: United States
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 513 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-246-982A-6
                                                                                                                                                                                                                                                                                  amino acid
                          FILING DATE: Ma
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08246982A
Patent No. 566288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Dayso, Mable P.
APPLICANT: Duyso, Mable P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 116; DB 4; Length 589;
Pred. No. 0.0025;
2; Mismatches 15; Indels
                                                                               APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                               ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
COUNTRY: U.S.A.
ZIP: Z0005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
PC Compatible
PC-DOS/MS-D
                 Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SED ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 39.1%;
1 Similarity 45.6%;
26; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 589 amino acids
                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-886-31
                                                                                                                                                                   NUMBER OF SEQUENCES: 7: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                  ADDRESSEE:
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US-09-041-886-31
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein – protein search, using sw model

7, 2003, 16:53:34 ; Search time 15.5911 Seconds May Run on:

(without alignments)
306.927 Million cell updates/sec

US-09-855-754B-15 297 Perfect score:

Sequence:

1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA 52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

349150 segs, 92025710 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 15, Appl		Sequence 18, Appl	Sequence 19, Appl	Sequence 6, Appli	Sequence 17, Appl	Sequence 16, Appl	14,	Sequence 20, Appl	21,	22,	Sequence 23, Appl	5,	24	43,	43,	· Sequence 43, Appl	٠,	Sequence 47, Appl
TD 01	US-09-855-754-15	US-09-855-754-4	US-09-855-754-18	US-09-855-754-19	US-09-855-754-6	US-09-855-754-17	US-09-855-754-16	US-09-855-754-14	US-09-855-754-20	US-09-855-754-21	US-09-855-754-22	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-09-976-740-43	US-10-023-529-43	US-10-023-523-43	US-09-976-740-47	US-10-023-529-47
Query Match Length DB	52 9	911 9	56 9	58 9	922 9	52 9	59	49 9	48 9	52 9	54 9	42 9	910 9	39	538 9	538 12	538 12	550 9	550 12
Query Match I	100.0	100.0	96.0	92.6	92.6	91.2	90.1	89.7	87.5	87.2	6.98	71.4	71.4	64.5	41.4	41.4	41.4	40.9	40.9
Score	297	297	285	284	284	27.1	267.5	266.5	260	259	258	212	212	191.5	123	123	123	121.5	121.5
Result No.	٦	7	e	4	ហ	9	7	80	6	10	. 11	12	13	14	15	16	17	18	19

Sequence 47, Appl Sequence 3, Appli Sequence 2, Appli	Sequence /, Appli Sequence 2, Appli Sequence 1002, Ap	Sequence 1, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli	. ~ ~ .	: 2	Sequence 62, Appl Sequence 2, Appli Sequence 10, Appl	Sequence 21, Appl Sequence 125, App Sequence 70, Appl	Sequence 967, App Sequence 1444, Ap Sequence 4, Appl1 Sequence 50, Appl Sequence 6, Appl1
12. US-10-023-523-47 9 US-10-171-384-3 10 US-09-823-240-2 10 US-09-004-097-7	10 US-US-94-967-7 9 US-09-959-987-2 9 US-09-925-299-1002 10 US-09-925-299-1002	9 US-10-171-384-1 9 US-10-077-584-4 9 US-10-020-215-2	9 US-10-077-584-9 10 US-09-765-272-160 9 US-10-067-457-5	10 US-09-850-887-4 12 US-10-042-417-32	9 US-U9-298-523B-5 9 US-09-298-523B-2 10 US-09-823-240-10	10 US-09-910-087-21 9 US-10-072-036-125 10 US-09-791-171-70	10 US-09-764-864-967 10 US-09-925-300-1444 9 US-10-038-010-4 9 US-10-001-873-50 9 US-09-978-167-6
550 827 802	641 647 647	824 171 1274	68 641 863	197	707	503 635 666	316 531 638 1134 578
0.044 0.09 0.09	0.00	38.2 37.9	37.7 37.5 37.5	37.4	2.00.0	37.0	8.98.98 86.99 86.99 7.
121.5	115.5	113.5 113 112.5	1112 111.5 111.5	1111	110.5	110	109.5 109.5 109.5 109.5
2220	462	272	30 31 32	ω ω υ ω 4- π	370	2 E 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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                                                                                           APPLICANT: GDISO-MACLOE, CHROLINE
APPLICANT: GGISO-MACLOE, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US,09/955,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSETWARE: PATEGITIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09855754;
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURGAUX-EDDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAEKPAPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 297; DB 9;
llarity 100.0%; Pred. No. 2.4e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
Sequence 15, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                              APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches | 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 15
LENGTH: 52
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CURRENT APPLICATION NUMBER: US/09/855,754
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVERTION: POLYMPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PRESIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDEFELLA PERTUGSIS, TITLE OF INVENTION: BONDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND STITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
FILE REFERENCE: 0495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 297; DB 9;
Pred. No. 2.6e-13;
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella bronchiseptica US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-855-754-18; Sequence 18, Application US/09855754 publication No. US20020192237A1; GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 92.9%;
Matches 52; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                    LENGTH: 911
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNICABLIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PRARPETUSSIS, AND BORDETELLA PRETUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT RELING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                            Score 284; DB 9;
Pred. No. 2e-13;
0; Mismatches 0;
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Pred. No. 2e-12;
0; Mismatches 0
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                                                                                                                                                          ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
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89.7%;
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1 Similarity 89.7%;
52; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Matches 52; Conserv
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Best Local Similarity.
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; ORGANIŜM: Bordetella bronchiseptica
US-09-855-754-20
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US-09-855-754-21
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BORNSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                Query Match 89.7%;
Best Local Similarity 94.2%;
Matches 49; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 92.3
Matches 48; Conservative
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PRIOR FILING DATE: 2000-0
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SOFTWARE: Patentin Ver.
SEQ ID NO 21
LENGTH: 52
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US-09-855-754-21
       US-09-855-754-14
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BEGINGS PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BROWGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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Publication No. US20020192237A1

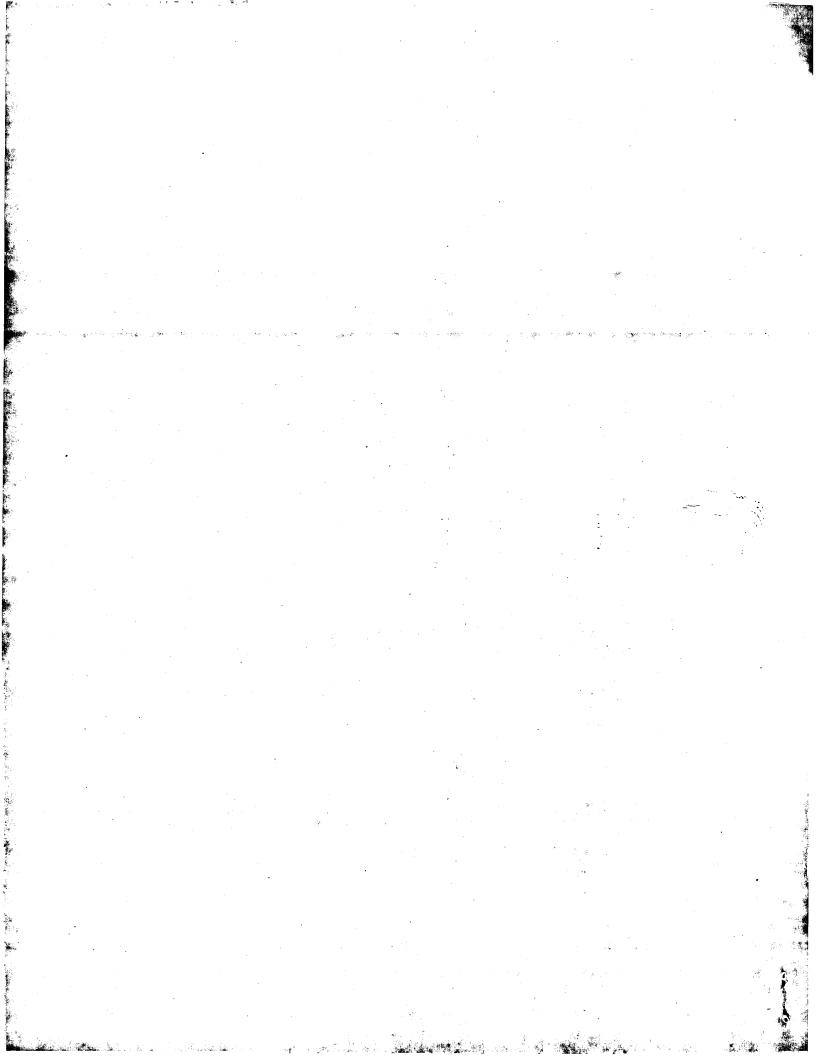
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
GUISS-UX-EUDE, CAROLINE
APPLICANT:
GUISS-UX-EUDE, CAROLINE
APPLICANT:
TITLE OF INVENTION:
BOUNTERELLA PERFUSSIS,
TITLE OF INVENTION:
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION:
IMMUNGENIC COMPOSITIONS
FILE REFERENCE:
03495-0206-00000
CURRENT APPLICATION NUMBER:
US/09/855,754
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Pred. No. 1.4e-12;
0; Mismatches 0;
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85.0%; Pred. No. 2.6e-12;
iive 0; Mismatches 0;
                                                              ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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US-09-855-754-16
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                          Query Match 91.2%;
Best Local Similarity 96.2%;
Matches 51; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
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Matches 51; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 14
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ENGTH: 59
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                                                                    Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT PAPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60,206,969
PRIOR FILLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
FILE REFERENCE: 0495-0206-00000
CURRENT APPLICATION NUMBER: USC/09/855,754
CURRENT **ILING** DATE: 2001-09-10
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                                                                                                                                         1 GAKAPPA, PKPAPQPGPQPG---PQPPQPPQPPQPPQPEAPAPQPPAGRELSAA · 49
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Score 266.5; DB 9;
Pred. No. 2.7e-12;
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92.3%; Pred. No. 7.2e-12;
11ve 0; Mismatches 0;
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92.5%; Pred. No. 8.9e-12;
ive 0; Mismatches 2;
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Best Local Similarity 92.5
Matches 49; Conservative
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RESULT 15
US-09-976-740-43
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LENGTH: 39
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                                                                                                                                                                                                                              APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERRACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BROWCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPEAPAPQPPAGRELSAA 42
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1.1e-11;
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Pred. No. 1.1e-08;
0; Mismatches 1;
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Pred. No. 1.1e
0; Mismatches
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
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                                                                                                                                                            Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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Best Local Similarity 89.1%;
Matches 49; Conservative
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Best Local Similarity 78.8%;
Matches 41; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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US-09-855-754-23
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LENGTH: 42
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LENGIH: 54
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRARAERUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION UNMBER: US/09/855,754
CURRENT FILING DATE: 2001-109-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PRAPERUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND SITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 1.4e-07;
0; Mismatches 1.
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                                                        CAROLINE
Sequence 5, Application US/09855754 Publication No. US20020192237A1
                                                                                                                   GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754-5
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Best Local Similarity 78.8%;
Matches 41; Conservative
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                                                      GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE,
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 5
LENGTH: 910
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Search completed: May 7, 2003, 17:30:50 Job time: 15.5911 secs



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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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	-							æ	ALIGNMENTS	
		RESULT 1 A47675 68K outer membrane protein P.68 pertactin C; Species: Bordetella bronchiseptica C;Date: 19-Dec-1993 #sequence_revision 18-C;Accession: A47675 R;Li, J.; Fairweather, N.F.; Novotny, P.; J. Gen. Microbiol. 138, 1697-1705, 1992	r me 19-18 10-18-19-19-19-19-19-19-19-19-19-19-19-19-19-	mbran ordet ec-19 A476 1rwea obiol	e pro ella 33 #8 75 :her,	otein P. bronchisequence	68 Sep Lre Nov	pertactin tica vision 18 otny, P.;	- Bordetella bronchiseptica Nov-1994 #text_change 08-Oct-19 Dougan, G.; Charles, I.G.	
	and and and and and and	A; Title: Cloning, A; Reference numbs A; Contents: CN75; A; Accession: A475; A; Status: prelimi A; Molecule type:	clc nce ts: lon: pr	nuing, numbe CN753 A476 elimin	nucl r: A4 1 75 nary nucle	leotide 17675; N	ged TOID	.9240	heterologous expression of the PMID:1527510	protective o
•		A; Kesidues: 1-911 <. A; Cross-references: A; Note: sequence ex	refe sequ			Stracted fr	. i	B:S46 NCBI	.11> GB:X54815; GB:S46416; NID:939396; PIDN:CAA38584.1; PID:939397 :racted from NCBI backbone (NCBIN:113318, NCBIP:113319)	1397
		Query Match Best Local S Matches 52	Matc ocal s	fai'	arit	larity 100 Conservative	90.0	Sr ;	Score 297; DB 2; Length 911; Pred. No. 4.5e-13; Mismatches 0; Indels 0; Gaps (0;
	y 1	Qy 1 . 559	- 6 - 6 - 6 - 6 - 6	KAPPAI 	PKPAE 	OPGPQPC	100 100 100 100 100	PQPPQ 	Gakappapkraropodopopopopopopopoporopeapapoppagkelsaa 52 	
	10 M2 0	RESULT 2 S15204 Pertactin N; Alterna C; Species	8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Bordet names ordete	ella out	Bordetella parapertussis names: outer membrane pr ordetella parapertussis	rtu	ssis e pro		
	J U M Z	C. Accessi R; Li, L. J fol. Micr	10n: J.; robi	5152(S152(Dougar ol. 5,	409	sequence 514659 .; Novot 9-417, 1	_re 991	V1810	on U/-Apr-1994 #text_change OB-Oct-1999 Charles, I.G.	
	~ ~ ~ ~ ~	A;Title: P.70 pertactin, an outen A;Reference number: S15204; MUID A;Accession: S15204 A;Molecule type: DWA	P.7	0 peri numbei S152(ype: L	tacti : S1)4 :NA	in, an c 15204; N	ute	r-mem:	outer-membrane protein from Bordetella parapertussis MUID:91251771; PMID:2041476	is: clo
		A, Cross-refe C, Genetics: A, Gene: prn C, Keywords:	refe lcs: prn ds:	rences membra	ine p	resides: 1 722 CLID. Cross-references: EMBL:X54547; Genetics: Gene: prn Keywords: membrane protein	47;		NID:g39761; PIDN:CAA38419.1; PID:g39762	
		Query Ma Best Loc Matches	altc.	h Simi 52;	(arit	95.68 Jarity 89.78 Conservative	78;	Score Pred. 0; Mis	e 284; DB 2; Length 922; . No. 3.3e-12; !smatches 0; Indels 6; Gaps	1;
	•	Oy 1	1 GA	KAPPAI	KPAF	gakappapkpapqpgpgpg 		0d	PQPPQPPQPPQPPQRDEAPAPQPPAGRELSAA 52 	

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Gaps

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C.Species: Brassica napus (rape)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C.Accession: S16748
R.Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991
A.Poscription: Cloning and characterization of a proline-rich gene expressed specific A.Reference number: S16748
A.Accession: S16748
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647.
J. Cell Biol. 109, 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri molecular structure of A;Reference number: A33647; MUID:90094551; PMID:2689458
A;Reference number: A33647; MUID:90094551; PMID:2689458
A;Reference number: A33647
A;Reference number: A33647
A;Reference number: A33647
A;Ression: A35647
A;Ression: A35647
A;Ression: G;Ression: A35647
A;Ression: C;Ression: A35647
A;Ression: C;Ression: A35647
A;Ression: C;Ression: A36648
A;Ression: C;Ression: A36648
A;Ression: C;Ression: C;Ression
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C; Species: human herpesvirus 4, Epstein-Barr virus
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Accession: $4244, $32988; $4244,
B; Sample, J; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KAPPAPKPAPQPGPQPGPQPPQPPQ-------PPQPPQRQPE---APAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.3%; Score 140.5; DB 2; Length 449; llarity 44.3%; Pred. No. 0.005; Conservative 4; Mismatches 13; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 485;
                                                                      Score 141; DB 2; Length 599;
Pred. No. 0.0058;
1; Mismatches 17; Indels
C; Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-449 <ROB>
A;Cross-references: EMBL:X60376; NID:g22596; PID:g22597
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                                                                                                                                                                                                                                             5 PPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 44
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46.1%; Score 137; DB 2;
Best Local Similarity 55.0%; Pred. No. 0.009;
Matches 22; Conservative 1; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sulfated surface glycoprotein 185 - Volvox carteri
C;Species: Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proline-rich protein - rape (fragment)
                                                                               47.5%;
55.0%;
                                                                                   Query Match
Best Local Similarity 55.0
Matches 22; Conservative
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27; Conserv
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Best Local S
Matches 27
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A; Residues: 1-599 <GOD>
A; Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A; Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A; Experimental source: strain HK 10; sub_species Nagariensis
A; Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-fre
                                                                                                                                                                                                                                                                                                                                                                    R.Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989

Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989

A;Title: Molecular cloning and characterization of protective outer membrane protein P.6

A;Reference number: A32560; MUID:89264462; PMID:2542937

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-910 CCHA>

A;Ross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054

A;Note: it is uncertain whether Met-1 or Met-3 is the initiator

A;Note: it sembrane protein

F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <NAT>
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C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Accession: JC2301
C;Accession: JC2301
Ni Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10798
R;Godl, K.: Hallmann, A.; Wenzl, S.; Sumper, M.
EWBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin
A;Reference number: 217154; MUID:97162277; PMID:9009264
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-430 <WAD>
A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
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                                                                                                                                                                                                              outer membrane protein P.69 precursor - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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    GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
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Best Local Similarity 50.8%; Pred. No. 0.00092;
Matches 30; Conservative 1; Mismatches 9; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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78.8%; Pred. No. 1.7e-07;
.ive 0; Mismatches 1; Indels
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Matches 41; Conservative
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Length 209;

Score 135; DB 2; Pred. No. 0.0064;

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A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;Ge S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding novel eA; Reference number: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: RMA
A;Residues: 33-209 <GGL>
A;Accession: EMBL:214020; NID:g19918; PID:g19919
A;Accession: EMBL:214020; NID:g19918; PID:g19919
A;Accession: EMBL:214020; NID:g19918; PID:g19919
A;Cross-references: EMBL:214020; NID:g19918; PID:g19919
A;Cross-references: EMBL:214020; NID:g19918; PID:g19919
A;Cross-references: Call and Light and Ligh
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A; Realdues: 1-487 < FARS
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
B; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A; Title: UZ region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2.
A; Recession: $42447
A; MOID: 95063846; PMID: 6209719
A; Accession: $42447
A; MOID: 95063846; PMID: 6209719
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: Loan
A; Molecule type: 
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C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
R;Wu, H; Zou, J; May B; Gu, Q; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
'fitle: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a 'Reference number: $42440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C;Species: Owenia fusiformis
C;Species: Ovenia fusiformis
C;Species: Ovenia fusiformis
C;Date: O'Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34043; B34043
B;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
B;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
B;Cochem. Blophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized by the repetition A;Reference number: A90159; MuID:90147742; PMID:2105723
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0.011;
ches 20;
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Pred. No. 0.0047;
0; Mismatches 20;
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                                                                                                                                                                                                                                                                     R;Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
AAccession: S3298B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.5%;
Matches 23; Conservative
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Best Local Similarity 53.5%;
Matches 23; Conservative
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A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
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A;Accession: B34043
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A; Residues: 1-141 <BAK>
                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-487 <SAM>
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A; Residues: 1-209 < WUA>
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                                                                                                                    A; Accession: S42442
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proline-rich protein APG - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.) Date: 13-Jan-1955 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 (C.) Accession: S21961 (C.) Accession: S21961 (C.) Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991 (C.) Areference number: S16748 (C.) Areference number: S16748 (C.) Areference number: S1961 (C.) Areference number: S1961 (C.) Areference number: S1961 (C.) Aresidues: 1-534 (C.) Aresidues: 1-534 (C.) Aresidues: EMBL:X60377; NID:922599; PID:922599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T48814
R; Schulte, U; Adgn, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatu submitted to the Protein Sequence Database, April 2000
A; Reference number: 224541
A; Reference number: 224541
A; Setults: preliminary
A; Molecule type: DNA
A; Residues: 1-1952 < SCH>
A; Essidues: 1-1952 < SCH>
A; Essidues: 1-1952 < SCH>
A; Esperimental source: cosmid contig 15E6; strain 74
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C.Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                     13; Indels
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                                                                                                                                                 5 PPAPKPAPQPGPQPGPQP-PQPPQPPQP-PQRQPEAPAPQPPA 45
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Pred. No. 0.021;
3; Mismatches. ]
45.5%; Sco...
55.8%; Pred. No. o....
... 4; Mismatches
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Matches 26; Conservative
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RingGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes A; Reference number: A30083; MUD:88274327; PMID:2839594
A; Accession: 130085
A; Accession: aid sequence not shown; translation not shown
A; Residues: 1-3164 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
                                                                                                                                                                                                                                       C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: I30085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                               UL36 protein - human herpesvirus 1 (strain 17)
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Best Local Similarity 66.7%;
Matches 30; Conservative
                                                                                                                                                                                                              C; Species: human herpesvirus 1
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Job time : 10.7445 secs
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                                                                                                                     RESULT 15
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C., L., J. H., Y.; Lin, X.; Liu, X.; Liu, X.; Liu, X.; Lin, X.; Liu, Z.S.X.; Liu, Z.S.X.; Liu, Z.S.X.; Liu, Z.S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Date: 28-0Ct-1996 *sequence_revision 07-Feb-1997 *text_change 10-Jul-1998
C;Date: 28-0Ct-1996 *sequence_revision 07-Feb-1997 *text_change 10-Jul-1998
C;Accession: S51939; $72115; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A. Plant Mol. Biol. 27, 21-216, 1995
Plant Mol. Biol. 27, 21-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
A;Title: A proline-rich chitinase from Beta vulgaris.
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A;Cross-references: GB:AE005172; NID:g8778985; PIDN:AAF79900.1; GSPDB:GN00141
C;GenetLos: A;Ap position: 1
                                                                                                                                                                                                                                                                                                    T20H2.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
                                 Gaps
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Note: the authors translated the codon TGC for residue 416 as Gly
Accession: S72315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 130.5; DB 2; Length 1137;
Pred. No. 0.047;
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Pred. No. 0.024;
2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 KPPPAAPSPSPCPSPPRRPQPKPVPPPACPPTPPKPQPKPAPPEPKPA 155
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                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Superfanily: plant chitinase homology
C.Keywords: glycosidase; hydrolase
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-439/Porduct: chitinase #status predicted <MAT>
F:183-423/Domain: plant chitinase homology <PCH>
                                                                                         5 PPAPKPA-PQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 44
                                                                                                                           12;
      Pred. No. 0.057;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chitinase (EC 3.2.1.14) precursor - beet
                              3;
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llarity 48.8%;
Conservative 2
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56.2%;
   Best Local Similarity 58.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 56.2
Matches 27; Conservative
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Residues: 191-397 <BER2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-439 <BER>
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Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: S51939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A86335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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5

Gaps

5

Length 3164; Indels

DB 1; .; 6

Score 129.5; DE Pred. No. 0.12; 2; Mismatches

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49; Search time 5.0494 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-15 297 1 GARAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 52 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q03035 bordetella		P14283 bordetella	P40603 brassica na		P12978 epstein-bar	P21260 owenia fusi	P40602 arabidopsis		083949 orgyta pseu		-		P02831 mus musculu	P51111 rattus norv	_	P78621 emericella	Q03211 nicotiana t		Q09442 caenorhabdi	Q24120 drosophila	_	_	P41467 autographa	O70324 mus musculu	P25050 herpesvirus		P05142 mus musculu	Q9pr99 ureaplasma	P22576 herpesvirus	P58840 homo sapien	m	P06915 plasmodium
SUMMARIES	ΙD	PERT_BORBR	PERT_BORPA	PERT_BORPE	APG_BRANA	SSGP_VOLCA	EBN2_EBV	YPRO_OWEFU	APG_ARATH	TEGU_HSV11	Y066_NPVOP	MOZ_HUMAN	ACRO_RABIT	GP1_CHLRE	HXA3_MOUSE	HD_RAT	G3PT_MOUSE	SEPA_EMENI	EXLP_TOBAC	BRD4_HUMAN	YP85_CAEEL	CAPU_DROME	RFX1_HUMAN	MEFD_MOUSE	Y066_NPVAC	MOT8_MOUSE	COLL_HSVS7	HD_HUMAN	PRP2_MOUSE	Y046_UREPA	COLL_HSVSC	ACRL_HUMAN	PRP3_MOUSE	CSP_PLABE
	Length DB	911 1	922 1	910 1	449 1	485 1	487 1	141 1	534 1	3164 1	875 1	2004 1	431 1	555 1	443 1	3110 1	440 1	1790 1	426 1	1362 1	379 1	1059 1	979 1	514 1	808 1	565 1	105 1	3144 1	261 1	791 1	102 1	232 1	296	339 1
d	Query Match Length	100.0	92.6	71.4	47.3	46.1	45.8	45.5	•	43.6		42.9	42.3	42.1	41.2	41.2	41.1	41.1	40.9	40.4	39.9	39.9	39.7	39.4	39.4	39.5	39.1	39.1	38.9	38.9	38.7	38.7	38.6	38.6
	Score	297	284	212	140.5	137	136	135	130.5	129.5	128	127.5	125.5	125	122.5	122.5	122	122	121.5	120	118.5	118.5	118	117	117	116.5	116	116	115.5	115.5	115	115	114.5	114.5
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P23093 plasmodium P06914 plasmodium (99014 trichoderma (05859 mus musculu (05860 mus musculu P08001 sus scrofa P42768 homo sapien (14003 homo sapien (14003 homo sapien P09791 trypanosoma P42859 mus musculu (1400 homo sapien P62859 mus musculu (1400 homo sapien P6285) muscul	P93329 medicago tr
CSP_PLABA CSP_PLAYO KPC1_TRIRE FW14_MOUSE FW14_MOUSE ACRO_PIG WASP_HUMAN PARB_TRYBB HD_MOUSE	NO20_MEDTR
347 367 1139 1206 1468 415 502 757 129 3119	268
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114.5 114.5 114.5 114.5 114.5 114.5 113.5 113.5 113.5	111.5
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ALIGNMENTS

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                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li L.J., Dougan G., Novotny P., Charles I.G.; "P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICTORIOL. 5:409-417(1991).

MICTORIOL. 5:409-417(1991).

FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN SUBUNIT: MONOMER.

SUBCULLAR LOCATION: Outer membrane.

BISEASE: MAY CONTRIBUTE TO THE DISBASE STATE OF WHOOPING COUGH.

MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                            Gaps
           3 X 5 AA TANDEM REPEATS OF G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERTACTIN (P.70).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                          ö
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                   Length 911;
                                                                                                                                                                                                                                                                                                                                                                       Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                                                                                          Indels
                                                     3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                            Score 297; DB 1;
Pred. No. 5.5e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Virulence; Repeat. 34 POTENTIAL. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CN2591;
MEDLINE-91251771; PubMed-2041476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rik; S14659; S14659.
InterPro; IPR004899; Pertact_sup.
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                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                    ..
Σ
                                                                                                              100.0%;
1larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03212; Pertactin; 1.
                                                                                   93995
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647
922
262
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                                                                                 911 AA;
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCENTRATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=519;
                                                                                                                  Local S.
52;
                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella.
                                                                                                                                                                                                                                                                      PERT_BORPA
P24328;
                                                                    DOMAIN
SEQUENCE
                                                                                                               Query Match
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                                        REPEAT
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                            REPEAT
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                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M.,
Novciny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordeteila pertusais.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i - FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

-1 SUBUNIT: MONOMER.

-1 SUBCELLULAR LOCATION: Outer membrane.

-1 DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.

-1 MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                            621
                                                                                                               X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                               22
                 LINES).
1 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G., "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
 ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                 9
                                                                                                                                                              Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                              Score 284; DB 1; Length 92
Pred. No. 3.4e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin precursor (Outer membrane protein P.69) (P.93). PRN OR OMP69A.
                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                          4 (APPROXIMATE)
9 X 3 AA APPROX
                                                                                                                                                                                                                                                                                                                                              910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 264 AND 332.
MEDLINE-92407514; Pubmed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96196517; PubMed-8609998
                                                                                                                                95178 MW;
                                                                                                                                                              95.6%;
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                290
270
275
280
285
603
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis.
                                                                                                                                922 AA;
                                                                                                                                                                                Similarity
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                                266
266
271
276
281
575
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                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                             PERT_BORPE
P14283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella.
                                                                                                                                 SEQUENCE
                                                                                                                                                              Query Match
                                                                                                                                                                                 Local
                                                                                                           DOMAIN
                                                                              REPEAT
REPEAT
                                  DOMAIN
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
NON_TER 1
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                                                                449 AA;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;

Broberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,

Draper J., Scott R.;

"Gametophytic and sporophytic expression of an anther-specific

Arabidopsis thaliana gene.";

Plant J. 3:111-120(1993).

-I TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.

-I DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING

MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING

MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                         X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
10-FEB-1995 (Rel. 31, Last sequence update)
11-ROV-1995 (Rel. 32, Last annotation update)
11-ROV-1995 (Rel. 32, Last annotation update)
11-ROV-1995 (Projectific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                    CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                     (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                      568 GAKAPPAPKPAPQPG-------PQPPQPPQPPQPPAPAPAPAPARGKELSAA 609
                                                                                                                                                                                                                                                                                                                                                         52
                                                                                                                                                                                                                                                                                                     71.4%; Score 212; DB 1; Length 910; 78.8%; Pred. No. 7.4e-07; 1ve 0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQREAPAPQPPAGRELSAA
                                                                                                                          PERTACTIN (P.69).
                                                                                                                                                                                                                                        (APPROXIMATE).
                                                                                      membrane; Signal; Virulence; Repeat.
                                                                                                                                         POTENTIAL
            InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfan; PF03212; Pertactin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001087; Lipase_GDSL
                                                            PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY
                                                                                                                                                                                                                                                                             93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus (Rape).
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                             910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3708;
                                                                                                                                                                                                                            276
281
286
579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                               APG_BRANA
P40603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR CEX
                                                                                                                                                                                                                                                                 DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                          CHAIN
PROPEP
                                                                                      Outer m
SIGNAL
                                                                                                                                                                                        DOMAIN
REPEAT
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                                                                                                                                                                                                                                                     REPEAT
                                                                                                                CHAIN
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APG_BRANA
                                                                                                                                                                                                                                                                                                                                Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the cellular compartment.*;
J. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. The Extracellular matrix (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC PRECURSOR OF THIS SUBSTITUTIONE (C3Z STRUCTURE). THE CONALENT (CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
I. PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                            3 KAPPAPKPAPGPQPGPQPPQPPQ------PPQPPQRQPE---APAPQPPA 45
                                                                                                                                                                                                                                                                                                                       7 КРРКРОРКРОРАРТРЯРСТРОРКРОРКРОРКРРАТТРЯРСТРОРКРОРКРОРАРДЯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nacariensis / HK10;
MEDLINE-90094551; PubMed-2689458;
Ertl H., Mendele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carterl: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                   Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.1%; Score 137; DB 1; Length 485; 55.0%; Pred. No. 0.016; 1ve 1; Mismatches 17; Indels
                                                                 9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50436 MW; A52216400A031421 CRC64;
                                                                                                                            47.3%; Score 140.5; DB 1;
44.3%; Pred. No. 0.0091;
11ve 4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 1851e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA.
BY SIMILARITY.
                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-PRO
                                                              48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X51616; CAA35953.1; -.
                                                                                                                                                               Local Similarity 44.3%; les 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.0%
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EBN2_EBV

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APG_ARATH
APG_ARATH
STANDALL,
APG_ARATH
APG_COST (093Z14; Oglun'8;
AC 4040602; 093Z14; Oglun'8;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-70N-2002 (Rel. 41, Last sequence update)
DT 15-70N-2002 (Rel. 41, Last annotation update)
DE Anter-specific prolline-rich protein APG precursor.
DE Anter-specific prolline-rich protein APG precursor.
ARADHADAS thaliana (Mouse-ear cress)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidae;
OC Spermatophyta; Magnollophyta; endicotyledons; core eudicots; Rosidae;
""rnsids II; "Assicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung W.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A chung W.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung W.K., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Fulla C.Y.,
Gill J.E., Jenkins J., Johnson Hopson C., Khan S., Khaykin B.,
A minter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin B.,
A minin Hooper S., Lee A., Lee J.M., Lenz C.A., Lil J.H., Li Y.-P.,
A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziall A.,
Millscher J., Maranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pai G., Peterson J., Pham P.K., Rizzo M., Kooney T., Rowley D.,
Sun H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
A treaded S., Vaysberg M., Yostekala V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Brasence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Biochem. Biophys. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
            Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                     15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                       POLY-PRO.
H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 реграморовороворовороворовороворовов 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 135; DB 1;
Pred. No. 0.0084;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                               Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%;
53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.55
Watches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Owenia fusiformis,
                                                                    NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana.";
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .. RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                            MEDLINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Harfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.,
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
Jurol. 65:2545-2554(1991).
-i- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90266473; PubMed-2161150;
Petti L., Sample C., Kieff E.;
Subbuclear localization and phosphorylation of Epstein-Barr virus
latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T01618; -.
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 136; DB 1; Length 487;
11arity 53.5%; Pred. No. 0.018;
Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rel. 18, Last sequence update)
Rel. 32, Last annotation update)
proline-rich protein (Fragment).
                                                                                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AA
                                               487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V01555; CAA24877.1; ALT_INIT.
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPRO_OWEFU STANDARD; PR
P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seque
01-NOV-1995 (Rel. 32, Last annot:
Hypothetical proline-rich proteii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- PTM: PHOSPHORYLATED.
                                               STANDARD;
                                                                                                                                                                      EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF LMP-1
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Matches 23;
                                             EBN2_EBV
P12978;
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YPRO_OWEFU RESULT 7

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Length 141; 20; Indels

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-1 - FÜNCTION: TEGUMENT PROTEIN.
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      SSSSSSSSSSSSSS
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                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                           STRAIN—cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
*RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
*Streng and the consortium (Salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-! TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL
TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-! DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOCENESS.S. DURING
MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88374327; PubMed-2839594;
MCGeoch D.J., Dalan A., Frame M.C.,
McGeoch D.J., Scott J.E., Taylor P.;
McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome."
                                                                                                                                                                                                                                                                      MATURATION.
SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ι,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.041;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KAPPAPKPAPQPGPQPGPQP---PQPPQPPQPPQRQPE-APAPQP-PA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S -> P (IN REF. 1)
E -> A (IN REF. 1)
E -> H (IN REF. 1)
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01-WAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large tegument protein (Virion protein UL36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 3164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X60377; CAA42925.1; -. EMBL, AK022472; AAF79900.1; ALT_SEQ. EMBL, AX058647; AAL24235.1; -. PIR; S21961; S21961. Lipase_GDSL. Pfan; PF001687; Lipase_GDSL. Pfan; PF001657; Lipase_GDSL, PF00167; Lipase_GDSL, IPASE_GDSL, IPASE_GDSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%;
Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGU_HSV11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
CONFLICT
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Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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TEGU_HSV11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyla pseudotsugata baculovirus DNA
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24; EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 083949; Q65364; O10323; Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical, 98.6 kba protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 X 2 AA TANDEM REPEATS OF P-Q. W; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97271300; Pubmed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIrology 210;372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 129.5; DB
Pred. No. 0.17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 AA
                                                                                                                                                                                                                                                                                                                                                                                  PIR; 130085, MMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; Pubmed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2911 2980 35
3164 AA; 335857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                       EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.6%;
itarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replication."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudosugata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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SEQUENCE
                                      DOMAIN
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                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                             Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; "The translocation t(8;16)(pl1;pl3) of acute myeloid leukaemia fuses a putetive acevyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: PART ALL CALLION: NUCLEAR.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL.
-!- DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL.
-!- SUBAPES OF ACUTE WRIGIOL LEUKEMIA.
-!- SIMILARITY: COMPAINS 2 PHD-TYPE ZINC FINGERS.
-!- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translocation; Zinc-finger; Repeat;
                                                                                                                                                   5 PPAPKPA-----PQPGPQPGPQPPQPPQPP-----QPPQRQPEAPAP--QPP 44
                                                                                                     Score 128; DB 1; Length 875;
Pred. No. 0.084;
3; Mismatches 10; Indels
                                                                                                                            10; Indels
                                                                     86 91 POLY-PRO.
875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                 PRT; 2004 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR001517; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Pfam; PP00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SWART; SW00249; PHD; 1.
PROSITE; PS01059; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_2; 2.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-96376968; PubMed-8782817;
                                                                                                                                                                                                                                                        (Rel. 36, Created)
         EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; IFOS.
                                                                                                     43.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene; Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:13013; ZNF220.
                                                                                                                              27; Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265
313
379
                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                       5-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 601408
                                                                                                                                                                                                                                 MOZ_HUMAN
Q92794;
                                                                              SEQUENCE
                                                                                                                              Matches
                                                                                                                                                                                                                     MOZ_HUMAN
CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULEIDE BONDS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-New Zealand white; TISSUE-Testis;
STRAIN-New Zealand white; TISSUE-Testis;
MEDLINE-9436861; Pubmed-8086468;
Richardson R.T., O'Rand MG;
Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
preproacrosin related cDNA.";
Blochim. Blophys. Acta 1219:215-218(1994).
IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                         GLN/PRO-RICH.
MET-RICH.
BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                     Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                        9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                5 PPAPKP----APQPGPQPGPQPPQP-PQPPQPPQRQPEAPAPQPP
                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB.1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                   Score 127.5; DE
Pred. No. 0.16;
1; Mismatches
                                                                   POLY-LYS.
GLU-RICH.
GLU-RICH.
                      POLY-ARG.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                            POLY-GLU
                                                                                                                                                                       POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                      2004 AA; 225054 MW;
                                                                                                                                                                                                                                                                                                                                     42.9%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
995
1026
1078
1150
1150
1302
1414
1597
1704
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACRO_RABIT
P48038;
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DEVELOPMENTAL STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL PRELIMINARY SEQUENCE FROM N.A. MEDLINE-91017504; PubMed-1699225; Adair W.S., Apt K.E.; "Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Glycosylated polyproline II rods-with-kinks as a structural motif plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                       Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
1 16 BY SIMILARITY.
                                                                                                                                                                                       (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                      SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIINE-21159092; Pubmed-11258910;
Ferris P.J., Weessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                           O9FP06; 003927; Created)
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
                                                                                                                                                                                                                                                                                        2 AKAPPAPKPAPQPGPQ------PGPQPPQPPQPPQPPQRPAPAPQPPA 45
                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                              DB 1; Length 431;
                                                                                                                                                                                                                                   Score 125.5; DB 1; Leus-
Pred. No. 0.071; Indels
                                                                                                  INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                      CHARGE RELAY SYSTEM (BY S. CHARGE RELAY SYSTEM (BY S. CHARGE RELAY SYSTEM (BY S. 1C015A4E0BCOC668 CRC64;
                                                      (BY :
                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .
N-LINKED (GLCNAC. . .
                                                      ACROSIN LIGHT CHAIN
ACROSIN HEAVY CHAIN
                                                                                       SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                      555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: Associates with GP2 and GP3.
-i- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                       SIMILARITY
                                                                             PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                      PRT;
 TRYPSIN_HIS; 1.
TRYPSIN_SER; 1.
                                                                                                                                                                                                                      46422 MW;
                                                                                                                                                                                                                                                      43.68;
                                                                                                                                                                                                                                            42.38;
                                                                                                                                                                                                                                                                   24; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                             223
264
                                                                           431
                                                                                                                                                                                                                      431 AA;
                                                                                                                                                                                                                                                       Local Similarity
 PROSITE; PS00134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3055;
                       Hydrolase;
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                                                                                                                                                                                      ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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CARBOHYD
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PROPEP
                                                                                       DOMAIN
                                             CHAIN
                                                      CHAIN
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"The homeo domain of a murine protein binds 5' to its own homeo box."; Proc. Natl. Acad. Sci. U.S.A. 83:9532-9536(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 185-258 FROM N.A.
MEDLINE-85024859; PubMed-6091896;
McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.;
Molecular cloning and chromosome mapping of a mouse DNA sequence homologous to homeotic genes of Drosophila.";
                                                                                                                                                                                                                   VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                                                                                                           POLY-PRO.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
6A584A90465502F5 CRC64;
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MEDLINE-96323206; PubMed-8710855;
Tan D., Shao X., Pu L., Guo V., Nirenberg M.;
"Sequence and expression of the murine Hoxd-3 homeobox gene.";
Proc. Natl. Acad. Sci. U.S.A. 93:8247-8252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87092283; PubMed-2879282;
Fainsod A., Bogarad L.D., Ruusala T., Lubin M., Crothers D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruddle F.H., Hart C.P., McGinnis W.; "Structural and functional aspects of the mammalian homeo-box
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
Hofmann M., Boehm T.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 APPAPKPAPQPGPQPGPQPPQPPQP----PQPPQRQPEAPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                         Score 125; DB 1.
Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P02831; 061197;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HOXA3 OR HOXA-3 (MOx-1.5) (MO-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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                                                                                                                                                                                             POTENTIAL
                                                                   Interpro: IPR002955; P_inch_extensn.
InterPro: IPR003882; Pistil_extensin.
PRINTS; PR01217; PRTCHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
Glycoprotein; Repeat; Signal.
EMBL; AF309494; AAG45420.1; -.
EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSulteDB; Q9FPQ6; -.
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                                                                                                                                                                                                                                                                                                                                                                                                         42.18;
54.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rends Genet. 1:48-51(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                 493
555 AA;
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es 25, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                CARBOHYD
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Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

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Thu May

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                             - PUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSITERIOR AXIS.

SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSITERIOR AXIS.

- SUBCELLULAR LOCATION: NUCLEAR.

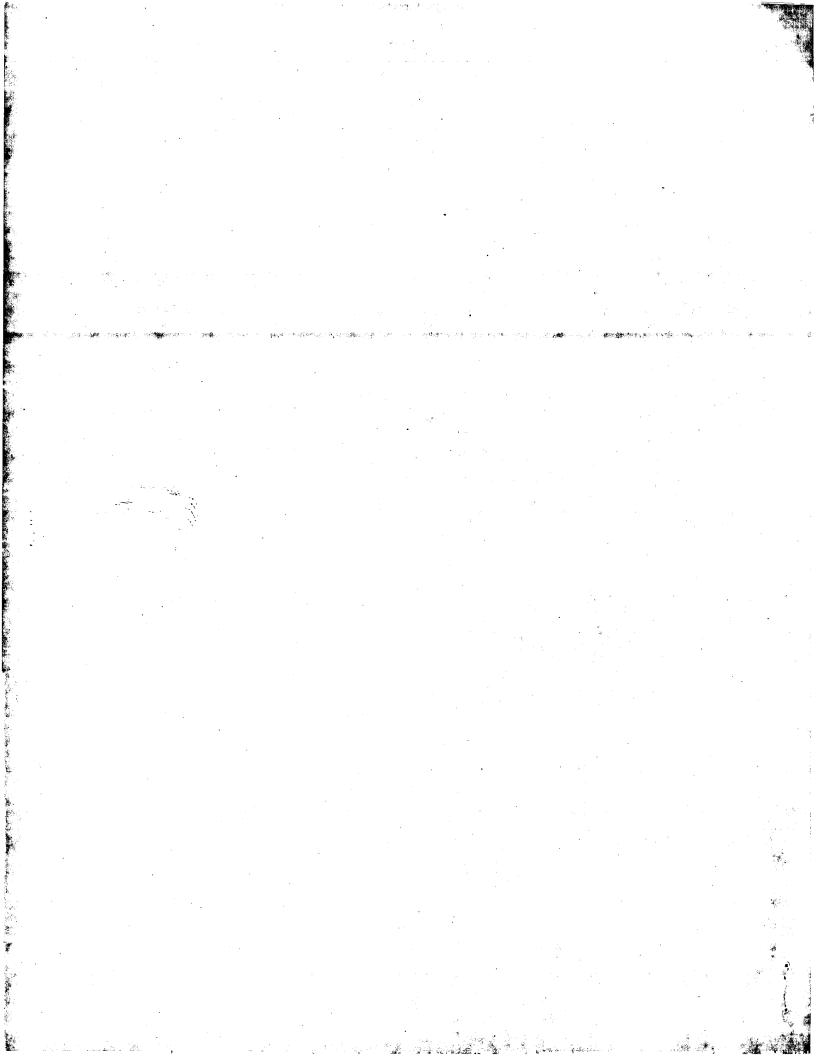
- SUBCELLULAR LOCATION: NUCLEAR.

- SUBCELLULAR LOCATION: NUCLEAR.

- SERPESSION IS LIMITED TO THE CRED MANNER IN EMBRYOS 8.5 DAYS P.C., EXPRESSION IS LIMITED TO THE CNS WITH AN ANTERIOR BOUNDARY IN THE HINDBRAIN AND EXTENDING POSTERIORLY THROUGH CAUDAL REGIONS OF THE SPINAL CORD. THE SAME SPATIAL EXPRESSION IS SEEN IN EMBRYOS 9.5 TO 12.5 DAYS P.C., STALLARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ′;
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PROSITE; PSO5071; HOMEOBOX_2; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S -> G (IN REF. 3 AND 4).
A -> G (IN REF. 3 AND 4).
SA -> RP (IN REF. 3 AND 4).
C -> M (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAP----QPP 44
MEDLINE-88030407; PubMed-2444477;
Fainsod A., Awgulewitsch A., Ruddle F.H.;
"Expression of the murine homeo box gene Hox 1.5 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6C0E184B0F6F2D40 CRC64;
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ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001827; Antennapedia
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46429 MW;
                                               embryogenesis.";
Dev. Biol, 124:125-133(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y11717; CAA72404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U56399; AAC52778.1; -. EMBL; K02591; AAA37822.1; -. PIR; A03315; A03315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T00378; -. MGD; MGI:96175; HOXA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P02833; 1SAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 AA;
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les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00389;
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DOMAIN
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Matches
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HD_RAT
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                                                                                                                                                                                     TISSUE-Brain;
MEDLINE-94100980; PubMed-8275091;
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K.,
Swaroop M., Kaatz K.W., Collins F.S., Albin R.L.;
"Widespread expression of the human and rat Huntington's disease gene in brain and noneural tissues.";
                   Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hamelster H., Epplen J.T., Aless O., "Expression of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
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                                                                                                                                                                                                                                                                                                                   Nat. Genet. 5:259-265(1993).
-1- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
VESICLE FUNCTION.
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MW; 33C357E8FC141550 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEATS DOMAIN 1. REPEATS DOMAIN 2. REPEATS DOMAIN 3.
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Pred. No. 0.45;
1; Mismatches
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POLY-PRO.
POLY-THR.
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                                                                                                                              Hum. Mol. Genet. 4:1173-1182(1995)
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MEDLINE-96133292; PubMed-8528205;
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Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
                                                                                                                                                                      SEQUENCE OF 1773-1926 FROM N.A.
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Hes 28; Conserv
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3110
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us-09-855-754b-15.rsp



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May 7, 2003, 16:38:52; Search time 26.5758 Seconds (without alignments) 403.166 Million cell updates/sec Run on:

US-09-855-754B-15 297 Title: Perfect score: Sequence:

1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA 52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_invertebrate:* sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

		dР				
Result No.	Score	Query Match	Query Match Length DB	DB		Description
-	297	100.0	107	2	Q9K5H5	09k5h5 bordetella
7	297	100.0	200	7	O9ALP9	
m	297	100.0	911	~	Q9L4E2 .	0914e2 bordetella
4	286.5	96.5	109	~	Q9K5H1	_
S	286.5	96.5	215	~	Q9ALQ4	_
9	285	96.0	111	~	Q9K5G9 ·	_
7	285	96.0	122	~	буклж9	_
8	285	96.0	252	7	Q9ALQ2	09alg2 bordetella
6	284	92.6	111	~	Q9K5G7	_
10	283	95.3	115	N	09к5н3	
11	266.5	89.7	104	7	09к5н9	_
12	266.5	89.7	105	~	Q9K5H7	_
13	266.5	89.7	115	~	Q9KJY1	-
14	266.5	89.7	115	~	09KJY0	-
15	266.5	89.7	198	~	овань0	Ogaĥpo bordetella
16	260	87.5	105	7	Q9K5G5	

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	Q9k5g4 bordetella	Q9k5g1 bordetella	Q9alp3 bordetella		0		Q9aix8 bordetella						088143 bordetella			_	Q9uvdl pneumocysti				Q93197 bordetella	Q9ull5 homo sapien	P93797 volvox cart	Q8s7y7 oryza sativ	091le9 rattus norv	Q8tly6 dictyostel1	069023 human herbe	Ol3305 pneumocysti	Q9rcx9 streptomyce
	09K5G4	Q9K5G1	Q9ALP3	Q9ALP7	Q9ALQ0	Q9ALP5	Q9AIX8	6M9S60	Q953M8	089860	Q9S6N1	069259	088143	093198	069257	Q8RSU0	090VD1	001823	09P944	096VI4	Q93L97	09ULL5	P93797	Q8S7Y7	Q9JLE9	Q8T1Y6	069023	013305	Q9RCX9
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	87.2	86.9	84.8	83.3	78.8	76.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	64.5	64.5	51.7	51.0	19.5	48.8	18.3	18.0	17.5	17.5	46.6	46.5	46.5	46.3	46.1
	259	258	252	247.5	234	227	212	212	212	212	212	212	212	212	191.5	191.5	153.5	151.5	146	145	143.5	142.5	141	141	138.5	138	138	137.5	137
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ALIGNMENTS

	is bronchisepticus). ision; Alcaligenaceae; Pertactin in Bordetella and Bordetella bronchiseptica."; 09D0238107 CRC64;	Gaps
	e; 11a hisept	07; 0;
	Borderial Proteobacteria; beta subdivision; Alcaligenecese; Bordetella. Bordetella. NCBLTaxID=518; (1) SEROUENCE FROM N.A. STRAIN=5; SEQUIENCE FROM N.A. STRAIN=5; BOLYMORPHISM Of Repeated Regions of Pertactin in Bordetella pertusis, Bordetella parapertussis, and Bordetella pertusis, Bordetella parapertussis, and Bordetella pertusis, Bordetella pertusis, Bordetella pertusis, Bordetella pertusis, Bordetella pertusis, Bordetella pertusis, and Bordetella bronchis. Intect. Immun. 68:4815-4817(2000). EMBL: A.0250081; CAB76435.1; - InterPro: IPR0004899; Pertact_sup. InterPro: IPR0004899; Pertact_sup. InterPro: IPR0004899; Pertact_sup. InterPro: IPR001265; Prich_extensn. Pfants; PR01217; PRICHEXTENSN. NON_TER 107 NON_TER 107 SEQUIENCE 107 AA; 11036 MW; 1AC13209D0238107 CRC64;	Length 107; Indels
nte) odate)	subdivision; Alcaligena subdivision; Alcaligena 96; ns of Pertactin in Bord siss, and Bordetella br 0). p	
107 AA. ence updē tation up	ronchi Dn; Al	DB 2 1.4e-1
107) quence notat:	nes bi ivisic f Pert , and	Score 297; DB 2; Pred. No. 1.4e-18; Mismatches 0;
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15, Cr 15, La 21, La nt).	10899 1 Reginater 17 (20) 17 (20) 17 (20) 17 (20) 17 (20) 17 (20) 18 (20) 18 (20) 19 (20) 10 (20) 10 (20) 10 (20) 10 (20) 10 (20) 10 (20) 10 (20) 1	100.0%; 100.0%; ive 0;
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T 1 5 99K5H5 PRELIMINARY; 909K5H5; 01-OCT-2000 (TEMBLrel. 15, 01-OCT-2000 (TEMBLrel. 15, 01-OTT-2002 (TEMBLrel. 21, Pertactin (P.689) (Eragment). PROPERTY.	Bacteria pronchiseptica (Alcaligenes bronchisepticus). Bacteria; Proteobacteria; beta subdivision; Alcaligenace Bordetella. NCBL_TaxID=518; [1] SEQUENCE FROM N.A. SERAIN=2015989; PubMed-10899896; SETAIN=2015989; PubMed-10899896; BOLISAUX-EUGE C., Guiso N.; FOLYMORPHISM OF Repeated Regions of Pertactin in Bordet pertusis; Bordetella parapertussis, and Bordetella bron Infect. Immun. 68:4815-4817(2000). EMBL; A.2550081; CAB76435-11; INTERPIC; IPR004899; Pertact_sup. INTERPIC; IPR002965; P.Ich_extensn. PRINTS; PR01217; PRICHEXTENSN. NOW_TER 107 AA; 11036 MW; IAC13209D0238107 CRC64;	ch Similarity 100. 52; Conservative
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1 1 5 5 09K5H5 09K5H5 01-0CT-2000 01-UCN-2002 Pertactin (CPRN)	Bacteria; Bacteria; Bacteria; Bordetella. NCBI_TaxID= (1) SEQUENCE FR STRAIN=5; STRAIN=5; STRAIN=6; BOLYMOPHI POLYMOPHI Infect! ism, Infect! ism, Infect! ism, InterPro; I InterPro; I InterPro; I Pfam; PF032 Pfam; PF032 NON_TER SEQUENCE	Match ocal S s 53
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Boursaux_Ende C., Guiso N.; Boursaux_Ende C., Guiso N.; Boursaux_Ende C., Guiso N.; Boursaux_Ende C., Guiso N.; pertussis, Bordetella parapertussis, and Bordetella parapertussis, and Bordetella parapertussis, and Bordetella parapertussis, and Bordetella parapertussis, natuso 1. Infect. Immun. 68:4815-4817(2000).

EMBL, AJ250085; CAB76439.1; -.

Enterpro, IPR004899; Pertuct_sup.
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                                                             DB 2; Length 109;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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bronchiseptica Pertactin.";
Embi. Ar007263; AAG38439.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR004895; Pertactin.
InterPro; IPR004895; Pertactin. 1.
                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQRQPEAPAPQPPAGRELSAA
0; Indels
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109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
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Pred. No. 1.1e-17;
0; Mismatches 0;
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PRINTS; PR01217; PRICHEXTENSN.
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ilarity 98.1%;
Conservative (
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Best Local Similarity
Matches 52; Conserv
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EMBL: AJZ45927; CABB2515.1; ...
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertactin.vir.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                          Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1197-1921(2001).
EMBL; ANO70271; AAG38447.1; InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
FinterPro; IPR018965; P. Frich_extensn.
Proj PR03121; Pertactin: 1.
PRINTS; PR03121; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNRAMLY.
SEQUENCE 911 Aa; 94093 MW; DF531A9EB4383A32 CRC64;
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Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 52; Conservative 0; Mismatches 0;
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Pred. No. 8.2e-18;
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MEDLINE=21117018; PubMed=11179374;
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100.0%;
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Best Local Similarity
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InterPro; IPR002965; P_rich_extensn.
                                   Pfam; PF03212; Pertactin; 1. PRINTS; PR01217; PRICHEXTENSN.
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Polymorphism of Repeated Regions of Pertactin in Bordetella
Perlumorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250087; CAB76441.1; -.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Prich_extensn.
Pf03212; Pertactin; I
                                                                                                                                                           Gaps
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"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
Submitted (JWN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF156773; AAP82397.1; ..
InterPro; IPR004899; Pertact_sup.
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                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 52
                                                                                          DB 2; Length 215;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%; Score 285; DB 2; Length 111; 92.9%; Pred. No. 1.5e-17; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                        Indels
                                5C21D45CF784B4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA; 11416 MW; 5140669692808F8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         09K5G9 PRELIMINARY; FKL; LLT.....
09K5G9;
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                       Query Match 96.5%; Score 286.5; DB 2; Best Local Similarity 98.1%; Pred. No. 1.9e-17; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BBCH;
MEDLINE-20359389; Pubmed-10899896;
   215
22327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 92.9 es 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111
   215 2
215 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella.
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Q9KJX9;
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                                                                                                                                                                                                                                                                                                                                                                                                     09K5G9
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                                                                                                                                                                                               42 GAKAPPARKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 97
                                                                                                                  . 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID-518;
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                                                                       Length 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 252
252 AA; 26107 MW; 368C142508D77057 CRC64;
                     122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-007-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P 68) (Fragment).
                                                                     Match 96.0%; Score 285; DB 2; L. Local Similarity 92.9%; Pred. No. 1.6e-17; les ; 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.0%; Score 285; DB 2. Best Local Similarity 92.9%; Pred. No. 3e-17; Matches 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       252 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dronchiseptica Pertactin.";
Infect. Immuh. 69:1917-1921(2001).
EMBL. ANGO7565, ARG38441.1;
Interpro; IPR003992; pertactin.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002965; Prich_extensn.
                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-21117018; PubMed-11179374;
Register R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
122
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Gaps

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Length 104;

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RESULT 10 **09K5H3**

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Boursaux-Ende C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250077; CAB76431.1;
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20359389; PubMed=10899896;

Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250079; CAB76433.1; ...

InterPro; IPR004899; Pertact_sup.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0170N-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                 104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.7%; Score 266.5; DB 2
94.2%; Pred. No. 5.2e-16;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 266.5; DB 2
Pred. No. 5.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                 MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.7%;
94.2%;
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NON_TER 104 104

SEQUENCE 104 AA; 10714 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                SEQUENCE FROM N.A.
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                         NCBI_TaxID=518;
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  Bordetella
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SEQUENCE
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Q9KJY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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09K5H7
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                      Boursaux_Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertusis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4615.4417(2000).
EMBL: AJ550089; CAB76443.1; Infect. Immun.geptica.min.geptica.min.geptica.min.geptica.min.geptica.min.geptica.min.geptica.min.geptica.geptica.geptica.min.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.geptica.gep
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 САКАРРАРКРА------РОРСРОРБРОРБРОРРОРРОРРОРРОРГОРГАРРАРИВИЕТСЯВ 52
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                                                                                                                                                                                                                                                                                                                                                                                 Score 284; DB 2; Length 111;
Pred. No. 1.8e-17;
0; Mismatches 0; Indels
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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86.7%; Pred. No. 2.3e-17;
tive 0; Mismatches 0; Indels
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                 111 AA; 11453 MW; 9B67012D3B9AEECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20359389; Pubmed-10899896; Boursaux-Eude C., Guiso N.;
MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                             PRINTS; PR01217; PRICHEXTENSN.
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                    95.6%;
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Best Local Similarity
Matches 52; Conserv
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Keil D.J., Fenwick B.;
Variability in the pertactin genes of Bordetella bronchiseptica variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR155772, ARF82396.1;
EMBL, AR156772, Pertact_sup.
Pfam; PP03212; Pertact_sup.
Pfam; PP03212; Pertactin; 1.
NON_TER 115 115
                                                                    Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                          89.7%; Score 266.5; DB 2; Length 115; 94.2%; Pred. No. 5.6e-16; 1ive 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 266.5; DB 2; Length 115;
Pred. No. 5.6e-16;
0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                  42 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQPPQRDPEAPAPQPPAGRELSAA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                             Submitted (JÜN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ARISG771; ARREA295.1; -.
InterPro; IPRO04899; Pertact_sup.
InterPro; IPRO02965; P_rich_extensn.
                                                                                                                                                                                                                                                115 AA; 11693 MW; FA3A76596F7097EB CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last anno
Pertactin (Fragment).
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Best Local Similarity 94.2%;
Matches 49; Conservative
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mes 49; Conserv
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             CBI_TaxID=518;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                      "Novel Genetic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
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94.2%; Pred. No. 8.7e-16;
Live 0; Mismatches 0;
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InterPro; IPR003992; pertactin.
InterPro; IPR004999; Pertact_sup.
InterPro; IPR004995; Pirch_extensn.
Pfam; PF03212; Pertactin; 1.
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                                                                                                                                                                        MEDLINE=21117018; PubMed=11179374;
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PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 198 198
SEQUENCE 198 AA; 20575 MW;
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Matches 49; Conservative
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Job time: 27.5758 secs
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  7, 2003, 16:31:28; Search time 30.6559 Seconds (without alignments) 256.453 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA
                GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Novel human diagno Sugar beet chitina Peptide BB05 deriv Streptococcus pneu Streptococcus pneu Herbicidally activ

AAW14573 AAW14569 ABB93838

AAW14570 AAW14574 ABB78538 AAE14305 ABB61362

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142 142 142 141.5 140.5

Database

AAW37148

AAO02124 ABG21919 AAR28150 AAR11739

ABG27250

Sugarcane proline Drosophila melanog Arabidopsis thalia Bioadhesive precur Mammallan Ena (Men

Streptococcus pneu Ser-Pro-Pro-Pro-Pr

Streptococcus pneu

Drosophila melanog Peptide 683 derive Novel human diagno Human polypeptide

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Novel Novel

ABB42321 ABG09876 ABG09877 ABB70063 AAR11737

ALIGNMENTS

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AAE16195 standard; peptide; 60

RESULT 1

B. bronchiseptica strain II-3 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II. Guiso-maclouf N, Boursaux-eude C; 25-MAY-2000; 2000US-206969P. 23-MAY-2001; 2001WO-EP06457 26-MAR-2002 (first entry) Bordetella bronchiseptica. (INSP) INST PASTEUR WPI; 2002-097639/13. WO200190143-A2. 29-NOV-2001 AAE16195;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

B. bronchiseptica
B. bronchiseptica
Bordetella paraper
Bordetella paraper
B. bronchiseptica
Pertactin antigen
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AAR25578 AAE16185 AAR14321 AAR16196 AAE16196 AAR16320

60 58 922 922 922 922 53 53 51 911

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331.5 298.5 298.5 294.5 283.5 274 267.5 267.5

AAE16195 AAE16198

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Query Match 1

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Description

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as blological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
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\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\overset{\circ}{\mathbf{x}}\over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Gaps
                                1;
    DB 23; Length 60;
                                0; Indels
96.9%; Score 331.5; DB 2.
98.3%; Pred. No. 1.6e-17;
Live 0; Mismatches 0
                               59; Conservative
    Query Match
Best Local Similarity
                               Matches
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1;

- 1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRQPPQRPPGREDAAA 60 1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59 à 셤
- AAE16198 standard; peptide; 58 AAE16198; RESULT 2

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26-MAR-2002 (first entry)

B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica,

WO200190143-A2.

29-NOV-2001.

91WO-GB02302 90GB-0027901

23-DEC-1991;

21-DEC-1990;

WO9211292-A.

(WELL) WELLCOME FOUND LID.

Charles IG;

WPI; 1992-250033/30. N-PSDB; AAQ26509.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

forPolypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Gaps
                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                               575.612 "contains 9 direct repeats of Pro-Gln-Pro" 712.712 "motte" "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                    260..262
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                            Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                        .;
m
                                                                                                                                                                                                                                                                  .285
.te= "contains 5 direct, tandem repeats"
                                       Length
                                                        Indels
                                                       ö
                                      Score 298.5; DB 2
Pred. No. 3.6e-15;
0; Mismatches 0
                                                                                                                                                                             Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                             AAR25578 standard; Protein; 922 AA
                                               95.08;
                                                                                                                                                                                                                                     35..643
/label- P70
                                                                                                                                                              (first entry)
                                    Query Match
Best Local Similarity 95.0°
Matches 57; Conservative
                                                                                                                                                                                                            Bordetella parapertussis.
                      58 AA;
                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                              08-JAN-1993
                       Sequence
                                                                                                                                              AAR25578;
                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                     Region
88.66
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comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen Acellular vaccine for immunisation against whooping cough -

Claim 1; Fig 1; 20pp; English.

recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the bamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (#P95) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kb. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino A cosmid library was constructed by transforming E.coli HB101 with

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Gaps

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Indels

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Mismatches

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Conservative

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SXC

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                    ÷
                                                                                                                                     DB 13; Length 922;
                                                                                                                                                                                                    Indels
                                                                                                                                 Score 298.5; DB 13;
Pred. No. 2.6e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
254..304
/note= "Pertactin region I"
/note= "Pertactin region II"
acids Pro577 to Pro612 or Ala574 to Pro612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16185 standard; Protein; 922
                                                                                                                                 87.3%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                              Best Local Similarity 95.0
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella parapertussis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-097639/13.
                                                                  922 AA;
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                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE16185;
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                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reg ton
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                  1 GAKAPPAPKAPAQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
1 GAKAPPASKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
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Pred. No. 6.7e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
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                                                                                                                                                                                                                       AAE16197 standard; peptide; 56
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Best Local Similarity 91.7%;
Matches 55; Conservative (
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                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2001.
                                                                                                                                                                                                                                                                                           AAE16197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR14321;
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Score 298.5; DB 23; Length 922; Pred. No. 2.6e-14;

87.3%; 95.0%;

Query Match Best Local Similarity

outer membrane protein; vaccine; Bordetella infection;

(first entry)

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B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                              therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                 AAE16196 standard; peptide; 53 AA.
                                                                                                                                                                                                                                                                                         23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                   25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                       Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-097639/13.
                                                                                                                                                               Pertactin; PRN;
                                                                                                                                                                                                                                   WO200190143-A2.
                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                              29-NOV-2001
                                                                            AAE16196;
                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. broochiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 283.5; DB 12; Length 922;
Pred. No. 3.1e-13;
0; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
                                                   Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                              595.597
                                                                                                                                                                                 281..285
/label= re-
75
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                                                                                                                                                                                                                                                              .s..585
/label= .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          510..612
/label= repeat
                                                                                                                                                                 label= repeat
                                                                                                                         266..270
/label- repeat
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Best Local Similarity 91.7%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90GB-0007416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-GB00487
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/label= r≏
20-JAN-1992 (first entry)
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7abel= re
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/label= re
                                                                                                                                                                               76..280
label= re
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Tabel = r
                                                                                Bordetella parapertussis.
                          Pertactin antigen P.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-325214/44.
N-PSDB; AAQ14320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1990;
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                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                     Peptide
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for

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                                                                                                                                                                                                                                 Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Bordetella bronchiseptica pertactin
Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

80.1%; Score 274; DB 23;
Best Local Similarity 86.7%; Pred. No. 1.9e-13;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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Gaps ; ;

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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPRPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 78.2%; Score 267.5; DB 23; Length Similarity 85.0%; Pred. No. 5.5e-13; 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; Pichia; B. pertussis; B. parapertussis.
therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
266..270
/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR14320 standard; Protein; 911 AA
                                                                                                                                                                                                      Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                    Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /1abel repeat
574..576
/label repeat
578..580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271..275
/label- repeat
                                                                                                               23-MAY-2001; 2001WO-EP06457.
                                                                                                                                          25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica.
                           Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin antigen P.68
                                                                                                                                                                       (INSP ) INST PASTEUR
                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                    Suiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AA;
                                                     WO200190143-A2
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                                                                                  29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR14320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively, or the B. pertussis P.59 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.2%; Score 267.5; DB 12; Length 911; 85.0%; Pred. No. 4.3e-12; 1ve 0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
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/label- RGD_tripeptide
701..703
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/label= Repeat_region
260..262
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/label= Repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1B; 38pp; English
            581..583
/label- repeat
584..586
/label- repeat
                                                                                                                                                                                                                                                                                                                                                       (WELL ) WELLCOME FOUNDATION LTD.
                                                                                           587..589
/label= repeat
599..601
/label= repeat
/label= repeat
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/label= P.68
                                                                                                                                                                                                                                                                             91WO-GB00487.
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Best Local Similarity 85.09
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sordetalla bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                             Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prn proteins.
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                                                                                                                                Peptide
                  Peptide
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                                                                                             Peptide
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The present invention relates to Bordetella bronchiseptica pertactin (cuter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, alycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as autigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the Bordetella in a materials can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.2%; Score 267.5; DB 2
85.0%; Pred. No. 4.3e-12;
ive 0; Mismatches 0
                                                                                                                                                                                                              Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boursaux-eude C;
Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 85.0 nes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guiso-maclouf N,
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica pertactin outer membrane protein, p.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 267.5; DB 13; Length 911; Pred. No. 4.3e-12; 0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
254..299
/note- "Pertactin region I"
559..610
/note- "Pertactin region II"
/label- RGD_tripeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 28pp; English.
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                                                                                                                                       92WO-GB00561
                                                                                                                                                                                      91GB-0006568
                                                                                                                                                                                                                                 (WELL ) WELLCOME FOUND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entire P.94 sequence
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                                                                                                                                                                                                                                                                                                                           WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
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                                                                                                                                                                                      27-MAR-1991;
                                                                                                                                          27-MAR-1992;
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                                              W09217587-A
                                                                                         15-0CT-1992.
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                                                                                                                                                                                                                                                                               Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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Region
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Gaps

DB 23; Length 911;

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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodsical and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKVPPAPKPAPKPAPGPGPQP-----PQP-PQPPQPQPQPQPQPQPQPGPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPPQPPQP-PQPPQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                     Score 249.5; DB 23; Leuy...
Pred. No. 1.1e-11;
Transparents 3; Indels
                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                  ch 73.0%;
1 Similarity 81.7%;
49; Conservative
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          54 AA;
                                                                                                                                                                                                                                                            Sequence
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 B. bronchiseptica strain II-1 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. Ş AAE16193 standard; peptide; 49 26-MAR-2002 AAE16193; RESULT a

Guiso-maclouf N, Boursaux-eude C; 25-MAY-2000; 2000US-206969P 23-MAY-2001; 2001WO-EP06457 Bordetella bronchiseptica WO200190143-A2 INSP) INST 29-NOV-2001

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

WPI; 2002-097639/13

for

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens an infinity chromatographic columns. Pertactin is useful as antigens and infinity chromatographic columns. Pertactin is useful as antigens and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. The present invention relates to Bordetella bronchiseptica pertactin

49 AA; Sequence

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AAE16199 standard; peptide; 48

RESULT 15

AAE16199 ID AAE1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin (outer membrene protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used to detect Bordetella antigens in biological preparations or in used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    B. bronchiseptica strain II-θ pertactin outer membrane protein region II.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                            Pertactin; PEN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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     Length 49;
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Pred. No. 3.4e-11;
1; Mismatches 3;
 Score 247; DB 23;
Pred. No. 1.6e-11;
                   Pred. No. 1.66
0; Mismatches
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                                                                                                                                                                                     AAE16200 standard; peptide; 52
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Llarity 81.4%;
Conservative
 72.2%;
80.0%;
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                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica.
Query Match
Best Local Similarity 80.0
Matches 48; Conservative
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                WO200190143-A2.
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                                                                                                                                                        RESULT 14
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AAE16199;

26-MAR-2002 (first entry)

B. bronchiseptica strain II-7 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Claim 26; Fig 1c; 47pp; English.

Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the artigens can be used for qualitative or quantitative determination of Bordetella in a materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin Bordetella bronchiseptica present invention relates to

48 AA; Sequence Score 240.5; DB 23; Length 48; Pred. No. 4.5e-11; 0; Mismatches 0; Indels 13; Gaps Ouery Match 70.3%; Best Local Similarity 78.3%; Matches 47; Conservative (

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1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59

ò a Search completed: May 7, 2003, 16:47:06 Job time : 31.6559 secs

us-09-855-754b-16.rai

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RESULT 1
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Sequence
Sequence
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                                                                                                                                                                                                                                              GAKAPPAPKPAPQPGPQPGP.......PQRPEAPAPQPPAGRELSAA
              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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seq length: 200000000
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Maximum DB s
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Sequence 29, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 12, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 16, Appl
Sequence 16,
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Sequence
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ZIP: 22201
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBE: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORIEY/ACBT INFORMATION:
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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US-09-535-008-65
US-09-535-008-77
US-09-535-008-73
US-09-041-886-28
US-09-041-886-29
US-09-041-886-31
US-08-246-982A-6
US-08-457-2738-42
US-08-457-2738-42
US-08-457-2738-42
US-08-457-2738-42
US-08-457-2738-42
US-08-6419-21
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-08-453-265-16
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Pred. No. 2e-18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            -09-041-886-15
-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-348-518C-4
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5470718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 32201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 87.3%;
Best Local Similarity 95.0%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
       1679
1681
1682
513
513
552
589
3144
3144
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3119
3119
366
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APPLICATION NUMBER: US/08/460,269C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY 1990
                                                                                                                                    TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           LENGTH: 910 amino acids
                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.18;
                                                                                                                                                                                                                                                                                                                                                                59.5%;
69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                Query Match 59.59
Best Local Similarity 69.59
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUSAN I.; MCCANDLISS, RUSS; WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No. 5202236
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5202236-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.2%; Score 267.5; DB 4; Length 911;
85.0%; Pred. No. 8.2e-16;
1.ve 0; Mismatches 0; Indels 9
                                                                                  GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROFEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                             Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REPERBECE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Ze
STREET: 2200 Clarendon Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                            Sequence 4, Application US/08460269C Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 911 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
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                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703)
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                                                                                                                                                                                                                                                                                                                                  22201
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Matches 51; Conserv
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4 APPAP------KPA-PQPGPQ--PGPQPGPQPPQPPQPPQPPQRPEAPAPQPP 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, N L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ** APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                        Score 203.5; DB 4;
Pred. No. 2.1e-10;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
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Pred. No. 1.9e-05;
0; Mismatches 19
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-M2-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
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Gaps

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NAME: Wilson, Mary J
REGISTRATION NUMBER:
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LENGTH: 490
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                                                                                                                                                                                4 APPAP------KPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPP 51
                                                                                                                                              11;
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                                                                                                          Length 331;
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                                                                                                      Score 138.5; DB 6; Length 3 Pred. No. 2.8e-05; 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
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Pred. No. 0.00014;
1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09095443
Patent No. 6342593
GENERAL INFORMATION:
APPLICANT: Poleman, Gregory
APPLICANT: Poles, Elor
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SECURANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.6 FOR MEDIUM TYPE: 3.6 MEDIUM TAPE. THE SETEM FOR WINDOWS 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/049,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 23 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3310
INFORMATION FOR SEQ ID NO: 2:
                                                                                                      40.5%;
illarity 44.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FILING DATE: 13-SEP-1984
;SEQ ID NO.37:
; LENGTH: 331
5202236-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 QPP--QPPQRPEAPAPQP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-095-443-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Los Angeles
California
                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/237,716
FILING DATE: US/08/237,716
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                4-Glucanases From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.2%; Score 134; DB 4; Best Local Similarity 45.1%; Pred. No. 9.3e-05; Matches 23; Conservative 8; Mismatches 18
                                                                     APPLICANT: Bjornvad, Mads E.
APPLICANT: Bjornvad, Matsin Martin
APPLICANT: Schilein, Martin
APPLICANT: Schilein, Martin
TITLE OF INVENTION: Endo-Beta-1, 4-Glucanas
TITLE OF INVENTION: Saccharchrix
TITLE OF INVENTION: Saccharchrix
TITLE OF INVENTION: Saccharchrix
CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 0812/97
EARLIER APPLICATION NUMBER: 0846/97
                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-07-11
EARLIER APPLICATION NUMBER: 60/053,506
BEARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fast;5EQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LIPSCOMBE, MARTIN J
APPLICANT: CHARLES, IAN G
APPLICANT: FAIRWEATHER, Neil F
IITLE OF INVENTION: FUSION PROTEINS
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Saccharothrix australiensis
US-09-109-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11.-UN-1992
APPLICATION NUMBER: GB 9112553.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence |11, Application US/08237716
Patent No. 5589384
GENERAL INFORMATION:
Sequence 2, Application US/09109841
Patent No. 6207436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDAN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201
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Gaps

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1 САКАРРАРКРАРОРОРОРОРОРОРОРОРОРОРОРОРОРОВРОЯ
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                                                                                                                                                              Length 60;
                                                     Length 60;
                                                                                                                                                                                                                                                                                                         APPLICANT: Fields, Gregg B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned,
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CAPPELLO, JOSEPh
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,140
FILING DATE: US/03/JUL-1996
CLASSIFICATION: 5.25
                                                   Score 130.5; DB 1;
Pred. No. 3e-05;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 130.5;
Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5726243west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 525
CRASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILIAN DATE: 30-JUN-1993
AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08642255 Patent No. 5773249 GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Sequence 12, Application US/08675140 Patent No. 5726243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 612-332-5300
                                                   38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 60 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Conservative
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
 unknown
                                                     Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 26; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
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; TOPOLOGY:
US-08-534-342-12
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US-08-642-255-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fields, Gregg'B.
TILE OF INVENTION: Mild Solid-Phase Synthesis of Aligned, NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 132.5; DB 1
Pred. No. 1.2e-05;
3; Mismatches 2
                                                                                                                                                                                                                                                         /label= LTB sequence
                                                                                                                                                                                                                                                                                                                                /label= hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 PGPQPGPQPPQPPQPPQPPQRPEAPAPQP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 600.253-US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Merchant & Gould
3100 No. 5576419west Center
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08534342
Patent No. 5576419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,977
                   TELECOMMUNICATION INFORMATION TELEPHONE: 703-816-4000
                                                   TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%;
69.7%;
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.79
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mueting, Ann M. REGISTRATION NUMBER:
                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region
COCATION: 10.31
COTHER INFORMATION:
US-08-237-716-11
                                                                                                                                                                                                                                        LOCATION: 1..2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                           LOCATION: 4..7
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                            NAME/KEY: Region
                                                                                                                                                                                                                     NAME/KEY: Region
                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Fields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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1 GAKAPPAPKPAPQPGPQPGP--QPGP----QPG-PQPPQPPQPPQRPEAPAPQPPA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65, Application US/08475411A
Patent No. 6140072
GENERAL INFORM/TION:
APPLICANT: Ferrari, Franco A.
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San'Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IIBM PC compatible
OPERATING $YSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                      REFERENCE/DOCKET NUMBER: A 55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-398-3249
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: alliear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CT-1987
PRIOR MAPPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/ASGNT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/475,411A FILLING DAFF: 07-2/04-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/609,716 PILLING DATE: 06-NOV-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/269,429 FILING DATE: 09-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  MOLECÜLE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-475-411A-65
                                                                                                                                                                                                                                                                                         us-07-609-716-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 130; DB 1; Length 330;
Pred. No. 0.00014;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPENDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400 n Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING_DATE: 1
                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELEPHONE: (415) 494-870
TELEPHONE: (415) 494-870
TELEFAX: (415) 494-8771
TELEFEX: (10 277299 FHT UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secure 65, Application US/07609716; Sequence 65, Application US/07609716; Patent No. 5514581; GENERAL INFORMATION:
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.0%;
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NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 330 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 47.5
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                        California
                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
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6 PAPKPAP-OPGPOPGP-OPGPOPGPOPPOP----PAGREL 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 160, Application US/08961083
Fatent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 641;
                                                                                                                                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                   Score 130; DB 4;
Pred. No. 0.00017;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 7, 2003, 16:57:17
Job time: 10.8405 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                               38.0%;
47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 166
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
                                                            Query Match
Best Local Similarity 47.57
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: slu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-961-083-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-961-083-160
      US-08-478-029A-65
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8
                                                                                                                                                                                                                                                           Length 408;
                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
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PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

GE-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 07/269,429

FILING DATE:

OF NOV-1988

PRIOR APPLICATION NUMBER:

TELING DATE:

APPLICATION NUMBER:

GO-NOV-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

TELING DATE:

APPLICATION NUMBER:

REGISTATION NUMBER:

NAME:

TECCOMMONICATION INFORMATION:

REGISTATION NUMBER:

TELECOMMUNICATION INFORMATION:

REGISTATION NUMBER:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           Score 130; DB 4;
Pred. No. 0.00017;
0; Mismatches 24
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APPLICATION NUMBER: US/08/478,029A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-478-029A-65
Equence 65, Application US/08478029A
; Patent No. 6184348
                                                                                                                                                                                                                                                           Query Match 38.0%;
Best Local Similarity 47.5%;
Matches 29; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                    single
                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-411A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                   TYPE: amino acid
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                                                                                              STRANDEDNESS:
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OM protein – protein search, using sw model

7, 2003, 16:53:34; Search time 17.6899 Seconds (without alignments) 306.927 Million cell updates/sec Мау Run on:

Title: Perfect score:

US-09-855-754B-16 342 I GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 59 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

349150 seqs, 92025710 residues Searched:

349150 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA: Database :

/cgn2_6/ptodata///pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:/ /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: ptodata/2/pubpaa/US08_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	9 Seguence	Sequence 19,	Sequence	3 Sequence 18	_		Sequence 4.	Sequence 22. Appl	14	1 Sequence 21,	20,	3 Sequence 23,	Sequence 5, A	24	Sequence 2,	Sequence 43.	13		Sequence 2, Appli
ID	US-09-855-754-1	US-09-855-754-1	US-09-855-754-6	US-09-855-754-1	US-09-855-754-17	US-09-855-754-1	US-09-855-754-4	US-09-855-754-2	US-09-855-754-1	US-09-855-754-2	US-09-855-754-2	US-09-855-754-2	US-09-855-754-5	US-09-855-754-2	US-09-823-240-	US-09-976-740-43	: US-10-023-529-	US-10-023-523-43	us-09-959-987-2
% Query Match Length DB	59 9	58 9	922 9	56 9	52 9	52 9	911 9	54 9	49 9	52 9	48 9	42 9	910 9	39 9	802 10	538 9	538 12	538 12	641 9
& Query Match I	100.0	87.3	87.3	86.1	83.2	78.2	78.2	73.0	72.2	70.9	70.3	59.5	59.5	53.5	40.9	40.1	40.1	40.1	39.8
Score	342	298.5	298.5	294.5	284.5	267.5	267.5	249.5	247	242.5	240.5	203.5	203.5	183	140	137	137	137	136
Result No.	1	7	m	4	Ŋ	9	7	æ	o	10	11	12	13	14	15	16	17	18	19

	Sequence 1002, Ap	Sequence 1002, Ap	Sequence 2, Appl1	٠,	Sequence 47. Appl	Sequence 47, Appl	4 .	70.	160.	App		_	Sequence 34988. A	Sequence 36844, A		Sequence 4. Appli		Sequence 967. App	Sequence 17, Appl	Sequence 10936, A	Sequence 61, Appl	Sequence 1, Appl1	Sequence 60. Appl	Sequence 43644. A	10.	Sequence 125, App	
	9 US-09-925-299-1002	70 OF-662-526-60-SD OT	9 US-10-020-215-2	9 US-09-976-740-47	12 US-10-023-529-47	12 US-10-023-523-47		-	10 US-09-765-272-160	9 US-10-171-384-3	9 US-09-298-523B-62	9 US-09-298-523B-2		10 US-09-864-761-36844	9 US-10-043-487-282	9 US-09-824-574-4		10 US-09-764-864-967	D		9 US-09-298-523B-61	9 US-09-298-523B-1	_	10 US-09-864-761-43644	10 US-09-823-240-10	9 US-10-072-036-125	
į	40	04	1274	550	550	550	274	999	. 641	827	701	707	171	171	416	1647	1543	316	274	1333	069	691	929	132	380	635	
	א מ מ	ر د د د د	39.B	39.6	39.6	39.6	39.0	38.2	37.6	37.6	37.4	37.4	37.1	37.1	36.7	36.4	36.3	36.1	35.8	35.7	35.4	35.4	35.4	35.1	34.9	34.9	
, ,	95.	0 C	136	135.5	135.5	135.5	133.5	130.5	128.5	128.5	128	128	127	127	125.5	124.5	124	123.5	122.5	122	121	121	121	120	119.5	119.5	
ć	2 6	7 0	7.7	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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TITLE OF INVENTION: POLYPEPIDE CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELA PERTUGSIS, TITLE OF INVENTION: BORDETELA PERTUGSIS, AND BORDETELA TITLE OF INVENTION: BORDETELA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 1205-00000

CURRENT PILLING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
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100.0%; Score 342; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bordetella bronchiseptica
US-09-855-754-16
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,969
Sequence 16, Aprilication US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Aprilication US/09855754 Publication No. US20020192237A1
                                                                              APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                          GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                          2000-05-25
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 16
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US-09-855-754-15
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BUISS-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PROFIDED FERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN PILE REFERENCE: 03495-0206-00000
CURRENT PELLOR NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                 TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGLISEPTICA, THEIR USE IN DIAGNOSTICS, AND FILLE OF INVENTION: IMMUNOCENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTIN VOR: 2.1
REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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Pred..No. 1.2e-13;
0; Mismatches 0;
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Pred. No. 1.1e-12;
0; Mismatches 0;
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95.0%;
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Best Local Similarity 95.0%;
Matches 57; Conservative
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Best Local Similarity
Matches 57; Conserv
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LENGTH: 58
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GENERAL INFORMATION:
APPLICANT: BOURSANTON:
APPLICANT: BOURSANTS EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PAPERRUSSIS,
TITLE OF INVENTION: BORDETELLA PAPERRUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, PHEIR USE IN DIAGNOSTICS, AND IN
FILLE REPEATENCE: OS495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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Pred. No. 8.7e-13;
0; Mismatches 0;
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Pred. No. 2.1e-13;
0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/855,754
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PRIOR FILING DATE: 2000-05-25
                                                      60/206,969
                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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Sequence 17, Application US/09855754
; Publication No. US20020192237A1
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Best Local Similarity 91.7%;
Matches 55; Conservative (
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Best Local Similarity 88.1%;
Matches 52; Conservative (
                                                                            2000-05-25
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05
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PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 24
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Gaps

SOFTWARE: PatentIn Ver. 2.1

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PRETACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNIOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: INMUNICORDIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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                                                   Length 54;
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                                                   DB 9;
                                              Score 249.5; DB 9
Pred. No. 1.7e-10;
1; Mismatches 3
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Pred. No. 2.2e-10;
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATE: NOS: 2.1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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US-09-855-754-14
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US-09-855-754-21
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Sequence 14, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUSSAUX: EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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                                              73.0%;
81.7%;
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Best Local Similarity 80.0%
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                                              Query Match
Best Local Similarity
Matches 49; Conserv
US-09-855-754-22
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: U5/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                    DB 9; Length 52;
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Pred. No. 1.1e-10;
0; Mismatches 0;
                                                                                                                                                               Score 267.5; DB 9;
Pred. No. 1.1e-11;
0; Mismatches 0;
                                                                                    ) ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
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Publication No. US20020192237A1
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Publication No. US20020192237A1
GENERAL INFORMATION:
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ilarity 85.0%;
Conservative (
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1 Similarity 85.0%;
51; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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SOFTWARE: Patentin Ver. 2
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Best Local Similarity
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                                         LENGTH: 52
TYPE: PRT
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LENGTH: 54
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US-09-855-754-24
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US-09-823-240-2
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LENGTH: 39
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNIOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                          APPLICANT: GUISO-MACLOUF, NICCLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 020206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
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Pred. No. 1.3e-07;
1; Mismatches 0;
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Pred. No. 5.8e-10;
0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
                                                                                                                                                       Sequence 20, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                          CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.58;
69.58;
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Best Local Similarity 78.3%;
Matches 47; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 41; Conserv
                                                                                                          RESULT 11
US-09-855-754-20
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US-09-855-754-23
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGGRIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPETER AND BORDETEL PARAPETER AND BORDETELLA PARAPETER PARAPETER AND BORDETER AND BORDETER AND BORDETER PARAPETER 
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Pred. No. 1.5e-06;
1; Mismatches 0;
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64.4%; Pred. No. 2.6e-06;
iive 1; Mismatches 0
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
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Sequence 5, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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; Patent No. US20020048813A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754-5
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Best Local Similarity 69.5%;
Matches 41; Conservative
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Best Local Similarity 64.4
Matches 38; Conservative
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outer membrane pro
hypothetical prote
proline-rich prote
hypothetical 47.8K
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68K outer membrane
                                                                       7, 2003, 16:41:02 ; Search time 11.0562 Seconds (without alignments) 513.008 Million cell updates/sec
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                                                                                                                         US-09-855-754B-16
342
1 Garappapkpapgpgpgp.....ppgrpeapapgppagrelsaa 59
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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A32560
AE2295
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A33647
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2: pir2:*
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•							ALIGNMENTS	
		RESULT 1 S15204 pertactin - Bordetella parapertussi N; Alternate names; outer membrane C; Species: Bordetella parapertussis C; Date: 07-Apr-1994 #sequence_revisis C; Accession: S15204; S14659 MOI. M.Croblol. 5, 409-417, 1991 A; Title: P.70 pertactin, an outer-n A; Reference number; S15204; MUID:91 A; Accession: S15204 A; Molecule type: DNA A; Residues; [1-922 < CILL>A; Cross-references: EMBL:X54547; NI C; Genetics: C; Genetics: C; Keywords: membrane protein	Borde Borde Aprile Borde Borde Aprile Douge 5101. 5101	atella p. s.; outer. (1941) a pa. 994; s.141 a pa. 994; s.141 a pa. 994; s.141 a pa. 994; s.152 a pa. 994; s.152 a p. 604 a pa. 994; s.152 a p. 604	araper membi rapert uence_ 659 659 novoti 17, 15 an ov 04; MC	rtus rane tuss russ russ russ Jy, Jy, J91 lter JID:	rotein P70 sion 07-apr-1994 #text charles, I.G. cembrane protein from [251771; PMID:2041476 ID:g39761; PIDN:CAA384	_change 08-Oct-1999 Bordetella parapertussis: clo 19.1; PID:g39762
		Ouery Match Best Local Matches 5	tch al Sim: 57;	h Similarity 95 57; Conservativ	87.3%; 95.0%; ative	.; .; .; .;	Score 298.5; DB 2; Length Pred. No. 1.6e-12; 0; Mismatches 0; Indels	gth 922; els 3; Gaps 3;
		Oy 1 (SAKAPPA SAKAPPA	apkpapop apkpapop	SPOPGE SPOPGE	00 - do	GAKAPPAPKPAPOPGPOPGPOPGPOPGPOPPOPPOPPOPPOR-PEAPAPOPPAGRELSAA 	POPPAGRELSAA 59 POPPAGRELSAA 621
		RESULT 2 A47675 68K outer membrane C;Species: Bordete C;Species: Bordete C;Staces: 19-Dec-199 C;Accession: A4767 A;Title: Cloning, A;Title: Cloning, A;Accession: A76731 A;Contents: Contents A;Coss.reference Coury Match Best Local Similia Matches S1; Cq	membrane pr Bordetella 	mbrane protein P.68 p cordetella bronchisept lec-1933 #sequence_rev A47675 A47675 ming, nucleotide sequ number: A47675; MUID: CN7531 A47675 eliminary ype: nucleic acid eliminary ype: nucleic acid 1-911 < LIL> Similarity 85.0%; Similarity 85.0%; 51; Conservative	in P.6 onchis uence. F.; N 1697-1 tide s 75; Mu acid acid 85.0 185.0	Sept Lyos Sept Lyos Lyos Sept Lyos Sept Lyos Sept Lyos Sept Lyos Lyos Lyos Lyos Lyos Lyos Lyos Lyos	RESULT 2 A47675 68 couter membrane protein P.68 pertactin - Bordetella bronchiseptica C; Species: Bordetella bronchiseptica C; Species: Bordetella bronchiseptica C; Date: 19-Pec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct C; Accession; A47675; Novotny, P.; Dougan, G.; Charles, I.G. R; Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. A; Title: Cloning, nucleotide sequence and heterologous expression of the A; Reference number: A47675; MulD:92407314; PMID:1527510 A; Contents: CN7331 A; Accession; A47675; MulD:92407314; PMID:1527510 A; Conservation: A47675 A; Status: prediminary A; Molecule type: nucleic acid A; Residues: 1-911 < Li.> A; Cross - references: GB:X54815; GB:S46416; NID:939396; PIDN:CAA38584.1; A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113 Query Match Best Local Similarity 85.0%; Pred. No. 1.5e-10; Batches 51; Conservative 0; Mismatches 0; Indels 9; G [- Bordetella bronchiseptica Nov-1994 #text_change 08-Oct-1999 Dougan, G.; Charles, I.G. heterologous expression of the protective o PMID:1527510 NID:939396; PIDN:CAA38584.1; PID:939397 cone (NCBIN:113318, NCBIP:113319) 7.5; DB 2; Length 911; t. 1.5e-10; tches 0; Indels 9; Gaps 2; PPOPPORPORPREAPAROPPAGRELSAA 59

pherophorin-S - vo hypothetical proli sulfated surface g UL36 protein - hum hypothetical prote cysteine-rich exte cysteine-rich exte proline-rich prote

S21961 EDBEIF

156.5 154.5 153.5 150.5 149.5

149 149 148.5 148.5

147 146.5 146

immediate-early pr proline-rich prote hypothetical prote protein-tyrosine-p nuclear protein EB T20HZ.9 protein -proline/lysine-ric proline-rich prote ORF2 protein - sai

proline-rich prote chitinase (EC 3.2. proline-rich prote

proline-rich prote proline-rich prote procyclin homolog ~

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Gaps

13;

Length 449;

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C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2201
R;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocyst
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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Ridodi, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A.Title: Differential targething of closely related ECM-glycoproteins: The pherophorial A.Reference number: 21154; MUID:97162277; PMID:9009264
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Rolecule type: MRNA
A.Residues: 1-599 <GODD>
A.Residues: 1-599 <GODD>
A.Residues: 1-599 <GODD>
A.Experimental source: EMBL:Y07752; NID:91655698; PIDN:CAA69032.1; PID:91655699
A.Experimental source: strain HK 10; sub_species Nagariensis
A.Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C; Keywords: extracellular matrix; 91ycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10798
                                                                                                                                                                                                                                                                                                              255 PPPPPPPRPERQPQPETQPPQPPQPPQPPQSETQPETQPETPEPEPEPEPE 314
                                                                                                                                                                                                                                                                          -----PQPGPQPGPQPPQPPQPPQRPEAPAPQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 161; DB 2; Length 43
Pred. No. 0.00046;
1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 РРАРКРАРОРСРОРСРОРСРОРСРОРСРОРРОРРОРРОВРАРОРР 51
                  A;Residues: 1-449 <ROB>
A;Cross-references: EMBL:X60376; NID:g22596; PID:g22597
                                                                                                                           Score 161.5; DB 2;
Pred. No. 0.00044;
4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 161; DB 2;
Pred. No. 0.0006;
2; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical 47.8K protein - Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 PKPAPQPGPQPGPQPGPQPGPQPPQPPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
47.1%; Score 161; DB
Best Local Similarity 50.0%; Pred. No. 0.00
Matches 32; Conservative 1; Mismatches
                                                                                                                           47.2%;
llarity 45.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%; 55.3%;
                                                                                                                                                                                                                                                                  3 KAPPAPKPAPQPGPQPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.3.
The 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carteri
                                                                                                                    Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-430 <WAD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JC2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 POPP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||
| PP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 POPP 51
                                                                                                                                                                                                                                                                                                                                                                                                     50 PP 51
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Nakazaki, N.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A.; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                    C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number, A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proline-rich protein - rape (fragment)
(Species: Brasalca napus (rape)
(S.Species: Brasalca napus (rape)
(S.Species: 13-3na-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
(S.Accession: S16748
(S. Robertz, M. R.; Foster, G. D.; Blundell, R. P.; Robinson, S. W.; Draper, J.; Scott, R.J.
(S. Robertz, M. R. Foster, G. D.; Blundell, R. P.; Robinson, S. W.; Draper, J.; Scott, R.J.
(S. Robertz)
(S. M.; Foster, G. D.; Blundell, R. P.; Robinson, S. W.; Draper, J.; Scott, R.J.
(S. Robertz)
(S. M.; Foster, G. D.; Blundell, R. P.; Robinson, S. W.; Draper, J.; Scott, R.J.
(S. Robertz)
(S. M.; Foster, S. S. M.; September, S. M.; Septem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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A.Molecule type: DNA
A.Residues: 1-383 <KUR>
A.Crossreferences: GB:BA000019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179
A.Experimental source: strain PCC 7120
C.Genetics:
559 GAKAPPAPKPA-----PQPGPQPGPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
K)Note: It is uncertain whether Met-1 or Met-3 is the initiator
C;Keywords: membrane protein
F:1-34/Domain: alguence #status predicted <SIG>
F:35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29

    САКАРРАРКРАРОРОРОРОРОРОРОРОРОРОРОРОРОРОВРАРАРОРРАСКЕЦЅАА

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein all3916 [imported] – Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 РРАРКРАРОРСРОРСРОРСРОРСРОРРОРРОРРОРРОВЕЛЬТЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 161.5; DB 2;
Pred. No. 0.00039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 203.5; DB 2;
Pred. No. 1.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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69.5%;
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                                                                                                                                                                              outer membrane protein P.69
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Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A32560
A; Molecule type: DNA
A; Residues: 1-910 <CHA>
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Matches 27; Conserv
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                                                                                                         RESULT 3
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20;

Length 430;

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Gaps

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19; Indels

Length 599;

us-09-855-754b-16.rpr

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ж.д., г., г.

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A; Molecule _type: mRNA
A; Residues: | 1-209 | <MNA
A; Cross-references: GB:L11439; NID:g310922; PIDN:AAA34059.1; PID:g310923
A; Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
R; de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A; Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A; Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine-rich extensin-like protein 1 precursor - common tobacco C;Species: Micotlana tabacum (common tobacco)
C;Date: 26-May-1994 #sequenc_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A4823:2; p00475; S24617
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. SCI. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE004091; NID:g9946031; PIDN:AAG03586.1; GSPDB:GN
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C; Keywords: cell vall; extracellular matrix; fertilization; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <WAT>
F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                   P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                  hypothetical protein PA0197 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AKAPPAPRPAPRPAPQPGPQPGPQPGPQ-----PPQPPQPPQPPQRPEAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: H83619
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, ...; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
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                                                          4
                                                                                                                                        Length 209;
        Length 3164;
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                                                                                                           PAPKPAPOPGPOPGPOPGPOP-POP-POP-POP-POPPORPEAPAPOPPAG
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A;Experimental source: stigma, style; strain Petit Havana SR1
                                                          11;
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48.2%; Pred. No. 0.00051;
ative 4; Mismatches 16;
  Score 158; DB 1;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 157; DB 2;
Pred. No. 0.00058;
4; Mismatches 17
                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain PAO1
C; Genetics;
A; Gene: PAO197
C; Superfamily: tonB protein
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%;
ilarity 50.0%;
Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Readiues: 1-270 < STO>
A, Cross-references: GB:AE004458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.29
Matches 27; Conservative
                                                       Conservative
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A; Residues: 39-209 <GOL>
Query Match
Best Local Similarity
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Matches 29; Conserv
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A; Status: preliminary
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                                                          Matches
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                                                                        C; Species: Owenia fusiformis
C; Date: 07-Un-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C; Accession: A34043; B34043 B34043 B34043
R; Bakalara, N.; Collet, J.: Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A; Title: Presence in invertebrate genomes of sequences characterized by the repetition A; Reference number: A90159; MUID:90147742; PMID:2105723
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A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WMBEH6
Ulj6 protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Caccession: 130085
S;McGech, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, J. Gen. virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of he A;Reference number: A30083; MUID:88274327; PMID:2839594
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                                                       hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Volvox carteri
C;Species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A3364, R; Wenzl, S; Engel, J; Sumper, W.
J; Cell Biol. 109, 3493-3501, 1989
A;Filte: The extracellular matrix of Volvox carteri: molecular structure of
A;Reference number: A33647; MUID:90094551; PMID:2689458
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C;Keywords: glycoprotein
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Pred. No. 0.00079;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR
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C;Superfamlly: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 158; DB 2;
Pred. No. 0.00031;
0; Mismatches 23
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sulfated surface glycoprotein 185 – Volvox carteri
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5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 46.2%;
Local Similarity 54.0%;
nes 27; Conservative
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1.141 <BAK>
A; Cross references: GB:M32217
A; Accession: B34043
                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
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Length 1460;

DB 1;

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A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies A;Reference number: S04713; MUID:89315207; PMID:2546124
                                                             .mmediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser); Species: suid herpesvirus 1
                                                                                                                                       C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PAPKPAPQPG------PQPGP--QPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 150.5; DB 1;
Pred. No. 0.0054;
4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 7, 2003, 16:55:25
Job time: 12.0562 secs
                                                                                                                                                                                        C; Accession: S04713
R; Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.2%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1460 <CHE>
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                                                                                                                                                                                                                                                                               Cysteine-rich extensin-like protein 2 precursor - common tobacco (Species: Nicotiana tabacum (common tobacco) (Cyate: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000 (Cyacession: B40232; P00474; S24616 (Cyacession: B40232; P00474; S24616 (Cyacession: B40232; P00474; S24616 (Cyacession: B40232; P00474; S24616 (Cyacer Call Way) (Cyace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Title: Developmental expression of tobacco pistil-specific genes encoding novel extens
A/Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proline-rich protein APG - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 (C.Accession: S21961 (C.Accession: S21961 (C.D.) Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. R.Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. A.Bescription: Cloning and characterization of a proline-rich gene expressed specificall A.Reference number: S16748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: glutelin
C;Reywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 *status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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                                                51
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             --PPOPPQRPEAPAPQPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 154.5; DB 2; Length 1
Pred. No. 0.00066;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 PAPKPAPQPGPQPGPQPGPQP-PQPPQPPQPPQRPEAPAPQPPA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 153.5; DB 2;
Pred. No. 0.0016;
2; Mismatches 19;
PPAPKPAPQPGPQPGPQPGPQPPQPPQ
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A;Gene: APG
A;Introns: 256/1; 299/3; 387/3; 470/1
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45.2%;
Best Local Similarity 54.2%;
Matches 26; Conservative
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ilarity 56.0%;
Conservative
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A;Residues: 'MAG',1-105 <GOL>
A;Cross-references: EMBL:214014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-196 <WUA>
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Best Local Similarity
Matches 28; Conser
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A; Residues: 1-534 <ROB>
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:49; Search time 5.72913 Seconds (without alignments) 427.133 Million cell updates/sec Мау Run on:

Title: Perfect score: Sequence:

US-09-855-754B-16 342 1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 59

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	p24328 bordetella		_	_	P21260 owenia fusi	volvox		Q9fpq6 chlamydomon		P40602 arabidopsis		_		_		Q83949 orgyta pseu			•	Q06084 trypanosoma	_	P70315 mus musculu	_		P23093 plasmodium	Q05859 mus musculu	Q05860 mus musculu	O60885 homo sapien	sns	P78621 emericella	_	0 homo	Q9umn6 homo sapien
SUMMARIES	ID	PERT BORPA	PERT_BORBR	PERT_BORPE	APG_BRANA	YPRO_OWEFU	SSGP_VOLCA	TEGU_HSV11	GP1_CHLRE	EBN2_EBV	APG_ARATH	COLL_HSVSC	PRP2_MOUSE	PRP3_MOUSE	ACRO_RABIT	EXLP_TOBAC	Y066_NPVOP	MOZ_HUMAN	PARB_TRYBB	PAR1_TRYBB	PARC_TRYBB	WASP_HUMAN	WASP_MOUSE	MOT8_MOUSE	CSP_PLABE	CSP_PLABA	FM14_MOUSE	FMN1_MOUSE	BRD4_HUMAN	ACRO_PIG	SEPA_EMENI	G3PT_MOUSE	RFX1_HUMAN	TRX2_HUMAN
	Length DB	922 1	911 1		449 1			3164 1	555 1	487 1	534 1	102 1	261 1	296 1	431 1	426 1	875 1	2004 1	129 1	143 1	145 1	502 1	520 1	565 1	339 1	347 1	•		•	415 1	•	•	979 1	2715 1
dP	Query Match	87.3	٠	•	47.2		٠	46.2	٠	٠		43.0	42.4	42.4	•		.i	•	ö	ď.	6	6	σ,	6	œ.	æ	.	в.	₩.	8	ω.	38.5	38.5	38.2
	Score	298.5	267.5	203.5	161.5	158	158	158	149.5	148.5	148.5	147	145	145	144	143	141.5	140.5	139	136	136	136	135.5	134	133	133	133	133	132.5	132	132	131.5	131.5	130.5
	Result No.	-	7	3	4	S	9	7	∞ •	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29	30	31	32	33

P25050 herpesvirus P04726 triticum ae P41473 autographa Q63627 rattus norv Q95107 bos taurus Q924h2 mus musculu Q93av1 arabidopsis Q00401 homo sapien	P04725 triticum ae P51532 homo sapien P58840 homo sapien
COLL HSVS7 GDA6_WHEAT Y091_WPVAC SRA4_RAT WASL_BOVIN WASL_BOVIN WASL_HUMAN WASL_HUMAN	GDAS_WHEAT SN24_HUMAN ACRL_HUMAN
105 296 224 1048 505 792 642 505 279	319 1647 232
	36.4 4.6 4.6
130 129.5 129.5 126.5 126.5 126.5	124.5
######################################	444

ALIGNMENTS

					ALIGNMENTS	MENTS		
	RESULT PERT_B	RESULT 1 PERT_BORPA ID PERT_BORPA	STANI	STANDARD;	PRT;	922 AA		
	8555	124320; 01-MAR-1992 01-MAR-1992 15-JUN-2002	(Rel. 21 (Rel. 21 (Rel. 41	21, Created) 21, Last seq	Created) Last sequence update) Last annotation update)	update) updat		
.,	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	PRN. PRN. Bordetella parapertussis Bacteria; Proteobacteria Bordetella.	ecursor arapertu oteobact	(Outer r issis. teria; be	(Juiter memorane protein F./U) ussis. teria; beta subdivision; Alcal	proteir /ision;	Feriacin precursor (Outer membrane protein P.70) (P.95). Bordetella parapertussis. Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella.	
	R R R C B R R R R R R R R R R R R R R R	NCBI_TaxID=519; [1] SEQUENCE FROM N.A. STRAILN=CN2591; MEDLINE=91251771; Li L.J., Dougan G. "P.70 pertactin, a	19; M N.A. 1771; Pt. 1771; Pt. tin, an	ubmed=204 Novotny outer-me Ing, nucl	1476; P., Char] umbrane pi	les I.C	NCBL Taxilla. NCBL Taxilla. [1] [2] [3] [4] [5] [6] [7] [7] [7] [7] [8] [8] [9] [9] [9] [9] [9] [9	
	# # S S S S	Escherichia Mol. Microbio -!- FUNCTION MEDIATED	coll."; ol. 5:4(: AGGLUT BY THE L ADHESI	09-417(19 FINGEN 1 R-G-D SE ION, AND	91). PAT BINDS QUENCE. F	S TO EU PERTACT	erichia coli."; Microbiol. 5:409-417(1991). MICTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.	
	888888	-1- SUBUNIT: MONOMER1- SUBCELLUIAR LOCAT -1- DISEASE: MAY CONT1- MISCELLANEOUS: SY.	MONOMER LAR LOCA MAY CON NEOUS: S ATIONS.	MONOMER. AR LOCATION: OUTE MAY CONTRIBUTE TO EOUS: SYNTHESIZED TIONS.	SUBDNIT: MONOMER. SUBCELLUIAR LOCATION: Outer membrane. DISEASE: MAY CONTRIBUTE TO THE DISEAS MISCELLANEOUS: SYNTHESIZED ONLY IN TH	rane. ISEASE IN THE	ATE OF WHOOPING C	
درست	388888 <u>88</u>	This SWISS-P between the the European use by non modified and entities requor	NOT entractions of the second	ry is cof Institute Drmatics institute atement license	yright. I tof Bloir Institute tions as is not re agreement	it is procedured to the second	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).	tion on - its way cial
.,,	*2	i " " 🖫	X54547; CAA38419.1; A26124; CAA01786.1; A19182; CAA01454.1; 315204; S15204 314659; S14659; Pro; IPR004899; Perta	CAA38419.1; CAA01786.1; CAA01454.1; S15204. S14659; Pertact_s	dns)	; ; ; ; ;		!
	DR DR DR DR FT FT	InterPro; IPR003992; pertact: InterPro; IPR003991; pertact: Pfan; PP03212; Pertactin; 1. PRINTS; PR01402; PERTACTIN. PRINTS; PR01404; PRTACTINAL. Outer membrane; Signal; Viru; SIGNAL 35 922 CHAIN 35 647 PROPEP 648 922 SITE 260 262	R003992; R003991; 2; Perta 4482; PER 484; PRI ne; Sign 35 35 648 260	1992; pertacti 1991; pertacti 1991; pertactin; 1. PERTACTIN. Signal; Virul 922 647 922	tactin. 'tactin_vir. 'i. 1. 'IN. 'IN. 'IN. Virulence; Repeat. P.95. P.95. PERTIAL. P.95. CELL ATPACHMENT	speat. NL. IN (P.70) NL.	70). WT SITE (INVOLVED IN	

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                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBDULT: MONOMER.
SUBGELLIQUAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANBOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                   LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
    ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchiseptica.";
J. Gen. Microbiol. 138:1697-1705(1992)
J. Gen. Microbiol. 138:1697-1705(1992)
MICROPION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                           Score 298.5; DB 1; Length 922;
Pred. No. 2.3e-11;
0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                               (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                     911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
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PRINTS; PRO1484; PRTACTNPAMLY.
Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92407514; PubMed-1527510;
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EEMBL; A19180; CAA01453.1; -.
PIR; A47675; A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
                                                                                                                               95178 MW;
                                                                                                                                                           87.38;
                                                                                                                                                                            95.0%;
                                                                                                                                                                          1 Similarity 95.0 57; Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                               266
271
276
281
575
922 AA;
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                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                           Query Match
                                                                                                                                                                            Local
                                               REPEAT
REPEAT
                                 DOMAIN
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                                                                                               REPEAT
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PERT_BORBR
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Matches
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                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89264462; PubMed-2542937; Charfield S., Smith M., Charles I.G., Dougan G., Pickard D., Charfield S., Smith M., Novotorp P., Morrissey P., Falrweather N.F.; "Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis."; Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-96196517; PubMed-8609998;
Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;
"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                            CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
   ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92407514; PubMed-1527510;
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                           6
                                                                                                                                                                      DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                                                         Indels
                                                                                                   (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                      0
                                                                                                                                                                  78.2%; Score 267.5; DB 1
85.0%; Pred. No. 1.4e-09;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Microbiol. 138:1697-1705(1992).
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                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                      MW.
                                                                                                                                  93995
                                                                                                                                                                                                      Conservative
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                               703
275
270
275
280
601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER
                                                                                                                                  911 AA;
                                                                                                                                                                                    Local Similarity
ses 51; Conserv
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P14283;
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Gaps

Indels

Length 449;

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3 KAPPAPKEAPQPGPQPG------PQPGPQPGPQPPQPPQPPQPPQRPEAPAPQ 49
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Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
"Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Owenidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PPAPKPAPOPGPOPGPOPGPOPGPOPPOPPOPPORPEAPAPOPPAGR 54
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                                                                                                                                                  9EFB6A3AB28EEA15 CRC64;
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                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                     47.2%; Score 161.5; DB 1;
llarity 45.2%; Pred. No. 0.0011;
Conservative 4; Mismatches 17;
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Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Blophys. Res. Commun. 166:66-73(1990)
PIR; A34043; A34043.
PIR; B34043; B34043.
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical proline-rich protein (Fragment).
Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AA
                                                                                        BY SIMILARITY.
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STRAIN-f. Nagariensis / HK10;
MEDLINE-90094551; PubMed-2689458;
                                                                                                                         POTENTIAL.
POLY - PRO.
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Best Local Similarity 54.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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NCBI_TaxID=3067;
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                                                                                                                                                                                                                                       Local Similarity
les 28; Conserv
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P21997;
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SSGP_VOLCA |
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Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nt J. 3:111-120(1993).
TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; "Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                              LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                 CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 203.5; DB 1; Length 910;
Pred. No. 6.9e-06;
1; Mismatches 0; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P. A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                             PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 AA
                                                                                                                                                                                                        Signal; Virulence; Repeat
                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                     InterPro; IPR001899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Profish; Pertactin_vir.
Profish; Pertactin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94004980; PubMed=8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL
                                                                                                                                           PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%;
69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
   PIR; A32560; A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                        Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APG_BRANA
P40603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
SEQUENCE
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ogo S

APG_BRANA

RESULT

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Plant

Query Match

Matches

Best

CHAIN PROPEP SITE

SIGNAL

CHAIN

DOMAIN REPEAT REPEAT REPEAT REPEAT

REPEAT

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Gaps

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23;

Pfam; PF03586; Herpes_UL36; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                the cellular compartment...

J. Cell Biol. 109:3493-3501(1989).

-!- FONGTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS

INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A

DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS

RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-!- FTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF

HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-88274377; Pubmed-2839594;
MCGOCH D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158; DB 1; Length 485;
Pred. No. 0.0019;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQRPEAPAPQPP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Sulfation; Hydroxylation.

DOMAIN 228 340 PRO-RTCH.

DOMAIN 260 295 POLX-PRO.

SEQUENCE 485 AA; 50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
01-AFR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X14112; CAA32311.1; -. PIR; 130085; WMBEH6. InterPro; IPR005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X51616; CAA35953.1; -. PIR; A33647; A33647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.2
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEGU_HSV11
P10220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glycosylated polyproline II rods-with-kinks as a structural motif in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGETATIVE CELL WALL PROTEIN GP1.
49 x 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
6AS84A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J., Goodenouch D.W.:
                                                                                                                                                                                                                                                         GP1_CHI.RE STANDARD; PRT; 555 AA.

G9FRGG; 003927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91017504; PubMed-1699255;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                                                                                                                                              35 X 2 AA TANDEM REPEATS OF P-Q. W; CC5D31FF4F9FE3F4 CRC64;
                                                                                   Length 3164;
                                                                                                                   11; Indels
                                                                                46.2%; Score 158; DB 1;
64.7%; Pred. No. 0.0069;
tive 3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        layer.
-1- SUBUNIT: Associates with GP2 and GP3.
-1- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003882; Pistil_extensln.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=211550910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF309494; AAG45420.1; -.
EMBL; M58496; AAA69706.1; ALT_SEQ.
                                                    335857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54219 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxyproline-rich
                                                                                                                   33; Conservative
                                       2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09FP06;
                                                    3164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
399
455
493
555 AA;
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlycoSuiteDB;
                   Repeat.
DOMAIN
SEQUENCE
                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                   Matches
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us-09-855-754b-16.rsp

APG_ARATH

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                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-842/U06); rupmed=cus/149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX
                                                Gaps
                                                                                                   255 APPSPKPPAPPPPPPPPPPPPPPPPPPPANTPMPPSPPSPPSPAPPTPPSPSPPS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen J.I., Wang F., Kieff E., "Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
                                                                               4 APPAPK-PAPQPGPQPGPQPGPQP-----GPQPPQPPQPPQPPQRPEAPAPQPPA
                                                6
              Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 X 2 AA TANDEM REPEATS OF R-G. DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 140.0, Pred. No. 0.0066;
                                                Indels
                                                                                                                                                                                                                                                                                                                       Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
Score 149.5; DB 1;
Pred. No. 0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90266473; PubMed-2161150;
Petti L., Sample C., Kleff E.;
"Subnuclear localization and phosphorylation of latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.4%; Score 148.5;
51.9%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION, AND PHOSPHORYLATION
                                                                                                                                                                                                     487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; V01555; CAA24877.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52544 MW;
            43.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 310:207-211(1984).
                                               28; Conservative

    -! - PTM: PHOSPHORYLATED.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation; Repeat.
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                      EBNA-2 nuclear protein.
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 AA;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF LMP-1
                                                                                                                                                                                                   EBN2_EBV
P12978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECURDING FROWN N.A.

STRAIN-CY. Columbia:

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MINCOLUMB M.K., Conn J., Chan H., Cheuk R.F., Chin C.W.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RA Lin C.J., Jonkins J., Johnson-Hopson C., Rhan S., Rhaykin E.,

RA Langin Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Langin Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Sakano, H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Wan Aken S., Vaysberg M., Wysotskala V.S., Walker M.,

R. Sequence and analysis of chromosome I of the plant Arabidopsis
APG_ARATH STANDARD; PRT; 534 AA.
P40602; 093214; 09LNT8;
01-FEB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
ARG OR AT1620;30 OR T20H2.9
Arabidopsis thallana (Mouse-ear cress)
Eukaryota; ViidIdIplantae; Streptophyta; Embryophyta; Tracheophyta; SpermatOphyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Prassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CAUTION: |Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. Cclumbia;
STRAIN-CV. Cclumbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
-! TISSUB SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL
TYPES IN THE ANTHER, ONLY IN MALE FERFILE PLANTS.
-! DEVELOPMENTAL SPAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                               MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X60377; CAA42925.1; -.
EMBL; AC022472; AAF79900.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID-3702;
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Gaps

PPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQP-PAGRE

3; Mismatches

27; Conservative

'n Matches

õ a

Local Similarity

Created) Last sequence update) Last annotation update)

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                     "The structure and organization of a proline-rich protein gene
                                              Proline-rich protein MP-2 precursor.
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-86059475; PubMed-2999141;
                                                                                                                                                           Ann D.K., Carlson D.M.;
                                                                    Mus musculus (Mouse)
                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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PRP3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and fils statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                         ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blesinger B., Trimble J.J., Desroslers R.C., Fleckenstein B.,
"The divergence between two oncogenic Herpesvirus saimiri strains in
a genomic region related to the transforming phenotype.";
Virology 176:505-514(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 534;
                                                                                                                                                                                                                                                    Score 147; DB 1; Length 102;
Pred. No. 0.0027;
1; Mismatches 18; Indels
                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
. Usage by an
                                                                                                                                                                                                                                       3 КАРРАРКРАРДРGРQРGРQРGРQРGРQ-РРQРРQРРQРРQRРEAPAPQPP
                                                                                                                             S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN-LIKE.
4C2CD389E78A03C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Herpesvirus saimiri (subgroup C / strain 488).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                  20:
                                                                                                                                                                                   Score 148.5; DB pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                              (Rel. 19, Last sequence update) (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                            102 AA
                                                                                                                                                                                                                2; Mismatches
                                                                                                                 POTENTIAL.
                                                                              POTENTIAL
                                     Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; AY058847; AAL24235.1; -.
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90266466; PubMed-2161148;
                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
01-MAY-1992 (Rel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B34770; B34770.
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                               58007 MW;
                                                                                                                                                                                       43.48;
54.08;
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                                                                                                                                                                                                              27; Conservative
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                                                                                                                                                             534 AA;
                                                                                                                                                                                                   Local Similarity
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P22576;
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CONFLICT
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                                                                                                                                                             SEQUENCE
                                                               Signal.
SIGNAL
                                                                                                                                      CONFLICT
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                                                                                       CHAIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86059475; PubMed-2999141;
Ann D.K., Carlson D.M.;
"The structure and organization of a proline-rich protein gene of
                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQP--GPQPGPQPGPQPPQ--PPQPPQRPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                                                                                                                                                                                                                         Score 145; ____Pred. No. 0.0068; ____thes 22; Indels
                                                                                                                                                                                                                                                                                                          PROLINE-RICH PROTEIN MP-2. 36E13BA7387F47D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Proline-rich protein MP-3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 AA
                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       42.4%; Score 145; 50.9%; Pred. No. 0
                                                                                                                                                                                                                                                                                         POTENTIAL
mouse multigene family.";
J. Biol. Chem. 260:15863-15872(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 260:15863-15872(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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13-AUG-1987 (Rel. 05, Last sequ
01-0CT-1994 (Rel. 30, Last anno
                                                                                                                                                                                                                                                                                                                             261 AA; 26034 MW;
                                                                                                                                                                                                                          EMBL; M12099; AAA40004.1; -.
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.99
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                             MGD; MGI:97773; Prp.
Repeat; Saliva; Signal.
                                                                                                                                                                                                                                                                                         15
261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97773; Prp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Saliva
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PRT;

STANDARD;

PRP2_MOUSE P05142;

PRP2_MOUSE

RESULT 12

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DISULFID
DISULFID
CARBOHYD
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REPEAT
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REPEAT
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   SHEETER
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                                                                                                                                                                        a
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                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAILM-New Zealand white; TISSUE-Testis;
MEDLINE-94368861; PubMed-8086468;
Richardson R.T., O'Rand M.G.;
Richardson R.T., O'Rand M.G.;
Cloning and sequencing of chas for rabbit preproacrosin and a novel preproacrosin-related coba.
Blochim. Blophys. Acta 1219:215-218(1994).
IF SHOWTION: ACROSIN IS THE MAJOR PROTEASE OF WAMMALIAN SPERMATOZOA.
IT IS A SERINE PROTEASE OF THYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROTEASE OF THYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                  23
                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
1 16 BY SIMILARITY.
17 431 ACROSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
                                                                              GAKAPPAPKPAPQPGPQP--GPQPGPQPGPQPPQPPQ--PPQPPQRPEAPAPQPPAG
                                                           *
                                  Length 296;
                                                       22; Indels
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INTERCHAIN (BY SIMILARITY)
BY SIMILARITY.
          7F146824E8AF3269 CRC64;
                                Score 145; DB 1;
Pred. No. 0.0074;
2; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE.
                                                                                                                                                             431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
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InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequen
15-JUN-2002 (Rel. 41, Last annota
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY
                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
 1
29521 MW;
                                 42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U05204; AAA61630.1; -.
                                                        Conservative
                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288
152
160
87
87
          296 AA;
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                                            Similarity
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                                                                                                                                                                                 01-FEB-1996
01-FEB-1996
                                                      29;
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                                                                                                                                                            ACRO_RABIT
NON_TER
SEQUENCE
                                Query Match
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                                             Best Loc
Matches
                                                                                                                                                ACRO_RABIT
                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTRAIN-CV. Petit Havana; TISSUE-Pistil;
MEDLINE-93065740; PubMed-1932607;
MEDLINE-93065740; PubMed-1932607;
GOldman M.H., Pezzotti M., Seurinck J., Mariani C.;
"Developmental expression of tobacco pistil-specific genes encoding novel extensia-like proteins.";
Plant cell 4:1041-1051(1992).
-1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
-1- DEVELOPMENTAL STACE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT FOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
Nicotiana tabacum (Common tobacco).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBL_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (POTENTIAL). 51A495CC94017812 CRC64;
                                                                                                                                                                                                                                                                                                                              2 AKAPPAPKPAPKPAPQPGPQPGPGP----QPGPQPPQPPQPPQRPEAPAPQPPA 52
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                                                                                                                                                                                                                             Score 144; DB 1; Length 431; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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InterPro; IPR000419; Pollen_Ole_e_I.
Pfam; PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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 Mismatches

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                                                                                                                                                                              46422 MW;
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208
140
238
431 AA;
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Best Local Similar
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                                                                                                     ACT_SITE
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                                                                              CARBOHYD
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Search completed: May 7, 2003, 16:48:08 Job time: 6.72913 secs

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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09k594 bordetella
09k594 bordetella
09alp7 bordetella
09alp7 bordetella
09alp5 bordetella
09alp5 bordetella
09asma bordetella
09s6n0 bordetella
09s5n1 bordetella
08s519 bordetella
08s529 bordetella
08s519 bordetella
08s197 bordetella
08s197 bordetella
09198 bordetella
09198 bordetella
09199 bordetella
09199 bordetella
09199 attus norv
09191 attus norv
09944 pneumocysti
09p34 pneumocysti
09p34 anabaena sp
09sbml volvox cart
08ygb7 anabaena sp
09sbml volvox cart
08ygb7 anabaena sp
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MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL: AJ250083; CAB76437.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID=518;
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115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99K5H3;
99K5H3;
01-OCT-2000 (TrEMBLrel, 15, Created)
01-OCT-2002 (TrEMBLrel, 15, Last sequence update)
01-UNN-2002 (TrEMBLrel, 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.9%; Score 331.5; DB 2; Best Local Similarity 98.3%; Pred. No. 3e-20; Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                          095649
0953M8
0955M1
0956N1
08143
08143
093149
0907D1
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P93797
Q9ARY7
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938
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                                                                                  7, 2003, 16:38:52; Search time 30.1533 Seconds (without alignments) 403.166 Million cell updates/sec
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342
1 Gakappapkpapgpgpgpgp.....porpeapapgppagrelsaa
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0.09k5h5 k
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0.09k5h3 k
0.09k5h3 k
0.09k5h3 k
0.09k5h3 k
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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09K5G7
09K5G9
09KJX9
09KJQ2
09K5H1
09K5H2
09K5H2
09K5H2
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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2: sp_bacteria:*
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Maximum DB seq length: 200000000
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sp_rodent:*
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bordetella bordetella bordetella

09K5H9 09K5H7 09KJY1 09KJY0

Q9ALP3

Score

Result ç S 331.5 298.5 294.5 294.5 274 274 267.5 267.5 249.5

RESULT 2 Q9K5G7

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1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kell D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

Best Local Similarity 91.7%; Pred. No. 3e-17;

Matches 55; Conservative 0; Mismatches 0; Indels 5;
                                                                                                                                                                                                                                                                                     Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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"Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AFR82397.1;
InterPro: IPR004899; Pertact_sup.
InterPro: IPR002965; P_rich_extensn.
Pfam: PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 12 122 NON_TER 122 AA; 12395 MW; RED00966A40FF994 CRC64;
                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AY007265, AAG38441.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact sup.
InterPro; IPR002965; P. rich_extensn.
Pfam; PF03212; Pertactin; 1.
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MEDLINE=21117018; PubMed=11179374;
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PRINTS; PR01217; PRICHEXTENSN
                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=518;
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Boursaux-Eude C., Guiso N.;

Infect. Immun. 68.4815-4817(2000).

EMBL: AJ250089; CAB7643.1;

EMBL: AJ250089; CAB7643.1;

Interpro: IPR0024899; Pertact_sup.

InterPro: IPR0024899; Prich_extensn.

Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ550087; CAB76441.1;
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
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Pred. No. 1.3e-17;
0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 86.1%; Score 294.5; DB 2; Length 111; 1 Similarity 91.7%; Pred. No. 2.8e-17; 55; Conservative 0; Mismatches 0; Indels 5.
                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus),
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA; 11416 MW; 5140669692808F8E CRC64;
                                                                         01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                        Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.3%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002965; P_rich
Pfam; PF03212; Pertactin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.0%
Matches 57; Conservative
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                                                  STRAIN-DEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BBCH;
                                                                                                                                                                                                                                                    Bordetella
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Q9K5G9;
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                                   Q9K5G7
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RESULT 6 **09K5H1**

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Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250081; CAB76435.1; ...
InterPro: IRR004899; Pertact.sup.
InterPro: IRR002965; P_rich_extensn.
Pfan; PF03212; Pertactin; I
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKAPPAFKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordecella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                      Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                             215 215
215 AA; 22327 MW; 5C21D45CF784B4AE CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.2%; Score 267.5; DB 2;
85.0%; Pred. No. 3.9e-15;
tive 0; Mismatches 0;
                                                                                                                                  80.1%; Score 274; DB 2; I
ilarity 86.7%; Pred. No. 2.1e-15;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AA.
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01-0CT-2000 (TEMBLE). 15, Last seq
01-JUN-2002 (TEMBLE). 21, Last ann
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MEDLINE-21117018; PubMed-11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20359389; PubMed-10899896;
                         PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01217; PRICHEXTENSN.
     Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 85.09
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                  Local Similarity
nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella.
NCBI_TaxID=518;
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NON_TER
SEQUENCE
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09ALP9;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERUBARIN-CYGEO;
STRAIN-CYGEO;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-108989;
PPolymorphism of Repeated Regions of Pertactin in Bordetella pertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250085; CAB76439.1;
INFERPLO: IPR004899; Pertact_Sup.
Pfam; PP03212; Pertactin; 1.
MON TER
                                                                                                                                  170 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 225
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRP-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GAKAPPAPKPAPQPGPQPGPQPGPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 74
                                                                             ŝ
                                        DB 2; Length 252;
                                   Query Match

86.1%; Score 294.5; DB 2; Length 25:
Best Local Similarity 91.7%; Pred. No. 5.3e-17;
Matches 55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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26107 MW; 368C142508D77057 CRC64;
                                                                                                                                                                                                                                                                                            01-077-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Pertactin (P.68) (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .80.1%; Score 274; DB 2;
86.7%; Pred. No. 1.2e-15;
tive 0; Mismatches 0
                                                                                                                                                                                                                                             109 AA.
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01-JUN-2001 (T.EMBLrel. 17, Created)
01-JUN-2001 (T.EMBLrel. 17, Last sequ
01-JUN-2002 (T.EMBLrel. 21, Last and
                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bronchiseptica Pertactin.;
Infect. Immun. 69:1917-1921(2001).
EMBL; ANO07263; AGG8439.1; --
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact Sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SO10328;
MEDLINE-21117018; PubMed-11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 86.7 ies 52; Conservative
                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=518;
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 SEQUENCE
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RESULT 7

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NCBI_TaxID=518;
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NON_TER
SEQUENCE
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SEQUENCE
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Q9K5H9;
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Q9ALP3
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Q9K5H9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (ANG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AJJ45927; CAB82515.1; InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.
Mooi F.R.;
                                                                                                                                                                                                                                                                                                                                                                                    ch 78.2%; Score 267.5; DB 2; Length 200; 1 Similarity 85.0%; Pred. No. 6.4e-15; 51; Conservative 0; Mismatches 0; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.2%; Score 267.5; DB 2; Length 911; 85.0%; Pred. No. 2.1e-14; tive 0; Mismatches 0; Indels 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
                                                                                                                                                                                                                                                                                                                                 20826 MW; 9F3AC6E4128942E6.CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09K5G1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA
                                                   Infect. Immun. 69:1917-1921(2001).
EMBL; AY007271; AAG38447.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact sup.
InterPro; IPR02965; Prich_extensn.
Pfam; PF03212; Pertactin; PRINTS; PR03121; PERRACTIN;
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                       200
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Best Local Similarity
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Q9L4E2
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Q9K5G1
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MEDLINE-20359389; pubmed-10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Broussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
Infect. Immun. 68:4815-4817(2000).
InterPro, IPR004899; Pertact.sup.
InterPro, IPR002865; P.rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPP-PQPPGRPEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
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Pred. No. 2e-13;
1; Mismatches 3; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
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EMBL; AXO07277; AAG38453.1; InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                   107 AA; 11073 MW; A0A339BFF0EAB8C6 CRC64;
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231 AA; 23930 MW; 5FB281B95E74678C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.0%; Score 249.5; DB 2; Best Local Similarity 81.7%; Pred. No. 1.1e-13; Matches 49; Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                          Pfam; PF03212; Pertactin; 1. PRINTS; PR01217; PRICHEXTENSN.
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PRINTS; PR01217; PRICHEXTENSN.
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73.0%;
Best Local Similarity 78.0%;
Matches 46; Conservative 1
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SEQUENCE FROM N.A.
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                              "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                 Pertactin (Frigment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        72.2%; Score 247; DB 2; Length 115; 80.0%; Pred. No. 1.8e-13; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156771; ARF82395.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                          115 AA; 11693 MW; FA3A76596F7097EB CRC64;
                  01-OCT-2000 ($rEMBLrel. 15, Created)
01-OCT-2000 ($rEMBLrel. 15, Last sequence update)
01-JUN 2002 ($rEMBLrel. 21, Last annotation update)
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Job time: 30.1533 secs
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PRINTS; PR01217; PRICHEXTENSN.
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hes 48; Conservative
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Keil D.J., Fenwick B.;
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BOUTSAUX-ENGC C., Gulso N.;
BOUTSAUX-ENGC C., Gulso N.;
FPOLYMOTPHISM of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL, ALSO0077; CAB76431.1;
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817 (2000).
EMBL: AJ250079; CAB76433.1;
InterPro; IPR004699; Pertact_sup.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GAKAPPAPKPAPQPGPQPG-------PQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 69
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                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                      Score 247; DB 2; Length 104;
Pred. No. 1.7e-13;
0; Mismatches 0; Indels 1
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                        104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-30N-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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                                               Pertactin (P.68) (Fragment).
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1 Similarity 80.0%;
48; Conservative
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nes 48; Conservative
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Best Local Similarity
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                                                                                                                                                                              STRAIN-9.73H+;
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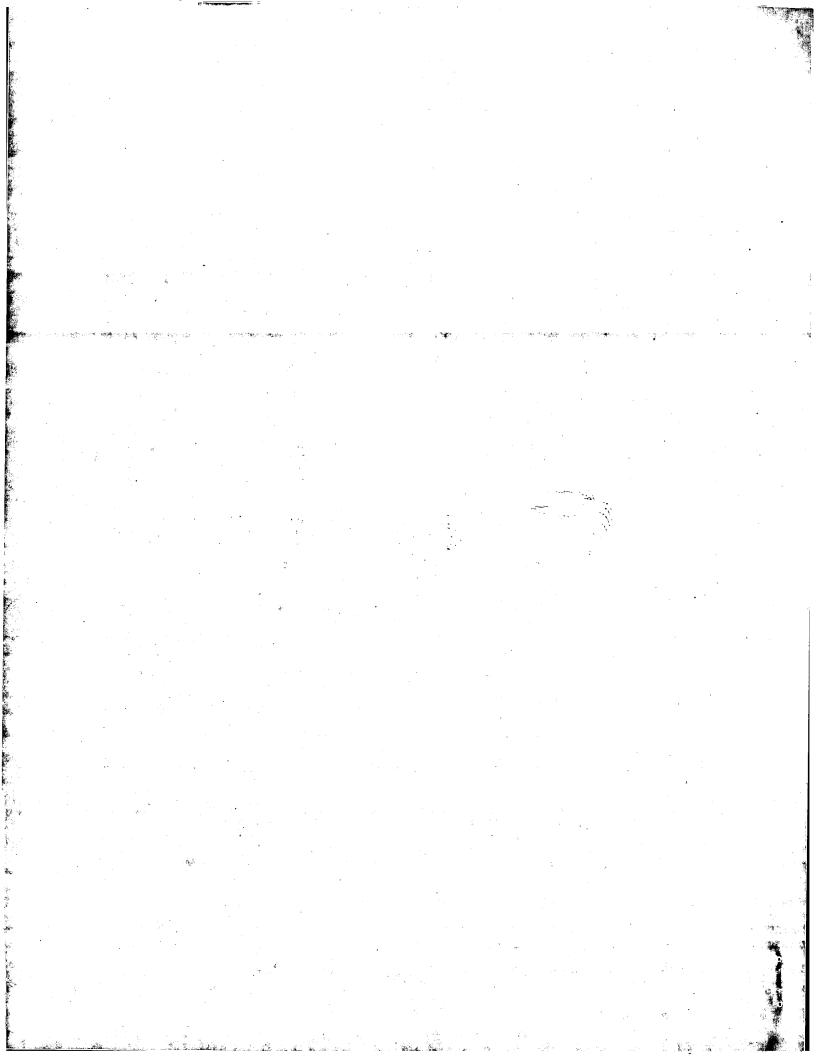
PRELIMINARY;

Q9KJY1 ID Q9KJY1

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Gaps

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us-09-855-754b-17.rag

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7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec
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298
1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 52
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	287.5	96.5	53	23	AAE16196	B bronchicontica
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4	271	6.06		23	AAE16194	B. bronchiseptica
Ŋ	271	90.9	911	12	AAR14320	Pertactin antigen
9	271	90.9		13	AAR26503	prn proteins. Bor
7	27.1	90.9		23		Bordetella bronchi
ω	267	9.68		23		B. bronchiseptica
6	267	89.6		13		Bordetella paraper
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Pertactin antigen B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica	Bordetella pertuss Bordetella pertuss B. bronchiseptica Peptide 683 derive	phila human polyp polyp ORFX human	Novel numan diagno Human polypeptide Herbicidally activ Sugar beet chitina Streptococcus pneu Human polypeptide Streptococcus pneu Ser-Pro-Pro-pro ge Streptococcus pneu	
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9 4 5 5 4 4 7 7	910 910 33 31	446 406 80 99 99 1217	1234 350 439 206 88 183 163	. 190 358 358 85 325 598 24 329 356
86.6 84.1 81.9 79.2 78.9	2000 0000 0000 0000 0000 0000	44444 000444 00088	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	222222111 008648984
250.5 244 236 235 207	207 207 186.5 153	134 134 1334 133.5 133.5	133.3 133 133 130 129 128	128 127.5 127.5 126.5 126.5 128 124.5
11 12 13 15 16	17 18 20 21 21	4.00000 4.00000	331 331 324 324 324	338 500 500 500 500 500 500 500 500 500 50

ALIGNMENTS

B. bronchiseptica strain II-4 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. AAE16196 standard; peptide; 53 AA. Guiso-maclouf N, Boursaux-eude C; 23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P. Bordetella bronchiseptica. 26-MAR-2002 (first entry) (INSP) INST PASTEUR. WPI; 2002-097639/13. WO200190143-A2. 29-NOV-2001. AAE16196; AAE16196 DXXXXXXXXX

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

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Courter membrane protein lorder by the contracting period period by vaccine. Pertractin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                  The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                 pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA;
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Gaps
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 Score 287.5; DB 23; Length 53; Pred. No. 1.6e-15;
                          0; Indels
                        0; Mismatches
96.5%;
98.1%;
                        52; Conservative
              Best Local Similarity
 Query Match
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA ö 셤

AAE16197 standard; peptide; 56 26-MAR-2002 (first entry) AAE16197; AAE16197

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B. bronchiseptica strain II-5 pertactin outer membrane protein region II. Pertactin; PRN;

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQ----RPEAPAPQPPAGRELSAA
                                                                                                                           Length 56,
                                                                                       Indels
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                                                            Score 282; DB Pred. No. 4.3e-1; Mismatches
                                                           Query Match
Best Local Similarity 91.1%;
Matches 51; Conservative
                                   56 AA;
                                     Sequence
2228
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B. bronchiseptica strain II-3 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. ¥ AAE16195 standard; peptide; 60 (first entry) 26-MAR-2002 AAE16195; SX BX B

RESULT 3

Bordetella bronchiseptica.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

60 AA; Sequence

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1 GAKAPPAPKPAPQPGPQPGPQPG-----PQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                    Indels
                                    ö
91.9%; Score 274; DB 23;
86.7%; Pred. No. 1.8e-14;
ive 0; Mismatches 0;
                                    Conservative
                 Best Local Similarity
Matches 52; Conserv
Query Match
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AAE16194;

RESULT 4 **AAE16194**

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Pichia microcrganisms are transformed for the expression of pertactin antigans. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAFKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pichia microcrganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271; DB 12;
Pred. No. 2.3e-13;
0; Mismatches 0;
                            Location/Qualifiers
266..270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR26503 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1B; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WELL ) WELLCOME FOUNDATION LTD.
                                                                        /label- repeat
                                                                                                        repeat
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Best Local Similarity 96.2%;
Matches 51; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-GB00487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1993 (first entry)
Bordetella bronchiseptica,
                                                                                                                         570..572.
                                                                                                                                                                                              578..580
/label= re
                                                                                                                                                                                                                                                                   . 586
                                                                                                                                                                                                                                                                                                       .589
                                                                                                                                                            576
                                                                                                                                                                                                                                  581..583
                                                                                                                                            /label=
                                                                                                        'label-
                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                    /label-
                                                                                                                                                                                                                                                                                    /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prn proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                         W09115571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                    Peptide
                                                                                     Peptide
                                                                                                                         Peptide
                                                                                                                                                           Peptide
                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used to detect Bordetella, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
?
                                                                                                                                                         B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                          Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.9%; Score 271; DB 23;
nllarity 96.2%; Pred. No. 2.8e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR14320 standard; Protein; 911 AA.
                                              AAE16194 standard; peptide; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001; 2001WO-EP06457
                                                                                                                       (first entry)
                                                                                                                                                                                                                                               Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin antigen P.68.
                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 AA;
                                                                                                                                                                                                                                                                              WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-1992
                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                  29-NOV-2001
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Gaps

5;

Sequence

Query Match Best Local S

Matches

AAR14320;

AAR14320

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ð

52

Key Protein

Region Region

Peptide Peptide

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271; DB 23; Length 911;
Pred. No. 2.3e-13;
0; Mismatches 0; Indels
           /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                               Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16198 standard; peptide; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.9%;
96.2%;
                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                                                       25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000; 2000US-206969P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.2
nes 51; Conservative
                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AAD26440
                                          WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200190143-A2.
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                                                                                29-NOV-2001
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Matches
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AAE16198
                                                               g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against arrophic rhinitis. The DNA sequence encoding these proteins was derived by attandard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 271; DB 13; Length 911;
Pred. No. 2.3e-13;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
                                                                                                                                                                  260..262
/label- RGD_tripeptide
                                                                                                                                                                                                   701..703
/label= RGD_tripeptide
                                                                                         266..279
/label= Repeat_region
                                                                                                                                                 'label- Repeat_region
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16183 standard; Protein; 911 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 28pp; English.
                                                       35..632
/label= P.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.9%;
96.2%;
                                                                                                                                                                                                                                                                                                                                   92WO-GB00561
                                                                                                                                                                                                                                                                                                                                                                     91GB-0006568
                                                                                                                                                                                                                                                                                                                                                                                                        (WELL ) WELLCOME FOUND LID.
Bordetalla bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica
                                                                                                                              570..589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-366258/44. N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 AA;
                                                                                                                                                                                                                                                                                                                                 27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                          WO9217587-A
                                                                                                                                                                                                                                                                                             15-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                          Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
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AAE16183;

RESULT 7 AAE16183 Reg ton Region

Sequence

Query Match

Best Loca Matches

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Gaps

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WPI; 1992-250033/30. N-PSDB; AAQ26509.

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                                                                                                                                             Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                   pertactin in Bordetella species, useful in immunogenic compositions for
treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                  present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                             260..262
/note= "motif associated with cell-cell adhesion"
266..285
/note= "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "contains 9 direct repeats of Pro-Gln-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "motif associated with cell-cell adhesion"
                                                     polymorphisms of the repeated regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                          Length 58;
                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                         Score 267; DB 23;
Pred. No. 6.1e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR25578 standard; Protein; 922 AA
Boursaux-eude C;
                                                                                                       Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35..643
/label- P70 .
                                                                                                                                                                                                                                                                                                                                                         89.6%;
87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-GB02302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "co
575..612
/note= "co
712..714
                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis.
                                                     Polypeptides containing
pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                         WPI; 2002-097639/13
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                              58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Charles IG;
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR25578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Protein
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with SauJA and cloning of 40-50kb fragments into the BamHI site of cosmid pH679. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (*P95*) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acellular vaccine for immunisation against whooping cough comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella parapertussis pertactin outer membrane protein, p.70.
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
89.6%; Score 267; DB 13;
Best Local Similarity 87.9%; Pred. No. 4.7e-13;
Matches 51; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254..304
/note= "Pertactin region I"
564..621
/note= "Pertactin region II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16185 standard; Protein; 922 AA.
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                                                                                                                   Claim 1; Fig 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2000; 2000US-206969P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella parapertussis.
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N-PSDB; AAD26442.
                                                                                                                                                                                                                                                                                                                                                                                               922 AA;
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91WO-GB00487.

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28-MAR-1991;
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                                Outer membrane protein) or their fragments. Pertactin (PRN) is used as and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquent to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
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                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                     ;
                                                                                                                                                                    Length 922;
                        present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                                                                               1 89.6%; Score 267; DB 23;
Similarity 87.9%; Pred. No. 4.7e-13;
il; Conservative 0; Mismatches 1;
          Page 34; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586..588
/label= --
                                                                                                                                                                                                                                                            AAR14321 standard; Protein; 922
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label= repeat
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/label= repeat
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//abel- re
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/label- re
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7. Tabel-
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'label- re
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| Jabel = re
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label- re
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label- re
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/label= re
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/label- r
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                                                                                                                                                                                                                                                                                                               Pertactin antigen P.70.
                                                                                                                                                 A)
                                                                                                                                                922
        Disclosure;
                                                                                                                                                             Query Match
Best Local Simi
Matches 51;
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                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                             AAR14321;
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Peptide
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17-0CT-1991

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B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
                                                                                                                                                                                                                                                              pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapartussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPGPQP-----PQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                   The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 922;
                                                                                                                                                                                                                                              Pichia microorganisms are transformed for the expression of
                                                                                                                                                       Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 258; DB 12;
Pred. No. 2.3e-12;
0; Mismatches 0;
                                                                                                                                                                                                              Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE16193 standard; peptide; 49 AA.
                                 (WELL ) WELLCOME FOUNDATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Fig 1c; 47pp; English.
 90GB-0007416.
                                                                                                                                                                                                                                                                                                                                                                                                                            86.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4
Matches 51; Conservative
                                                                     Clare JJ, Romanos MA;
                                                                                                   WPI; 1991-325214/44.
N-PSDB; AAQ14320.
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                                                                                                                                                                                                                                                                                                                                                                                          922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN;
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02-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodgical and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                 Score 250.5; DB 23; Lens-
Pred. No. 9.5e-13;
Orientales 0; Indels
                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                             84.18;
90.68;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                             49 AA;
                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                               Query Match
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   88888888888888
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bronchiseptica strain II-7 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. Ž AAE16199 standard; peptide; 48 23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P (first entry) Bordetella bronchiseptica 40200190143-A2 26-MAR-2002 AAE16199; AAE16199

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13

(INSP) INST PASTEUR

Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. present invention relates to Bordetella bronchiseptica pertactin The

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48 AA;
 Sequence
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    B. bronchiseptica strain II-8 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the repeated regions of
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        Length 48;
      Score 244; DB 23;
Pred. No. 2.9e-12;
                      Pred. No. 2.96
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides containing polymorphisms pertactin in Bordetella species, usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                               AAE16200 standard; peptide; 52
   81.9%;
llarity 88.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
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Query Match
Best Local Similarity
Matches 47; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                            WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2001
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ID AAE1
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B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                outer membrane protein; vaccine; Bordetella infection;
                                Pertactin; PRN; outer membrane protein; vaccin
therapy; antibiotic; antibacterial; region II.
             26-MAR-2002 (first entry)
    AAE16201;
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23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P (INSP) INST PASTEUR 29-NOV-2001.

Bordetella bronchiseptica

WO200190143-A2

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fillids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

54 AA; Sequence

6; Gaps Length 54; 1; Indels Score 235; DB 23; Pred. No. 1.5e-11; 1; Mismatches 1; 78.9%; 85.7%; 48; Conservative Query Match Best Local Similarity Matches 48; Conserva

4

1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP---PQ-RPEAPAPQPPAGRELSAA 52 ò g

Search completed: May 7, 2003, 16:47:07 Job time: 28.0187 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2003, 16:41:51; Search time 8.59284 Seconds
(without alignments)
178.054 Million cell updates/sec
Fitle: US-09-855-754B-17
Perfect score: 298
Sequence: 1 GAKAPPAPKPAPQPGPPGPP......PQRPEAPAPQPPAGRELSAA 52
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: \cgn2_6/ptodata1/1/aa/5A_COMB.pep:*
2: \cgn2_6/ptodata1/1/aa/6A_COMB.pep:*
3: \cgn2_6/ptodata1/1/aa/6A_COMB.pep:*
4: \cgn2_6/ptodata1/1/aa/6A_COMB.pep:*
5: \cgn2_6/ptodata1/1/aa/PCTUS_COMB.pep:*
6: \cgn2_6/ptodata1/1/aa/PCTUS_COMB.pep:*
6: \cgn2_6/ptodata1/1/aa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 4, Appli	Ġ	Sequence 2, Appli	11	11,	52	N	16	16,		Sequence 8, Appli	4	4	~	32,	65,	Sequence 65, Appl	65,	Sequence 8, Appli	Sequence 4, Appli	4	Sequence 160, App	28,	Sequence 29, Appl	30,	31,	Sequence 6, Appli
ID	US-08-460-269C-4	US-08-460-269C-6	US-08-460-269C-2	US-08-237-716-11	US-08-750-624-11	5202236-3	US-09-095-443-2	US-08-246-982A-16	US-08-453-265-16	5202236-37	US-08-460-269C-8	US-09-026-587-4	US-09-227-420-4	US-09-109-841-2	US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65	US-08-457-273B-8	US-08-348-518C-4	US-08-476-509B-4	US-08-961-083-160	US-09-041-886-28	US-09-041-886-29	US-09-041-886-30	US-09-041-886-31	US-08-246-982A-6
D38	4	4	4	-	4	9	4	-1	-4	ø	4	7	~	4	-	н	4	4	~	٣	m	4	4	4	4	4	-
å Query Match Length DB	911	922	910	33	24	334	1274	3119	3119	331	23	380	380	490	330	408	408	408	3118	454	454	641	513	530	552	589	3144
& Query Match	90.9	9.68	69.5	45.0	41.9	40.9	40.8	40.8	40.8	40.6	39.6	39.6	39.6	38.4	38.1	38.1	38.1	38.1	38.1	37.9	37.9	37.8	37.1	37.1	37.1	37.1	37.1
Score	271	267	207	134	125	122	121.5	121.5	121.5	121	118	118	118	114.5	113.5	113.5	113.5	113.5	113.5	113	113	112.5	110.5	110.5	110.5	110.5	110.5
Result No.	1	7	e	4	2	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	. 22	23	24	25	36	27

5

Gaps

5;

oy G

Query Match

Query Match

Best Local Similarity 96.2%; Pred. No. 1.3e-16;
Matches 51; Conservative 0; Mismatches 0; Indels

Sequence 6, Appli Sequence 12, Appli Sequence 15, Appli Sequence 15, Appli Sequence 61, Appli Sequence 67, Appli Sequence 75, Appli Sequence 75, Appli Sequence 77, Appli Sequence 71, Appli Sequence 71, Appli Sequence 12, Appli	s PROTEIN IN gan, P.C.
US-08-453-265-6 US-08-08-457-245-4 US-08-08-556-419-21 US-09-041-086-15 US-09-535-008-63 US-09-535-008-67 US-09-535-008-72 US-09-535-008-72 US-09-535-008-73 US-09-535-008-69 US-09-535-008-69 US-09-535-008-69 US-09-535-008-73 US-09-535-008-73 US-09-535-008-73 US-09-535-008-73 US-08-54-342-12 US-08-54-140-12 US-08-675-140-12	n US/08460269C E, JEFFREY J. NOS, MICHAEL A. ION: EXPRESSION OF HETEROLOGGUS PR YEAST ADDRESS: ADDRESS: ALILen, White, Zelano & Branigan, 00 Clarendon Blvd., Suite 1400 Millen, White, Zelano & Branigan, 00 Clarendon Blvd., Suite 1400 NGTON SA SYSTEM: PC-DOS/MS-DOS SYSTEM: PC-DOS/MS-DOS PATENTIN Release #1.0, Version #1. TION DATA: WINDHER: US/08/460,269C E: OZ-Jun-1995 INFORMATION: WINDHER: 37,067 DOCKET NUMBER: 3
37.1.3144.1.3144.1.3144.2.3144.3144.3.3144.3144.304.3144.304	NE, JE NE, JE NOS. IION: IION: NOON 111 NO OU OU NEE: FI NO OU NEE: FI NO N
228 1110.5 30 1110.5 30 31 31 31 31 31 31 31 31 31 31 31 31 31	RESULT 1 US-08-460-269C-4 Sequence 4, Application Patent No. 6197548 GENERAL INFORMATION ROWA TITLE OF INVENT ROWA TITLE OF SEQUENCE STREET: 22201 CORRESPONDENCE STREET: 22201 COMPUTER IREADA MEDIUM TY: COMPUTER IREADA SOFTWARE: LEBO SOFTWARE: LEBO SOFTWARE: LEBO SEQUENCE CHARA INFORMATION FCR SEQ SEQUENCE CHARA SEQUENCE CHARA TYPE: AMOLECHIE TYPE: TYPE: AMOL

Gaps

10;

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568 GAKAPPAPKPA------PQPGPQPPQPPQPPQP--QPEAPAPQPPAGRELSAA 609
                                                                                                                                                                                                                                                                                                                                                                                      Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;- Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Nixon & Vanderhye, P.C.
1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,716
FILING DATE: US/MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   Score 207; DB 4;
Pred. No. 4.7e-11;
1; Mismatches 0;
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                        REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08237716
Patent No. 5589384
                                                                                                                                                                           (703) 243-6410
                                                                                                                                                                                                                                            LENGTH: 910 amino acids
                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        69.5%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wilson, Mary J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia
                                                                                                                                                                         FELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-237-716-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                        APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 267; DB 4; Length 922;
Pred. No. 3e-16;
                                                                                                                                                                                                                                       ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703) 243-6333
                                     Sequence 6, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.6%;
milarity 87.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQP
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-460-269C-2
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                                                                               ;Patent No. 5202236;
3 APPLICAMT: MAÖGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
5:SUSAN L.;AMCANDISS, RUSS;WEI, TENA;FILPULA, DAVID
5: TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 APPAPAFAPAPALAPAPPNPNPQSPPSPPSPPTPPPTPPSP+PAPPS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 APPAPKPAPQPG-----PQPGPQPGPQPPQPPQRPEAPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%; Score 122; DB 6;
51.1%; Pred. No. 0.00044;
tive 2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                           NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: FASTSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/049,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09095443
Patent No. 6342593
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Plowman, Gregory
APPLICANT: Peles, Eior
TITLE OF INVENTION: DIAGNOSIS
TITLE OF INVENTION: OF ALP RE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICÄTION DATA:
APPLICATION NUMBER: 60/049
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i. (213) 489-1600
(213) 955-0440
67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.19
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: U.S.A.
90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                       5202236-3
                                                                                                                                                          PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
TILLE OF INVENTION: ALICHAL COMPOSITIONS COMPRISING A
TILLE OF INVENTION: ALICHAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                              /label= P69 BB05 epitope of Bordetella pertussis sequence
                                                                                                                                                                                                                                                                             Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/750,624
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                         Score 134; DB 1;
Pred. No. 5.1e-06;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125; DB 4;
Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                       /label- LTB sequence
                                                                                                                /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                               14 PGPQPGPQPGPQPPQPPQRPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-660
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 POPGPQPPQPPQP--OPEAPAPQPP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 PQPGPQPPQPPQRPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         ch 45.0%;
1 Similarity 76.7%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity ·88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
NAME/KEY: Region LOCATION: 1..2 OTHER INFORMATION:
                                                                                              LOCATION: 4..7
OTHER INFORMATION:
                                                                                                                                                                           COCATION: 10.31
CTHER INFORMATION:
CTHER INFORMATION:
US-08-237-716-11
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                          FEATURE:
NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                        NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-750-624-11
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                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                 Matches
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Gaps

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RESULT 10
5202236-37
;Patent No. 5202236
                                                                                                                                                                                                           ADDRESSEE:
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; LENGTH: 331
5202236-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
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                                                                                                                                                                                                                                         Gaps
                                                                                                                                            DB 4; Length 1274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.8%; Score 121.5; DB 1; Length 3119;
48.0%; Pred. No. 0.0035;
tive 3; Mismatches 12; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacOpold, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof CORRESPONDENCES. 25
CORRESPONDENCES. 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 QPGPQPGPQPPQPPQPPQRPEAPAPQPP-----AGRELSA 51
                                                                                                                                        Score 121.5; DB 4; Length
Pred. No. 0.0016;
1; Mismatches 11; Indels
                                                                                                                                                                                                               1 GAKAP-----GPQPPQ----GPQPPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.C.

COUNTRY: U.S.A.

ZIP: ZOD05

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

RPLICATION NUMBER: US/08/246,982A

FILING DATE: MAY 20, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge, A.

REGISTRATION NUMBER: 29,021

REJEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2600

TELEFHONE: (202) 371-2540

INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                    Query Match 40.8%;
Best Local Similarity 39.7%;
Matches 31; Conservative
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                              625 QAPGLLPPQSPYPYAPOP 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                           31 Q----PPQRPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.09
Matches 24; Conservative
                           TYPE: amino acid
STRANDEDNESS: single
                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                 US-09-095-443-2
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RESULT 9 US-08-453-265-16

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Gaps
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Pred. No. 0.0035;
3; Mismatches 12; Indels 11;
                                                                     APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MAGGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, ; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID ; TILE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

40.6%; Score 121; DB 6;
Best Local Similarity 47.7%; Pred. No. 0.00053;
Matches 21; Conservative 2; Mismatches 21.
                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOKNET ALGERY STEVEN R.
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-MG11987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP. 20005
COMPUTER READABLE FORM:
MEDIUM TYPER: RIAPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
5, Application US/08453265
5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
FELECOMMUNICATION INFORMATION
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 40.8%;
Best Local Similarity 48.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-453-265-16
                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQ------PPQRPEAPAPQPPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 2; Length 380;
0.0011;
ches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4. Application US/09227420
Patent No. 5990087
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: dal, Preett
APPLICANT: dal, Preett
APPLICANT: corley, Mail C.
TILLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                              COPERATING SYSTEM: DOS

SOFTWARE: FastESD for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/026,587

FILING DATE: Filed Herewith
CLASSIFICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOMNEY AGAIN: INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: BF-0471 US

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMFUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB
Pred. No. 0.001
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0471 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 43.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
COMPUTER READIABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11near
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-227-420-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                       Sequence 8, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun 1995
ATTORNEY/AGENT INFORMATION:
             GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESSPENDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 118; DB 4;
Pred. No. 9.1e-05;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 antho acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-460-269C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PQPGPQPPQPPQP--QPEAPAPQP 23
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US-09-026-587-4
; Sequence 4, Application US/09026587
; Patent No. 5912128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 PQPGPQPPQPPQRPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.6%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
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4 Embarcadero Center, Suite 3400
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                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.0027;
6; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                      Length 380;
                                                                                                                                                                                                                                                                                                                         21; Indels
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                                                                                                                                                                                                                                                                                    Score 118; DB 2;
Pred. No. 0.0011;
0; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bjornvad, Mads E.
APPLICANT: Bjornvad, Mariko
APPLICANT: Batakeyama, Mariko
APPLICANT: Schulein, Maritin
APPLICANT: Schulein, Maritin
APPLICANT: Schulein, Maritin
TITLE OF INVENTION: Endo-Beta-1, 4-Glucanas,
TITLE OF INVENTION: Saccharothrix
TITLE OF INVENTION: Saccharothrix
TITLE OF INVENTION: Saccharothrix
CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 0812/97
EARLIER FILING DATE: 1997-07-11
EARLIER FILING DATE: 1997-07-11
EARLIER FILING DATE: 1997-07-13
EARLIER FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharothrix australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09109841
Patent No. 6207436
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFFAX: 650-845-4166
                                                                                                                                                                                                                                                                            Query Match 39.6%;
Best Local Similarity 43.1%;
Matches 25; Conservative
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Best Local Similarity 44.2%;
Matches 19; Conservative (
                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
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LIBRARY: Gendali
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US-09-109-841-2
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TYPE: PRT
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APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVERTION: High Molecular Weight Collagen-Like
TITLE OF INVERTION: Protein Polymers
NUMBER OF SEQUENCES: 135

Sequence 32, Application US/08642255 Patent No. 5773249 GENERAL INFORMATION:

FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HC

5

Gaps Length 330; 1 GAKAPPAPKPAPQPGPGPGP-----QPG-PQPPQPPQPPQRPEAPAPQPPAG 46 SYSTEM: PC-DOS/MS-DOS Patentin Release #1.0, Version #1.30 5; 0.0024; 15; Score 113.5; 1 Pred. No. 0.00; 0; Mismatches CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255 7, 2003, 16:57:18 IBM PC compatible CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A TELEFAX: (415) 494-6771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID 00: 32:
SEQUENCE CHARACTERISTICS: (415) 494-8700 Floppy disk : 330 amino acids amino acid Conservative ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy single ; MOLECULE TYPE: protein US-08-642-255-32 California COMPUTER: IBM PC OPERATING SYSTEM: Query Match Best Local Similarity Matches 28; Conserve linear

us-09-855-754b-17.rapb

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7, 2003, 16:53:34; Search time 15.5911 Seconds (without alignments) 306.927 Million cell updates/sec
                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 52
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                 349150 seqs, 92025710 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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ptodata/2/pubpaa/US06_NEW_PUB. /ptodata/2/pubpaa/US08_NEW_

Published_Applications_AA:

Database :

/cgn2_6,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 17, Appl	16,	Sequence 18, Appl	Sequence 15, Appl	Sequence 4, Appli	Sequence 19, Appl	, ,	14,	20,	Sequence 21, Appl	Sequence 22, Appl	Sequence 23, Appl	5, A	24,	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 43, Appl	Sequence 43, Appl
SUMMARIES	ID	US-09-855-754-17	US-09-855-754-16	US-09-855-754-18	US-09-855-754-15	US-09-855-754-4	US-09-855-754-19	US-09-855-754-6	US-09-855-754-14	US-09-855-754-20	US-09-855-754-21	US-09-855-754-22	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-10-171-384-3	US-10-020-215-2	US-09-823-240-2	US-09-976-740-43	US-10-023-529-43
	DB	6	0	σ	σ	σ	6	6	σ	6	σ	6	σ	σ	6	6	о	10	6	12
•	Match Length	52	59	26	52	911	28	922	49	48	25	54	42	910	39	827	1274	802	538	538
e Ouerv	Match	100.0	95.5	94.6	6.06	6.06	89.6	9.68	84.1	81.9	79.2	78.9	69.5	69.5	62.6	43.8	40.8	40.6	39.8	39.8
	Score	298	284.5	282	271	271	267	267	250.5	244	236	235	207	207	186.5	130.5	121.5	121	118.5	118.5
Result	NO.	н	7	9	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 43, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 17, Appl Sequence 125, Appl Sequence 1002, Ap Sequence 1002, Ap Sequence 1002, Ap Sequence 1, Appl 1 Sequence 4, Appl 1 Sequence 4, Appl 1 Sequence 67, Appl 2 Sequence 61, Appl 3 Sequence 61, Appl 3	Sequence 10936, A Sequence 4, Appl1 Sequence 56, Appl Sequence 5, Appl1
12 US-10-023-523-43 10 US-09-823-240-10 12 US-10-023-529-47 12 US-10-023-529-47 12 US-10-023-529-47 12 US-10-023-529-47 13 US-10-023-529-47 14 US-09-955-987-2 10 US-09-955-299-1002 10 US-09-925-299-1002 10 US-09-925-299-1002 10 US-09-864-761-36844 10 US-09-864-761-36844 10 US-09-864-761-36844 10 US-09-864-761-36844 10 US-09-864-761-36844 10 US-09-781-721-160 10 US-09-781-721-160 10 US-09-781-721-160 10 US-09-298-5238-62 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1	10 US-09-815-242-10936 9 US-09-824-574-4 10 US-09-866-562-56 10 US-09-770-689A-5
533 380 550 550 643 647 171 171 171 171 171 171 171 171 171 1	1333 1647 510 780
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ALIGNMENTS

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARABERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 0209-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
                       Sequence 17, Aprilcation US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-855-754-16
; Sequence 16, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
                                                                                                             APPLICANT: BOURSAUX-EUDE, CAROLINE
-09-855-754-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 17
LENGTH: 52
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CURRENT APPLICATION NUMBER: US/09/855,754
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Matches 51; Conserv
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Matches 51; Conserv
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                                                                                                                                                         SEQ ID NO 15
LENGIH: 52
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Publication No. US20020192237A1

GENERAL INFORMATION:

APPLICANT: BOUNSAUX-EUDE, CARCLINE

APPLICANT: BOUNSAUX-EUDE, CARCLINE

TITLE OF INVENTION: POLYPEFTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,

TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS

TITLE OF INVENTION: UMUNOSEN: US/09/855,754

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATCHE NOS: 24
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TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PRESIONS OF PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHIELPA PRAAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHIESPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 0409-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 284.5; DB 9; Length 59;
Pred. No. 1.1e-13;
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Pred. No. 1.6e-13;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica US-09-855-754-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bordetella bronchiseptica US-09-855-754-18
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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91.1%;
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ilarity 88.1%;
Conservative
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Matches 52; Conserv
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Best Local Similarity
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US-09-855-754-15
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISSEPTICA, THERE USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSINIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND STRILE AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQR-PEAPAPQPPAGRELSAA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                                                                                                                                                                                                              Length 52;
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                                                                                                                                                                                                                                                                                                                  90.9%; Score 271; DB 9;
illarity 96.2%; Pred. No. 8.3e-13;
Conservative 0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; Publication No. US20020192237A1
; GENERAL INFORMATION:
; APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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                                                                                                                     SOFTWARE: Patentin Ver.
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Gaps

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERRACTININI BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MANDOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ. ID NOS: 24
SOFTWARE: PATCHIL VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: INMUNOERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILLING JATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,960
NUMBER OF SEO THE 
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                                                                                  Length 49;
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                                                                                  DB 9;
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88.7%; Pred. No. 5.4e-11;
tive 0; Mismatches 0
                                                                              Score 250.5; DB
Pred. No. 2e-11;
0; Mismatches
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Best Local Similarity 88.9%; Pred. No. 2e-10;
Matches 48; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
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US-09-855-754-21
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; Publication No. US20020192237A1
; GENERAL INFORMATION:
                                                                              84.1%;
90.6%;
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Best Local Similarity 88.73
Matches 47; Conservative
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                                                                          Query Match
Best Local Similarity
Matches 48; Conserv
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US-09-855-754-20
          US-09-855-754-14
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Publication No US20020192237A1

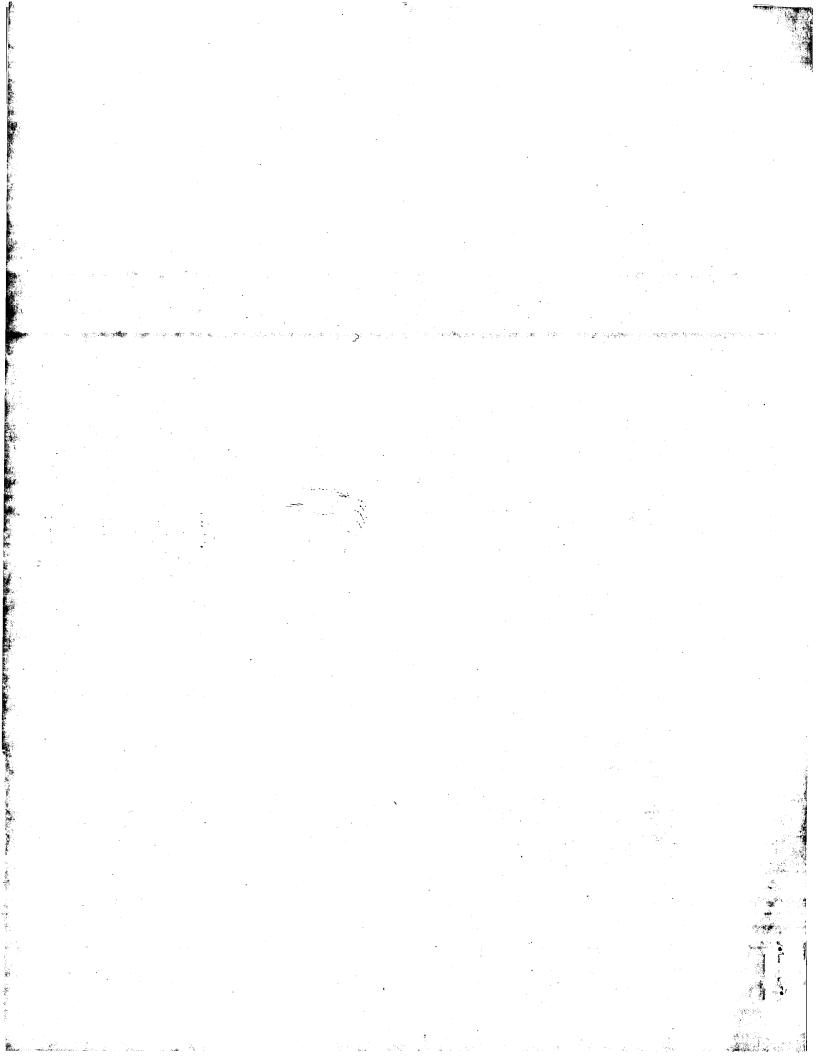
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: UNMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUISO-MACLOE, NICCLE
TITLE OF INVENTION: PEGFPLIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGFELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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Pred. No. 1.7e-11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                           Length 58;
                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                    Score 267; DB 9;
Pred. No. 1.7e-12;
0; Mismatches 1
                                                                                                                                ; ORGANISM: Bordetella bronchiseptica US-09-855-754-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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Best Local Similarity 87.9%;
Matches 51; Conservative
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l Similarity 87.9%;
51; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: PatentIn Ver
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Best Local Similarity
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LENGTH: 922
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                                                                                                   TYPE: PRT
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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US-09-855-754-24
                                                                                                                        APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09855754
Publication No. US20020192237A1
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                                                      Sequence 5, Application US/09855754
Publication No. US20020192237A1
                                                                                                                                             GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bordetella pertussis US-09-855-754-5
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78.8%;
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Best Local Similarity 73.1%;
Matches 38; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 78.8
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05
                                                                                                   GENERAL INFORMATION:
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US-09-855-754-24
                            US-09-855-754-5
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LENGTH: 910
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-00000
CURRENT APPLICATION NUMBER: 105/09/985,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PEGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND SINVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: MANUNCHORNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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  GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQP-PQ-RPEAPAPQPPAGRELSAA 52
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2.5e-10;
ches 1;
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Pred. No. 1.6e-08;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica US-09-855-754-23
                                                                                                                                                         Sequence 22, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUBSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09855754
Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.9%;
Best Local Similarity 85.7%;
Matches 48; Conservative
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Best Local Similarity 78.8%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 54
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                    US-09-855-754-22
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                              REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
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Pred. No. 2.1e-07;
1; Mismatches 0; Indels
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PETITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETE TITLE OF INVENTION: BONCHISEPTICA, THEIR USE IN DIAGNOST TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186.5; DB 9;
Pred. No. 3.9e-07;
1; Mismatches 0;
                                                                                                        TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT PELLOATON NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-171-384-3; Sequence 3, Application US/10171384; Publication No. US20030031680A1
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

7, 2003, 16:41:02 ; Search time 9.7446 Seconds (without alignments) 513.008 Million cell updates/sec Run on:

US-09-855-754B-17 298 1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
!: pir1:*
!: pir2:*
!: pir3:*
:: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hypothetical prote pherophorin-S - Vo sulfated surface g nuclear protein EB hypothetical proli UL36 protein - hum 58K outer membrane pertactin - Bordet outer membrane pro hypothetical 47.8K cysteine-rich exte proline-rich prote hydroxyproline-ric cysteine-rich exte Description S16748 T07907 B48232 H83619 AE2295 S42442 A34043 WMBEH6 \$21961 \$51939 T17737 A33647 Query Match Length DB 446 196 270 383 599 485 Score 135 134 132.5 132 145.5 145 140.5 138.5 138 Result ŝ

proline-rich prote hypotherical prote hypothetical prote circumsporozoite p circumsporozoite p acrosin (EC 3.4.21 ORF2 protein - sai	extensin-like prot pistil extensin-li proline-rich prote extensin - Volvox	excessin-like prot acrosin (BC 3.4.21 lysine/proline-ric proline-rich prote proline-rich prote
28 KB 1 3 5	1962	00744
T17525 C96623 T31611 OZZQMB OZZQBK S47538	T1074 J0169 C2914 S2269	71788 71788 71788 71788 72426
9994499	00000	77077
549 929 1585 332 348 431	461 227 464	415 415 456 240 240
444444 6.1111111 9.6.8.8.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.	4444 6444	4 4 4 4 0 0 0 0 0 0 0 0 0
125 125 125 126 124 - 5 124 - 5 124 - 5	124 123.5 122.5 122.5	122 122 121 121.5 121.5
30 32 33 34 35	7 8 8 8 4 4 7 8 8 6 0 5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

RESULT 1 A47675 68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica C;Species: Bordetella bronchiseptica C;Species: Bordetella bronchiseptica C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-oct-1999 C;Accession: A47675 R;Li, J.;Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. R;Lii, J.;Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. R;Lii, J.;Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. A;Title: Cloning, nucleotide sequence and heterologous expression of the protective of A;Totestics: A47675; MUID:92407514; PMID:1527510 A;Cocession: A47675 A;Status: preliminary A;Rocession: A47675 A;Status: preliminary A;Rocession: A47675 A;Status: preliminary A;Rocession: A47675 A;Rolecule type: nucleic acid A;Rocession: A47675 A;Roc
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52 õ

Perfactin - Bordetella parapertussis
N.Alternate names: outer membrane protein P70
C; Species: Bordetella parapertussis
C; Date: O'Apr-1994 #text_change 08-Oct-1999
C; Accession S15204; S14659
R; Li, L.J.; Dougan, G; Novotny, P; Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
Mol. Microbiol. 5, 409-417, 1991
A; Ritle: P; 70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A; Reference number: S15204; MUID:91251771; PMID:2041476

proline-rich prote chitinase (EC 3.2. proline-rich prote T20H2.9 protein -

prote tyrosine-p hypothetical prote proline-rich prote

protein-

439 288 1137 1494 165

130 129.5 129.5 129.5 129.5 129.5 129.5 126.5 126.5 126.5

A; Molecule type: DNA A; Residues: 1-922 <LIL> A; Cross-references: EMBL:X54547; NID:g39761; PIDN:CAA38419.1; PID:g39762 C; Genetics: A; Gene: pro| C; Keywords: membrane protein

hypothetical prote hypothetical prote proline/lysine-ric

hypothetical proline-rich proline-rich proline-rich

T02632 T17547 T17636 T17815

Gaps ; 9 Length 922; Ouery Match

89.6%; Score 267; DB 2; Length 92
Best Local Similarity 87.9%; Pred. No. 3.6e-11;
Matches 51; Conservative 0; Mismatches 1; Indels

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1 GÄKAPPAPÄPAPQPGPQPGPQP-----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52

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Gaps

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proline-rich protein - rape (fragment)
C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Date: 13-Jan-1995 #text_change 09-Sep-1997
C; Accession: S16748
R; Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL. Data Library, August 1991
A; Reference number: S16748
A; Reference number: S16748
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: RNB>A; CROB>A; C
                                                                                                                                                                                                                                        A.Accession: PQ0475
A.Molecule type: mRNA
A.Residues: 39-209 <GOLD-
A.Cross-references: EMBL:Z14020; NID:g19918; PID:g19919
A.Experimental source: stigma, style; strain Petit Havana SR1
A.Experimental source: stigma, style; strain Petit Havana SR1
C.Superfamily: glutelin
C.Superfamily: glutelin
C.Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F.1-19/Domain: signal sequence estratus predicted <SIG>
F.20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
F:146/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                            R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani,.C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
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C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
C;Accession: T07907
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F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-446/Product: hydroxyproline-rich glycoprotein GAS28 #status predicted
                                 3:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
Pezzotti, M.; Seurinck, J.; Mariani,.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KAPPAPKPA-----PQPGPQPGPQPGPQPPQPPQP-PQRPEAPAPQPPAG 46
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A. Reference number: 216207
A. Stackus: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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Pred. No. 0.0046;
3; Mismatches 14
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Pred. No. 0.0013;
2; Mismatches 1:
                                      GB:L13439; NID:g310922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.7%;
57.5%;
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50.98;
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Matches 27; Conservative
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Matches 23; Conservative
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Best Local Similarity
Matches 24; Conserv
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A: Residues: 1-209 <WUA>
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BDNA Res. 1, 163-168, 1994
A; Title: No age of cluster encoding major cell surface glycoproteins of rat Pneumocystis
A; Reference number: JC2299; MUD: 96051989; PMID: 8535973
A; Accession: JC3301
A; Molecule type: DNA
A; Residues: 1-430 < WADD
A; Residues: 1-430 < WADD
A; Cross-references: GB: D31909; GB: D17441; NID: 9559718; PIDN: BAA06706.1; PID: d1007278; PI
                                                                                                                                                                                                                                                                              C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
C;Accession: A32560
C;Accession: A32560
A;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number: A32560; MUID:89264462; PMID:2542937
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Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
A;Status: preliminary
A;Molecule type: mRNA
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May.1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48232; PQ0475; S24617
                                                                                                                                                                                                  outer membrane protein P.69 precursor - Bordetella pertussis.
C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pneumocystis carinil
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Cross-references: GB: J04560; NID: g144053; PIDN: AAA22980.1; PID: g144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
C; Keywords: membrane protein
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 1-34/Domain: outer membrane protein P6: 9 #status predicted <MAT>
564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQPQPQPAPAPQPPAGRELSAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPEA--------
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Pred. No. 0.0021;
5; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.5%; Score 207; DB 2; 78.8%; Pred. No. 3.2e-07; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical 47.8K protein - Pneumocystis carinii
N;Alternate names: ORF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 48.8%;
1.Similarity 40.9%;
27; Conservative
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Best Local Similarity
Matches 41; Conserv
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Best Local, Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A32560
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A;Ncterior Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE2295 R;RaneAco, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 Squence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
R;Godl, K; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophori
A;Reference number: Z17154: MUID:97162277; PMID:9009264
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Y0752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to tC;Keywords; extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession; A33647; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of shacession: A33647; MUID:90094551; PMID:2689458
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Length 383;
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A;Molecule type: mRNA
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Pred. No. 0.0069;
1; Mismatches 1
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Pred. No. 0.0097;
2; Mismatches
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55.0%;
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A;Molecule type: DNA
A;Residues: 1-383 <KUR>
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Matches 22; Conserv
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Best Local Simi
Matches 22;
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A.; Larbig, K.; Lim,
                                                                                                                                                                                                                       C.Species: Nicotiana tabacum (common tobacco)
C.Date: 2-6-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C.Date: 2-6-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C.Accession: 846232; PQ0414; S24616
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Scl. 10.S.A. 90; 6822-6833; 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83619
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A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Title: Developmental expression of tobacco pistil-specific genes encoding Reference number: P00474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C;Keywords: cell wall; extracellular matrix; fertilization
C;T1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 #status
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Pred. No. 0.0035;
3; Mismatches 15; Indels
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                A; Residues: 1-196 GMTA>
A; Residues: 1-196 GMTA>
A; Cross-references: GB:L13440; NID:g310924; PIDN:AAA34060.
R; de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                       common
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Pred. No. 0.0045;
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52.0%;
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Best Local Similarity 55.0%;
Matches 22; Conservative
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A; Residues: 'MAG',1-105 <GOL>
A; Cross-references: EMBL:214014
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les 26; Conserva
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A;Molecule type: DNA
A;Residues: 1-270 <STO>
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2 AKAPPAPKPAPQPGPQPGPQPGPQP-----PQPPQPPQRPEAPAPQPPA 45

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Search completed: May Job time: 10.7445 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
roc. Natl. Acad. Sci. U.S.A. 83, 5095-5100, 1986
;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins; a
;Reference number: 842440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Blochem. Blophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized by the repetition
A;Reference number: A90159; MUID:90147742; PMID:2105723
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: human herpesvirus 4, Epstein-Barr virus
Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Owenia fusiformis
:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
:Accession: A34043; B34043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A;Residues: 1-88,'PPP',89-487 <DAM>
A;Residues: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                          A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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                                                                                                                                                      Length 485;
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                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                             5 PPAPKPAPQPGPGPGPGPQPPQPPQRPEAPAPQPP 44
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Pred. No. 0.011;
); Mismatches 20;
                                                                                                                                                    Score 136; DB 2;
Pred. No. 0.0096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  March 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farrell, P.J.

Ubmitted to the EMBL Data Library,
Federence number: S32973
Accession: S32988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S42442; S32988; S42447
                                                                                                                                                 45.6%;
55.0%;
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53.5%;
                                                                                                                                            Query Match
Best Local Similarity 55.0%
Matches 22; Conservative
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Matches 23; Conservative
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A; Cross-references: GB:M32217
A; Accession: B34043
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A; Residues: 59-136 <BA2>
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-487 <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear protein EBNA2
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7, 2003, 16:55:26

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Riwiceoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: I30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-3164 <MCG>
A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C;Genetics:
A;Gene: UL36
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         Length 141;
                                                    Indels
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  Score 134; DB 2; L
Pred. No. 0.005;
); Mismatches 20;
                                                                                                                            5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.5%; Score 132.5; DF Best Local Similarity 62.8%; Pred. No. 0.07; Matches 27; Conservative 3; Mismatches
                           Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                           protein - human herpesvirus 1 (strain 17)
Query Match
Best Local Similarity 53.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                      Species: human herpesvirus
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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2003, 16:31:49; Search time 5.0494 Seconds

(without alignments)

427.133 Million cell updates/sec
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Title: US-09-855-754B-17
Perfect score: 298
Sequence: 1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 52

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description			P24328 bordetella	P14283 bordetella	P40603 brassica na	P21997 volvox cart	P12978 epstein-bar	P21260 owenia fusi			P40602 arabidopsis	Q83949 orgyia pseu			P23093 plasmodium			Q03211 nicotiana t	P08001 sus scrofa	P05142 mus musculu	P05143 mus musculu	O70324 mus musculu	Q64467 mus musculu	P78621 emericella	P09791 trypanosoma		P25050 herpesvirus			P08469 trypanosoma	Q06084 trypanosoma	_	P58840 homo sapien	Q05859 mus musculu
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SUMMARIES	11	`	PENI_BURBR	PERT_BORPA	PERT_BORPE	APG_BRANA	SSGP_VOLCA	EBN2_EBV	YPRO_OWEFU	TEGU_HSV11	GP1_CHLRE	APG_ARATH	Y066_NPVOP	MOZ_HUMAN	CSP_PLABE	CSP_PLABA	ACRO_RABIT	COLL_HSVSC	EXLP_TOBAC	ACRO_PIG	PRP2_MOUSE	PRP3_MOUSE	MOT8_MOUSE	G3PT_MOUSE	SEPA_EMENI	PARB_TRYBB	RFX1_HUMAN	COLL_HSVS7	VASP_HUMAN	CAPU_DROME	PAR1_TRYBB	PARC_TRYBB	HXA3_MOUSE	ACRL_HUMAN	FM14_MOUSE
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dР	Query	0		89.0	69.5		45.6	45.3	٠.	٠	43.8	43.6	43.5	41.9	41.8	41.8	41.8	41.6	41.4	40.9						-	39.8			39.6	39.1	39.1	39.1	38.9	38.9
	Score	1.46	1 1	197	207	140.5	136	135	134	132.5	130.5	130	129.5	125	124.5	124.5	124.5	124	123.5	122	121.5	121.5	121.5	120	120	118.5	118.5	118	118	118	116.5	116.5	116.5	116	116
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			Q9savl arabidopsis									P42858 homo sapien	
	FMN1_MOUSE	WASP_HUMAN	MB11_ARATH	Z219_HUMAN	HD_MOUSE	YAP1_HUMAN	WASP_MOUSE	HD_RAT	ACRO_HUMAN	CDNC_HUMAN	BAI1_HUMAN	HD_HUMAN	
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	38.9	38.4	38.1	38.1	38.1	37.9	37.8	37.4	37.2	37.1	37.1	37.1	
=-	116	114.5	113.5	113.5	113.5	113	112.5	111.5	1111	110.5	110.5	110.5	
	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                    STRAIN-CN2591,
MEDLINE-91251771; PubMed-2041476;
MEDLINE-91251771; PubMed-2041476;
MEDLINE-91251771; PubMed-2041476;
MI L.J., Dougan G., Novotny P., Charles I.G.;
P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coli.";
Mol. Microbiol. 5:409-417(1991).
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                            ä
                                                                                                                                              22
                                                                                    Score 271; DB 1; Length 911;
Pred. No. 1.6e-10;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA

    Last sequence update)
    Last annotation update)
    (Outer membrane protein P.70) (P.95).

                                           3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERTACTIN (P.70). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Juter membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pertactin_vir.
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004899; Pertact_sup. InterPro; IPR003992; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seqi
15-JUN-2002 (Rel. 41, Last anno
                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                        90.9%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03212; Pertactin; 1.
                                                                   93995
                                                                                                              51; Conservative
                                                                                                                                                                                                               STANDARD;
                      270
275
280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                   Pertactin precursor
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PIR; S14659; S14659.
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                                                                   911 AA;
                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=519;
                                                                                                                                                                                                              PERT_BORPA
P24328;
                                                                                                                                                                                                                                                                                                             Bordetella
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PERT_BORPA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EmsLoy P., Charles I.G., Fairweather N.F., Isaacs N.W.;
EmsLoy P., Charles I.G., Fairweather N.F., Isaacs N.W.;
Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
--- FUNCTION. AGGLOTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
--- FUNCTION. AGGLOTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novotup P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLUTAR LOCATION: Outer membrane.
-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AA APPROXIMATE REPEATS OF P-Q-P
                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                               LINES). 4 \times 5 \text{ AA} \text{ TANDEM REPEATS OF G-G-A-V-P}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                   Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRN OR OMF089A.
                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                  3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                Score 267; DB 1;
Pred. No. 2.8e-10;
                                                                                                                                                                    4 (APPROXIMATE)
9 X 3 AA APPROX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 AA.
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 264 AND 332.
MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                           MM.
                                                                                                                                                                                                                                                                                             89.6%;
87.9%;
                                                                                                                                                                                                                                        95178
                                                                                                                                                                                                                                                                                                                               1 Similarity 87.9 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                          290
270
275
280
285
603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONCENTRATION.
                                                                                                                                                                                                                                        922 AA;
                                                          266
266
271
271
281
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CN2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERT_BORPE
P14283;
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us-09-855-754b-17.rsp

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PIR; A33647
                                                                                                                                                                                                                SSGP_VOLCA
P21997;
                                     ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                           NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                        SSGP_VOLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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81118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
-!- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-94004980; Pubmed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
Draper J., Scott R.;
                                                                                                                                                                  LINES).
5 x 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURATION.
-!- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                      ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                                                                                   69.5%; Score 207; DB 1; Length 910;
78.8%; Pred. No. 1.2e-06;
Live 1; Mismatches 0; Indels 10;
                                                                                                                                         CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draper J., Scott R.; "Gametophytic expression of an anther-specific
                                                                                                                                                                                                                                                  X 3 AA TANDEM REPEATS OF P-Q-P. A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                568 GAKAPPAPKPA------PQPGPQPPQPPQP--QPEAPAPQPPAGRELSAA 609
                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
                                                                                                                   PERTACTIN (P.69).
                                                                                                                                                                                                                             (APPROXIMATE).
                                                                                                                                                                                                                                        (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                     449 AA.
                                                                                Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                POTENTIAL
         InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001087; Lipase_GDSL
                                           Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                             93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
 PIR; A32560; A32560.
                                                                                                                                                                                                                                                             910 AA;
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3708;
                                                                                                                                                                            266
2266
271
276
281
286
579
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                                                                                                                                                                                                                                                                                                                                                                                                                    APG_BRANA
P40603;
                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                     Query Match
                                                                                             SIGNAL
                                                                                                                                                                           DOMAIN
REPEAT
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REPEAT
                                                                                                                              PROPEP
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                                                                                                                                         SITE
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                                                                                                                                                                                                                                                                                                                                                                                                       APG_BRANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the cellular compartment.";
J. Cell Biol. 109:349-3501(1989).
-!- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
-!- FUNCULULE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-F. Nagariensis / HKI0;
MEDLINE-90094551; PubMed-2689458;
Erti H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPFOLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                47.1%; Score 140.5; DB 1; Length 449; 50.9%; Pred. No. 0.0079; tive 3; Mismatches 14; Indels 9
                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                  45.6%; Score 136; DB 1; Length 485; 55.0%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                               3 KAPPAPKFA-----PQPGPQPGPQPGPQPPQPPQP-PQRPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                            POTENTIAL.
9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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1; Mismatches
                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfation; Hydroxylation.
28 340 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                       428 428 PH 449 AA; 48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 AA;
                                                                                                                                                                                Query Match
Best Local Similarity
Matches | 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; |A33647
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nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
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ID EBN2_EBV
AC P12978;
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Gaps

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47

Length 141; 20; Indels

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MEDLINE-90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Brasence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine."
Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; A34043; A34043.
                                                                                                                                                              58 POLY-PRO.
116 H-T-H MOTIF (POTENTIAL).
1141 15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                           5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR
                                                                                                                                                                                                                                                                                                             Score 134; DB 1;
Pred. No. 0.0086;
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                    \begin{array}{c} \operatorname{Hypothetical\ protein;\ DNA-binding.} \\ \operatorname{NON\_TER} & 1 \end{array}
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juery Match
Best Local Similarity 62.8%,
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3164 AA;
                                                                                                                                                                                                         141 AA;
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         TEGU_HSV11
P10220;
                                                                                                                                                                            DNA_BIND
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                          SECUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149; MEDLINE-84270667; PubMed-6087149; Baer R. Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G., "Na sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                   Cohen J.I., Wang F., Kleff E.;
"Epstein Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
J. Virol. 65:2546-2554 (1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90266473; PubMed-2161150;
Pettl L., Sample C., Kleff E.;
Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 X 2 AA TANDEM REPEATS OF R-G. DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.3%; Score 135; DB 1; Length 487; 53.5%; Pred. No. 0.018; live 0; Mismatches 20; Indels
                                                                       Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR 47
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPRO_OWEFU STANDARD; PRT; 141 AA. P21260; P21261; A. P21260; P21261; B. Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-WAY-1995 (Rel. 32, Last annotation update) Hypothetical proline-rich protein (Fragment). Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; V01555; CAA24877.1; ALT_INIT. TRANSFAC; T01618; -.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 AA; 52544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - ! - PTM: PHOSPHORYLATED.
                                            EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                  NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6347
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF LMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                            DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPRO_OWEFU
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                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.

MEDLINE-88274327; Pubmed-2839594;

MEDLINE-88274327; Pubmed-2839594;

MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,

MCMBD D., Perry L.J., Scott J.E., Taylor P.;

"The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1.";

J. Gen. Virol. 69:1531-1574(1988).

-I- FUNCTION: TEGUNENT PROTEIN.

-I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,

EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 35 X 2 AA TANDEM REPEATS OF P-Q. 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2941 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPG 2982
                                                                                                                                                                                                                             Herpes simplex virus (type 1 / strain 17).
Viruses: deDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID-10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 PAPKPAPQPGPQPGPQP-PQP-PQPPQRPEAPAPQPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 132.5; DB 1;
Pred. No. 0.098;
3; Mismatches 10;
                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                Large tegument protein (Virion protein UL36)
Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; 130085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
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Q93Z14; Q9LNT8;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                             "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                       encoding cell wall hydroxyproline rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-! FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGETATIVE CELL WALL PROTEIN GP1.
                                                                                                                                                                   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                               MEDLINE-21159092; PubMed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S.; Kilz S., Drees J.,
Goodenough U.W.;
                                       OFFQ6; Q03927;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
91ycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91017504; PubMed-1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%; Score 130.5; DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 APPSPRPPAPPPPSPPPPPPPPPPPPANTPMPPSPPSPPPPPPP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 130.0, Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 APPAPK-PAPQPGPGPGPGPQP-----PQPPQPPQRPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. SUBUNIT: Associates with GP2 and GP3.
1. PTM: N-glycosylated and O-glycosylated.
                             555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF309494; AAG45420.1; --
EMBL, M58495, AAA69706.1; ALT_SEQ.
G1ycoSutteDB, G9FP06; --
InterPro; IPR003965; P_rich_extensn.
InterPro; IPR003965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                            PRT;
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                                                                                                                                                      Chlamydomonas reinhardtii.
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                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
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299
399
455
455
555 AA;
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                                                                                                                                                                                                  NCBI_TaxID=3055;
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SIGNAL
                            CHLRE
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             GP1_CHLRE
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RESULT 9
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534 AA.

PRT;

STANDARD;

APG_ARATH

RESULT 10 APG_ARATH

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                                                                                                                                                                                                                                                                                                                                                                                                                      A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buhte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buhte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buhte O., Chan L., Conway A.B., Conway A.R., Creasy T.H., C.W., Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., C.W., Conn L., Conway A.B., Fong B., Fujii C.Y., Col H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin Hooper S., Lee A., Lee J.M., Lea J. H., Li Y.-P., A. Lin X., Liu S.X., Liu S.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I., A. Bakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Wu Utterback I., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; Fabildopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huizar L.,
           01-FEB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline rich protein APG precursor.
APG OR ATIG20130 OR T20H2.9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; wagnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATURATION.
-1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
-1- CAUTION: Ref. 2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                          Draper J., Scott R., "Gametophytic expression of an anther-specific Arabidopsis thallana gene."; Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X60377; CAA42925.1; -.
EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AX058847; AAL24235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Columbia;
MEDLINE-21015719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=3702;
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MOZ_HUMAN
Q92794;
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                                                                                                                                                                                                                                                                                                                                    ;
;
                                                                         ANTER-SPECIFIC PROLINE-RICH PROTEIN APG.
BY SIMILARITY.
BY SIMILARITY.
S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 806-875 FROM N.A.
MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             083949; 065364; 010323; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 98.6 kDa protein (ORF71). Orgyla pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
                                                                                                                                                                                                                                                                                Score 130; DB 1; Length 534; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene essential for Orgyia pseudotsugata baculovirus DNA replication.";
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                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                 3 KAPPAPKPAPQPGPQPGPQPPQ--PPQPPQRPEAPAPQP
                                                                                                                                                                                                                                                                                                          Pred. No. 0.039
2; Mismatches
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     PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97271300; Pubmed-9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seudosugata.";
7. Gen. Virol. 77:825-837(1996).
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875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U75930; AAC59070.1; -.
                                                                                                                                                                                                                                                                                43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U39145; AAB04047.1; -. EMBL, D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
DOMAIN 86 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleopolyhedrovirus.
                                                                                                                                                                                                                              534 AA;
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudosugata.
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PROSITE; I
Signal.
SIGNAL
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ACT_SITE
ACT_SITE
CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                  Matches
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     NA LILLE LILL SO LILL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOTTOW J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; The translocation t(8;16)(pl1;pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).

I. FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.

I. SUBCELLUTAR LOCATION: Nuclear.

DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL TRANSLOCATION THAT PRODUCES A MOX-CBP CHIMAERA OBSERVED IN THE M4/AB SUBTYPE OF ACUTE MYELOID LEUKEMIA.

SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocation; Zinc-finger; Repeat;
        Length
                                                             Indels
                                                                                                                                              44
                                                                                                              5 PPAPKP----APQPGPQPGPQPPQPPQPPQRPEAPAPQPP
Score 129.5; DB 1;
Pred. No. 0.059;
1; Mismatches 12;
                                                                                                                                                                                                                                                                                                               2004 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=96376968; Pubmed=8782817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01359; ZF_PHD_1; 1. PROSITE; PS50016; ZF_PHD_2; 2. Proto-oncogene; Chromosomal tra
43.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U47742; AAC50662.1;
Genew; HGNC:13013; ZNF220.
MIM; 601408; -.
                                                          26; Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1150
1242
1302
1414
Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear prote
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RESULT 14

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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                 BREAKPOINT FOR TRANSLOCATION TO FORM MOZ-CBP.
                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 X 8 AA TANDEM REPEATS.
16 X 2 AA TANDEM REPEATS OF P-Q.
E8068A6D11D9551B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 339;
                                                                                  Length 2004;
                                                                                                                                                                                                                                                                                         Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                           9FFBBAC3792854BA CRC64;
                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                 PROBABLE.
CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                 5 PPAPKPAPQPGPQPGPQPPQPPQPPQ----RPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PAP----KPAPQPGPQPGPQPGPQPPQPPQPPQRPEAPAPQP 43
                                                                                  Score 125; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.8%; Score 124.5; DB 58.1%; Pred. No. 0.061; tive 1; Mismatches 1
                                                                                                                                                                                                                                                        06, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                   339 AA
                                                                                               Pred. No. 0.2;
2; Mismatches
            GLN/PRO-RICH.
MET-RICH.
                                                                                                                                                                                                                                                                                Circumsporozoite protein precursor (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A25083; OZZOMB.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00090; tsp_1; 1.
PRINTS, PR0130; CRMSPRZOITE.
SMART; SM00209; TSD1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 238 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malaria; Sporozoite; Repeat;
                                                                                  41.9%;
53.3%;
                                                           2004 AA; 225054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M14135; AAA29577.1; -.
                                                                                                           24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, 01-JAN-1988 (Rel. 06,
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel.
1593
1643
1897
1546
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5821;
                                                                                                                                                                                                                     CSP_PLABE
P06915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                  Query Match
                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
DOMAIN
DOMAIN
DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                           Matches
                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                         CSP_PLABE
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                                                                                                                                                                                SEQUENCE FROM N.A.

MEDILINE-90221834; Pubmed-2183186;
LOCKYGT M.J./ Davies C.S., Suhrbier A., Sinden R.E.;
LOCKYGT M.J./ Davies C.S., Suhrbier A., Sinden R.E.;
LOCKYGT M.J./ Davies C.S., Suhrbier A., Sinden R.E.;

Mucleotide sequence of the Plasmodium berghel circumsporozotte
T. Mucleotide sequence of the Plasmodium berghel circumsporozotte
T. Mucleotide sequence of the 234L.";
Protein gene from the MRA clone 2.34L.";
INUCLEOT ACIGS Res. 18:376-376(1990).

-1- FUNCTION: THE CIRCUMSPOROZOTTE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).

-1- MINCRELIANDOSIS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.

-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 347;
                                                                                                                               Eukaryota; Alyeolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_raxID=5823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIRCUMSPOROZOITE PROTEIN.

13 X 8 AA REPEATS.

17 X 2 AA REPEATS OF P-Q.

0EC240EE35681AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PAP----KPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 PAPPOGNINPQPQPRPQPQPQPQPQPQPQPQPPPQPPPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.8%; Score 124.5; DB
                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
101-FUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                          Circumsporozolite protein precursor (CS).
Plasmodium berghei (strain Anka).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X17606; CAA35608.1; -.
PIR; S07873; OZZQBK.
InterPro; IPPR003067; Crcmsprzolte.
Interpro; IPPR00084; TSP1.
Pfam; PPR00099; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00209; TSP1; 1.
PROSITE, PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA; 37776 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Matches 25;
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P48038;
CSP_PLABA
P23093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACRO_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                  ACROSOME.

CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
                                    SEQUENCE FROM N.A.

STRAIN-New Zealand white; TISSUE-Testis;

STRAIN-New Zealand white; TISSUE-Testis;

STRAIN-New Zealand white; TISSUE-Testis;

Richardson R.T., O'Rand M. S.

"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";

Biochim. Biophys. Acta 1219:215-218(1994).

IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY.
                                                                                                                                                                                                                                                                                                            CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.8%; Score 124.5; DB 1; Length 431;
43.6%; Pred. No. 0.072;
Live 0; Mismatches 20; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACROSIN LIGHT CHAIN (BY SIMILARITY)
ACROSIN HEAVY CHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . ) (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AKAPPAPKPAPQPGPQ------PGPQPGPQPPQPPQPPQRPEAPAPQPPA 45
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                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.223; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 43.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 AA;
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CARBOHYD
ACT_SITE
ACT_SITE
ACT_SITE
SCT_SITE
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271 271 250.5 250.5 250.5 250.5 250.5 250.5

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1 GAKAPPAPKPAPQPGPGPGPGPGPPPGPPQPPQPPQRQPEAPAPQPPAGRELSAA 76
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                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
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94.6%; Score 282; DB 2; Length 12.
Best Local Similarity 91.1%; Pred. No. 5.7e-17;
Matches 51; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR156773; ARF82397.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IRR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
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122 Aa; 12395 MW; 8ED00966A40FF994 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Infect. Immun. 69:1917-1921(2001).
EMBL: AV07265; AAG34441...
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR00265; P.rich_extensn.
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                  Bordetella
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                                                                                                          RESULT 4
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Boursaux-Eude C., Gulso N.;
Boursaux-Eude C., Gulso N.;
Boursaux-Eude C., Gulso N.;
Folymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
Infect. Immun. 68:4815-4817(2000).
InterPro; IPR004899; Pertact.sup.
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96.5%; Score 287.5; DB 2; Length 215;
Best Local Similarity 98.1%; Pred. No. 3.2e-17;
Matches 52; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                  Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL; APO07263; AAG38439.1; ...
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
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                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fregment).
      215 AA.
      PRT;
                                                                                                                                                                                                                                                STRAIN=S010328;
MEDLINE=21117018; PubMed=11179374;
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22327 MW;
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PRINTS; PR01217; PRICHEXTENSN.
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PRINTS; PR01217; PRICHEXTENSN.
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  PRELIMINARY;
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                                                                                            Pertactin (Fragment).
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                          NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                      Register K.B.;
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SEQUENCE
09ALQ4
09ALQ4;
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InterPro; IPR002965; P_rich_extensn.
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                          STRAIN=335;
MEDLINE-20359389; PubMed=10899896;
MEDLINE-20359389; PubMed=10899896;
MEDLINE-20359389; PubMed=1080 N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250083; CAB76437.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250081; CAB76435.1; ...
InterPro; IPR004899; Pertact_sup.
                                              Gaps
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                                                                              1 GAKAPPAPRPAPQPGPQPGPQPPQPPQPPQ----RPEAPAPQPPAGRELSAA 52
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacterla; Proteobacterla; beta subdivision; Alcaligenaceae;
                       DB 2; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 115;
                     Score 282; DB 2; Length 25
Pred. No. 1e-16;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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SEQUENCE 115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
26107 MW; 368C142508D77057 CRC64;
                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.9%; Score 274; DB 2;
86.7%; Pred. No. 2.5e-16;
tive 0; Mismatches 0
                                                                                                                                                115 AA
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Interpro; IPR00286; P_ich_extensn.
Pfan: PF03212; Pertactin; il.
PRINTS; PR01217; PRICHEXTENSN.
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                      94.6%;
                    Query Match
Best Local Similarity 91.1
Matches 51; Conservative
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                                                                                                                                               PRELIMINARY;
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252 AA;
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 SEQUENCE
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Q9K5H5;
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                                                                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                            Length 107;
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Bacteria; Prcteobacteria; beta subdivision; Alcaligenaceae;
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EMBL, ANGO1291; AAG38447.1; ...
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P.rich_extensn.
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107 AA: 11036 MW; 1AC13209D0238107 CRC64;
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Last annotation update)
                                                                                                                       Match 90.9%; Score 271; DB 2; I Local Similarity 96.2%; Pred. No. 4.2e-16; les 51; Conservative 0; Mismatches 0;
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Pred. No. 7e-16;
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-JUN-2001 (TrEMBLrel. 17, Last seq
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MEDLINE-21117018; Pubmed-11179374;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PRO1217; PRICHEXTENSN
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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nes 48; Conserv
                                                                                                                 SEQUENCE FROM N.A.
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Bordetella.
NCBI_TaxID=518;
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Matches
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL, A.250089; CAB76443.1; InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
Prim; PR03212; Pertactin; 1.
PRINTS; PR01217; PRICEEXTENSN.
                                                                "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (AnG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJJ45927; CAB82515.1; -
InterPro; IPR003992; pertactin.

InterPro; IPR004999; pertactin.

InterPro; IPR004999; pertactin.

InterPro; PR004999; Pertactin.

PRINTS; PR01484; PRTACTINALY.
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Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.,
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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87.9%; Pred. No. 9.3e-16;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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96.2%; Pred. No. 2.3e-15;
1ve 0; Mismatches 0;
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hes 51; Conservative
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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815.4817(2000).
EMBL; AJ250077; CAB76431.1;
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertuasis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4815.4817(2000).
EMBL; AJ250079; CAB76433.1;
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                                                                                                                                                                                                                                                                                                                                              Score 250.5; DB 2; Length 104;
Pred. No. 2.1e-14;
0; Mismatches 0; Indels 5;
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01-CCT-2000 (TEMBLE) 15, Last sequence update)
01-JUN-2002 (TEMBLE) 21, Last annotation update)
Pertactin (Fragment).
Bordetalla bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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llarity 90.6%; Pred. No. 2.1e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AA
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01-0CT-2000 (TrEMBLrel, 15, Last seq
01-JUN-2002 (TrEMBLrel, 21, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LAPR;
MEDLINE=20359389; PubMed=10899896;
MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                          InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.6%;
Matches 48; Conservative
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                               Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 AA; 20575 MW; AC940EC331A725AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.1%; Score 250.5; DB 2; Best Local Similarity 90.6%; Pred. No. 3.5e-14; Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               InterPro; 1PR003992; pertactin.
InterPro; 1PR004899; Pertact_sup.
InterPro; 1PR002965; P_rich_extensn.
PFam, PF03312; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 7, 2003, 16:53:14
Job time: 27.5758 secs
                                                                                                                                             STRAIN-MBORD031;
MEDLINE-21117018; PubMed-11179374;
                                                                                                                                                                                                                                                             E. Immun. 69:1917-1921(2001).
AF298590; AAK16691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                       bronchiseptica Pertactin.
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                                                                                                                     SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=518;
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                                                                                                        Kell D.J., Fenwick B., "Warlability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ell D.J., Fenwick B.; variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                       Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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115 AA; 11693 MW; FA3A76596F7097EB CRC64;
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115 AA; 11705 MW; EIABD4D347D20652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 250.5; DB 2;
Pred. No. 2.2e-14;
0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                EMBL; AF156771; AAF82395.1; -...
INTERPRO; IPRO0A899; Pertact_sup.
INTERPRO; IPRO02965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
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Similarity 90.6%;
8; Conservative
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PRN.
                                                                                                                                                                                 amino acid repeats.
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                                                                 SEQUENCE FROM N.A.
Bordetella.
NCBI_TaxID=518;
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Kell D.J.,
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SEQUENCE
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Best Local ?
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Q9AHP0
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Drosophila melanog Human low density Rabbit low density

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Streptococcus pneu Ser-Pro-Pro-Pro Drosophila melanog

Human polypeptide Human polypeptide Human polypeptide Drosophila melanog

Searched:

Database

4567860

Result ş

Sequence:

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    B. bronchiseptica strain II-5 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                   AAR28150
AAG49660
AAC02036
ABC21919
ABB93838
AAP82971
AAP82971
AAP82949
AAB82403
AAB864403
AAB864403
                                       AAE16200
AAE16201
AAE16201
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AAE16184
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AAE1779
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AAR1177
AAR1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16197 standard; peptide; 56 AA.
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130.5
130.5
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133.5
133
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138
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B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
Bordetella paraper
Bordetella paraper
Pertactin antigen
B. bronchiseptica
B. bronchiseptica
Pertactin antigen
princhinalica
                                                                                             7, 2003, 16:31:28; Search time 29.0971 Seconds (without alignments) 256.453 Million cell updates/sec
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322
I GARAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
           5.1.4_p5_4578
Compugen Ltd.
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           GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAE16196
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AAR14320
AAR26503
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Gapop 10.0 , Gapext 0.5
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fourter membrane protein) or their fragments. Pertactin present invention or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens at identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                    present invention relates to Bordetella bronchiseptica pertactin
1c; 47pp; English
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  Length 56;
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100.0%; Score 322; DB 23;
100.0%; Pred. No. 1.2e-17;
ive 0; Mismatches 0;
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                        56; Conservative
  Query Match
Best Local Similarity
                          Matches
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQPPQPPQPPAGRELSAA 56 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA ò g

AAE16195 RESULT

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AAE16195 standard; peptide; 60
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AAE16195;

26-MAR-2002 (first entry)

B. bronchiseptica strain II-3 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fullds, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiques can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                B. bronchiseptica strain II-6 pertactin outer membrane protein region
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                                                                                                                                                                 1 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPGRELSAA 56
 B. bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to Bordetella bronchiseptica
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                                                                                Length 60;
                                                                                                                 Indels
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 sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 94.1%; Score 303; DB 23;
Best Local Similarity 94.8%; Pred. No. 3.2e-16;
Matches 55; Conservative 0; Mismatches 1;
                                                                                                                 .
                                                                                96.3%; Score 310; DB 23;
                                                                                               Pred. No. 9.9e-17;
0; Mismatches 0
Bordetella in a material. The present sequer pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                             AAE16198 standard; peptide; 58
                                                                                                   93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica.
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097639/13.
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 AA;
                                                 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISNI ( dSNI)
                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                 26;
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                                                                                                                                                                                                                                                                                               AAE16198;
                                                   Sequence
                                                                                Query Match
                                                                                                 Best Local
                                                                                                                 Matches
                                                                                                                                                                                                                              AME16198
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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.

254..304 /note= "Pertactin region I" 564..621 /note= "Pertactin region II"

Location/Qualifiers

Key Region Region

Bordetella parapertussis.

Bordetella parapertussis pertactin outer membrane protein, p.70.

26-MAR-2002 (first entry)

AAE16185;

AAE16185 standard; Protein; 922 AA.

RESULT 5 AAE16185

us-09-855-754b-18.rag

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A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (#995") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
35..643
7[label- P70
260..262
7/note. "motif associated with cell-cell adhesion"
266..285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 575.612
//note="contains 9 direct repeats of Pro-Gln-Pro"
712.714
/note="motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                      Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 303; DB 13; Length 922;
Pred. No. 2.3e-15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                Bordetella parapertussis P95 antigen precursor.
                                                        AAR25578 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 20pp; English
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94.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WELL ) WELLCOME FOUND LID.
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                              Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-250033/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ26509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1990;
                                                                                                                                                                       08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9211292-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                 AAR25578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reg 1on
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RESULT 4
AAR25578
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Suiso maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

N-PSDB; AAD25442

(INSP.) INST PASTEUR

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P

WO200190143-A2. 29-NOV-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Couter membrane protein) or their fragments. Pertactin (PRN) is used as waccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens and infinity chromatographic columns. Pertactin is useful as antiquens animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal leals, as well as biological and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 303; DB 23;
Pred. No. 2.3e-15;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR14321 standard; Protein; 922 AA.
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94.8%;
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Matches 55; Conservative
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Best Local Similarity 94.8 Matches 55; Conservative

B. bronchiseptica strain II-4 pertactin outer membrane protein region II.

(first entry)

26-MAR-2002

AAE16196;

AAE16196 standard; peptide; 53 AA

AAE16196 RESULT

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2.

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The 46 %s represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 294; DB 12; Length 922;
pred. No. 1.1e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
                                  Pertactin; Pichia; B. pertussis; B.bronchiseptica;
                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                          583.585
/label= re-
                                                                                                  276..280
/label= ren
                                                                                                                    281.285
/label- ro
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                                                                                                                                                                                                                                       repeat
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                                                                                                                                                                                                                                                                                                   610..612
/label= repeat
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                                                                                          repeat
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Best Local Similarity 93.2%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                   90GB-0007416.
                                                                                                                                                                                                                                                                                                                                                                91WO-GB00487
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'label= re
20-JAN-1992 (first entry)
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/label= re
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/label= re
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/label= re
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Tabel- re
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Tabel= re
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                                                                                266..270
/label= r
                                                     Bordetella parapertussis.
                                                                                                 ..275
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                Pertactin antigen P.70.
                                                                                                                                                                                                                                                                                                                                                                                                                       Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 AA;
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                                                                                                                                                                                                                                                                                                                                                                 28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1990;
                                                                                                                                                                                                                                                                                                                              WO9115571-A.
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                                                                        Key
Peptide
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Boursaux-eude C;

Guiso-maclouf N,

WPI; 2002-097639/13.

(INSP) INST PASTEUR

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P

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Ϊ
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 291.5; DB 2
illarity 94.6%; Pred. No. 2.1e-15;
Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ż
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1c; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 53; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 AA;
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1 GAKAPPAPKPAPQPGPQPGPQPGPQP---PQPPQPPQPPQPPAPAPQPPAGRELSAA 56

564

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/label= repeat

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28-MAR-1991;
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                                                                                                                                                                           17-0CT-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR26503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Protein
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                  Peptide
                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 285; DB 23;
Pred. No. 6.4e-15;
0; Mismatches 0
therapy; antiblotic; antibacterial; region II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14320 standard; Protein; 911 AA
                                                                                                                                                                                                     Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                  Claim 26; Fig 1c; 47pp; English.
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574..576
/label= repeat
578..580
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/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271..275
/label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.5%;
Best Local Similarity 92.9%;
Matches 52; Conservative
                                                                                                               23-MAY-2001; 2001WO-EP06457
                                                                                                                                            25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica.
                              Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570..572
                                                                                                                                                                                                                                                          Polypeptides containing
pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin antigen P.68
                                                                                                                                                                        (INSP ) INST PASTEUR
                                                                                                                                                                                                                                WPI; 2002-097639/13.
                                                                                                                                                                                                    Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AA;
                                                       40200190143-A2
                                                                                    29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR14320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pept1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQRPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 285; DB 12; Length 911;
Pred. No. 5e-14;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260..262
/label= RGD_tripeptide
701..703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1B; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR26503 standard; Protein; 911
581..583
/label= repeat
584..586
/label= repeat
                                                                                                                                                                                                                                                                                                                                                          (WELL ) WELLCOME FOUNDATION LTD
                                                                                                          repeat
                                                                                                                                             /label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.5%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35..632
/label= P.68
                                                                                                                                                                                                                                                                             91WO-GB00487
                                                                               587..589
/label= re
599..601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetalla bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266..279
/label= Re
570..589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 92.9
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325214/44.
N-PSDB; AAQ14319.
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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285; DB 23
Pred. No. 5e-14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                       Disclosure; Page 28; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą.
      Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . AAE16193 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.5%;
Best Local Similarity 92.9%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.
                                          WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 AA;
    Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16193;
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AAE16193
    88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; p.68.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.68 antigen is formed by alternative cleavage of this protein.
P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                            DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence given is the P.94 antigen from B. bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 285; DB 13; Length 911;
Pred. No. 5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
/label- RGD_tripeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.5%;
92.9%;
                                                                                                                                                               91GB-0006568
                                                                                                                       92WO-GB00561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                    (WELL ) WELLCOME FOUND LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                  WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entire P.94 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2
                                                                                                                     27-MAR-1992;
                                                                                                                                                             27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                      WO9217587-A
                                                                            15-0CT-1992
                                                                                                                                                                                                                                            Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Signatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Region
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Gaps

Indels

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23; Length 911;

26

for

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Gaps

8;

Indels

Length 48;

Score 258; DB 23; Pred. No. 6.1e-13; ; Mismatches 0;

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Conservative

48;

Similarity

Query Match Best Local S Matches 48

80.1%; 85.7%;

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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, alycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \mathbf{for}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                       Length 49;
                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                    Score 264.5; DB
Pred. No. 2e-13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                               AAE16199 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                    82.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4PI; 2002-097639/13.
                                                                                                                                                                                                                  Local Similarity
hes 49; Conserv
                                                                                                                                                                       49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSP ( INST
                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
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                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                           AAE16199;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                     RESULT 13
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    888888888888888%
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                                                                                                                                                                                                       8. bronchiseptica strain II-8 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                               48
   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA
                  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPAPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 257; DB 23;
Pred. No. 7.7e-13;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude
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                                                                                                           AAE16200 standard; peptide; 52
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86.0%;
                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000; 2000US-206969P
                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AA;
                                                                                                                                                                                                                                                                                                                     WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                     29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                           AAE16200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AAE16201
ID AAE162
                                                                              RESULT 14
AAE16200
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens an infinity chromatographic columns. Pertactin is useful as antiquens and lumin tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B bronchiseptica pertactin outer membrane protein region II.

48 AA;

sequence

The present invention relates to Bordetella bronchiseptica

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 4jycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                        B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                  Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                      23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                         25-MAY-2000; 2000US-206969P
                                                       26-MAR-2002 (first entry)
                                                                                                                                                                                       Bordetella bronchiseptica,
                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 AA;
                                                                                                                                                                                                                           WO200190143-A2
                                                                                                                                                                                                                                                                29-NOV-2001
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1 GAKAPPAPRPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56 ò qq

Gaps

5

Length 54; 5; Indels

Score 256; DB 23; Pred. No. 9.4e-13; 0; Mismatches 5;

79.5%; 87.5%;

49; Conservative

Query Match Best Local Similarity Matches 49; Conserv

Search completed: May 7, 2003, 16:47:07 Job time: 29.0971 secs

Sequence

Appl ddy

Sequence 6 Sequence 5 Sequence 7 Sequence 7 Sequence 6 Sequence 7 Sequence 7 Sequence 2 Sequence 2 Sequence 4 Sequence 4 Sequence 4 Sequence 4 Sequence 4 Sequence 4

May

Run on:

OM protein

Perfect score:

Sequence:

Scoring table:

searched:

Minimum DB Maximum DB

Database

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APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: IBM PC COMPATIBLE
COMFUTER: BATCHION PC-DOS/MS-DOS
SOFTWARE: PATCHION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: 37,067
TELECAMUNICATION INFORMATION:
TELECAMUNICATION INFORMATION:
TELECAMUNICATION INFORMATION:
TELEFAX: (703) 243-6410
INFORMATION FCR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan,
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 303; DB 4;
Pred. No. 4.7e-19;
0; Mismatches 1
                              US-08-478-029A-65
US-09-535-008-63
US-09-535-008-67
US-09-535-008-7
US-09-535-008-7
US-09-535-008-7
US-09-535-008-69
US-09-535-008-69
US-09-535-008-69
US-09-535-008-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11near MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5470718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1 | 101-08-06 | 101-08-460-269C-6 | 101-08-460-269C | 101-08-460-260C | 101-0
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LENGTH: 922 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.1%;
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Best Local Similarity 94.8
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON STATE: VA
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NUMBER OF
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Patent No. 57
                                                                                                                                                                                                                                                                                                                                                                                                                             322
1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Query

Score

Result No.

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Gaps 26

5

Length 922; Indels ä g

Sequence Sequence Sequence Sequence

121.5 120.5 120.5 120.5

120 115.5 115

121.5 121.5 121.5 121.5 121.5 121.5 121.5 121.5

Sequence

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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQRPGRPAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PACHOETIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          Score 210; DB 4;
Pred. No. 4.1e-11;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
                                                        NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REBERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 911253.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: 11 NIXON & Vanderhye, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08237716
Patent No. 5589384
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 11
TELECOMMNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                            65.2%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECUMA: 703-616-4100
                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 73.2
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08460269C
Sequence 2, Application US/08460269C
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                               APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 285; DB 4; Length 911;
Pred. No. 1.6e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                               ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWANE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: ILINear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                               Sequence 4, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.59
Best Local Similarity 92.99
Matches 52; Conservative
                                                                                                                                                                                                                                                                                            CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                  US-08-460-269C-4
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APPLICANT: Kandil, Ali
APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
APP
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APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER, OF SEGUENCES: 25
                                     Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 24;
                                                                                                                                                                                      20 APAPPNPNPQSPPSPPSPPTPPTPPSPPAPPSPPPSPPS 67
                                                                                                                                                 2 AKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750 CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 127; DB 4; L. 79.3%; Pred. No. 2.1e-05;
                                     Score 134; DB 6;
Pred. No. 5.4e-05;
1; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 РОРСРОРРОРРОРРОРОВЕЛЬНОРР 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PQPGPQPPQPPQPP-----QPEAPAPQPP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-FEB-1997
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENE/POOKET NUMBER: 1038-660
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16. Application US/08246982A Patent No. 5886288 GENERAL INFORMATION:
APPLICANT: Ambrose, Christine M.
                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08750624 Patent No. 6290971 GENERAL INFORMATION:
                                     41.68;
ilarity 47.98;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 79.39
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronce
STATE: Ontario
                               Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-246-982A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                          /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
;SUSAN L.;MCCANTISS, RUSS;WEL, TENA;FILPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, ; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 АКАРРАРКРАРОРСРОРСРОРСРОРРОРРОРРОРРОРРОРОВАРАРОРРА 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 6;
Pred. No. 5.4e-05;
1; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 136; DB 1;
Pred. No. 4.7e-06;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 PGPQPGPQPGPQPPQPPQPPQRQPEAPAPQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PGPEIAPQPGPQPPQP-----QPEAPAPEP 32
                                                          /label- LTB sequence
                                                                                                                                                                          /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
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CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 83,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.6%;
Matches 24; Conservative
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Best Local Similarity 47.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                 CTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: EUS-08-237-716-11
                                                                                                                                        LOCATION: 4.7
OTHER INFORMATION:
FEATURE:
                                                       OTHER INFORMATION:
   Region
                                                                                                               NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO:37;
; LENGTH: 331
                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , LENGTH: 334
5202236-3
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:3
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5202236-3
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1 GAKAP-----PAPKPAPQPGPQPGPQP----GPQPPQPPQPPQ----PP 36
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                                                                                                                                                             Length 3119;
                                                                                                                                                                                                                                                                         13 OPGPOPGPOPGPOPPOPPOPPOROPEAPAPOPPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAGNOSIS AND TREATMENT
OF ALP RELATED DISORDERS
                                                                                                                                                             Score 123.5; DB
Pred. No. 0.0031
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTESG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Poles, Elor
APPLICANT: Peles, Elor
TITLE OF INVENTION: DIAGNOSIS AND
TITLE OF INVENTION: OF ALP RELATE,
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Lyon
STREET: Salle 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
FILING DATE: JUNE 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                       US-09-095-443-2; Sequence 2, Application US/09095443; Patent No. 6342593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.0%;
Best Local Similarity 41.0%;
Matches 32; Conservative
                                                                                                                                                                   38.4%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1274 amino acids
               SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino act
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-095-443-2
INFORMATION FOR SEQ ID NO
                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GRELSA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/246,982A
FILING DATE: MAY 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 QPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPA----
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STREET: 1100 New York Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.0031;
  Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 123.5;
                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: GOLGStein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SED ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                       1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISCRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.4%;
Best Local Similarity 51.9%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-246-982A-16
                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 20005
                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                      COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bredeson, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE DE INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: PolyPeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
COMPUTER: Floppy disk
COMPUTER: The PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENTINON:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 2626
TELECOMMULICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.7%; Score 121.5; DB 4;
48.2%; Pred. No. 0.00092;
tive 2; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09041886 Patent No. 6235372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/OCKET NUMBER: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 43/0 C.C.C.T. San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 513 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query.Match
Best Local Similarity 48.29
Matches 27; Conservative
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-041-886-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 GPGAPQGPGAPQEPPQQPPQQPPQQPPQQP-PQQPPQQPPQQPRPQP 374
                                                                                                                                                                                                                                                            APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, Martha
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTEC:
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
NUMBER OF SEGUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121.5; DB 3;
Pred. No. 0.00087;
3; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Naval Medical Res. & Dev. Cmd. STREET: Bldg. 1, T-12 8901 Wisconsin Ave. CITY: Bethesda STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/CDOCKET NUMBER: 24,743
REFERENCE/CDOCKET NUMBER: N. C. 75,851
TELECOMUNICATION INFORMATION:
TELEPRATIC (202) 295-6759
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                         RESULT 11
US-08-155-888-2
; Sequence 2, Application US/08155888
; Patent No. 6066623
; GENERAL INFORMATION:
; APPLICANT: HOffman, Stephen L.
                                                                                                                                                                                                                                         Hoffman, Stephen L.
Hedstrom, Richard C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.7%;
Best Local Similarity 51.1%;
Matches 24; Conservative
                                          625 QAPGLLPPQSPYPYAPQP 642
                37 QR----QPEAP---APQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 478 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-155-888-2
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STREET: 43,
CITY: San Diego
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20889-5606
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                                                                                                                                         5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                                                                                                                                   5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                         Score 121.5; DB 4; Length 530;
Pred. No. 0.00095;
2; Mismatches 20; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 121.5; DB 4; Length 552;
Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brodesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Proapoptotic Peptides, Dependen TITLE OF INVENTION: PolyPeptides and Methods of Use NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.7%; Scor. 48.2%; Pred. No. v... 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
                                                         Query Match 37.7%;
Best Local Similarity 48.2%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 48.29
Matches 27; Conservative
; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                US-09-041-886-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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US-09-041-886-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 589;
                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 121.5; DB
Pred. No. 0.001;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 7, 2003, 16:57:20 Job time: 11.3447 secs
Campbell & Flores LLP
                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/POCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.7%;
Best Local Similarity 48.2%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (619) 535-9001
                                                   : California
RY: United States
92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-041-886-31
                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
               STREET: 43/0 LL CITY: San Diego
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                            STATE: Ca
COUNTRY:
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us-09-855-754b-7.rsp

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CHAIN
DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT TASSEL GROWTH UP UNTIL MATURE POLLEN IS PRODUCED IN THE ANTHERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. BEIO; TISSUE-Tassel;
MEDILNE-94004997; Pubmed-8401606;
Wilght S.Y., Suner M.-M., Bell P.J., Vaudin M., Greenland A.J.;
"Isolation and characterization of male flower cDNAs from malze.";
Plant J. 3:41-49(1993).
                                                                                                                                                            CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                            PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                        DB 1; Length 911;
                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGAVPGGAVPGGRGPGLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                 (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                       ch 85.5%; Score 232.5; DB 1
1 Similarity 90.2%; Pred. No. 5.9e-16;
46; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                        p32439;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                              Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
EMBL; A19180; CAA01453.1; -.
PIR: A47675; A47675.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.
Pfan; PF03212; Pertactin_vir.
PRINTS; PR01482; PERTACTIN.
                                                                                                                                                    LINES)
                                                                                                                                                                                                                    93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X67324; CAA47738.1; -. PIR; S25103; S25103.
Maizebb; 78601; -.
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               MFS18 protein precursor.
                                                                                                  911
712
911
262
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266
266
271
276
570
911 AA;
                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                                       Query Match
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DOMAIN
REPEAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS reformenty is copyright. It is produced through a collaboration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- FUNCTION MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-I- SUBDUIT: HE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D METHORA.

-I- SUBCELLUIAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.

-I- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-Lung;
MEDLINE-95130669; PubMed-7829060;
MEDLINE-95130069; PubMed-7829060;
Mydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                       X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.2%; Score 74; DB 1; Length 860; 43.6%; Pred. No. 2.9;
                                                                                                                            AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
ELASTIN.
; OCOBESAAE1EDD7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                       7661ECC596E0D778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Repeat; Signal; Connective tissue.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 1;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
10-CT-1996 (Rel. 34, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GDAPAGGAVPGGAVPGGAVPG----GFGPLLDGW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MFS18 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                 1-3.
8 x 4.
2-1.
                                                                                                                                                                                                                                                                                                                                                     12535 MW;
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U08210; AAA80155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                               113 1
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 860 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELS_MOUSE
P54320;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                      REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                 REPEAT
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
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"Sequence analysis upstream of the gene encoding the precursor to the major merozoite surface antigens of Plasmodium yoelii."; MOI. Blochem. Parasitol. 39:285-288(1990).
             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (230 kDa).
                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 85:602-606(1988).
                                                                                                                                                                                                                                                                                                               MEDLINE-88124889; PubMed-2448778;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
"The 3' portion of the gene for a Plasmodium yoeli1 merozoite surf
antigen encodes the epitope recognized by a protective monoclonal
                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5862;
                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=90205979; PubMed=2320061;
                                                                                                                                                                                                                                                                                 SEQUENCE OF 1093-1772 FROM N.A. STRAIN=17XL;
                                                                                                           Plasmodium berghei yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                      Lewis A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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 Gaps
                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Cytoplasmic antigen) (74.6 kDa
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-93050041; Pubmed-1426134;
Eckert V., Sanchez L., Cochrane A.H., Enea V.;
"Plasmodium cynonojg: the hsp 70 gene.";
Exp. Parasitol. 75:323-328(1992).
-1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN THE ASEXUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 X 4 AA TANDEM REPEATS OF G-G-M-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
 8;
                                                                                                                                                                                                                                                                                                                                                                                                        BLOOD STAGE FORMS.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 686;
                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5828;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FF31F448FFCBF286 CRC64;
11;
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                           2 RATIRRGDAPAGGAVPG----GAVPGGFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70.5; DB Pred. No. 5.2; 4; Mismatches
                                                                                                                                          686 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GDAPAG----GAVPGGAVPGGAVPGGFGPLLD 35
                                                                                                                                                                                                                                                    Plasmodium cynomolgi (strain Berok)
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Repeat
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; PO8109; ICKR.
InterPro; IPR01023; Hsp70.
Pfam. PF00012; HSP70. 1.
PRINYS; PR00301; HEATSHCCK70.
ProDom; PD000089; Hsp70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M90978; AAA29625.1;
PIR; A49242; A49242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                        HS70_PLACB
Q05746;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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REPEAT
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                                                                                                         RESULT 6
HS70_PLACB
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Matches
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merozoite surface

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | |: |:||
----GTDTRVAGSSVD 1379
(Potential).
PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TIRRGDAPA-----GGAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.

MEROZOITE SURFACE PROTEIN 1.

N-LINKED (GLCNAC. . . ) (POTE

N-LINKED (GLCNAC. . ) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> V (IN REF. 2).
9A6291658EB0F45D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.5; DB 1;
Pred. No. 12;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1330 TILAADAPATPEGAVPGAVPGAVPGAVPGAVPGS----
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                                                                                                                                                                                                                                                                                                                                                                              EMBL; J03612; AAA29762.1; -. EMBL; J04668; AAA29702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04668; AAA29702.1; -.
PIR; A28121; A28121.
PIR; A45532; A45532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%;
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1680
1521
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RESULT 8 CUT2_CAEEL

PRT; 1772 AA

STANDARD;

RESULT 7 MSP1_PLAYO ID MSP1_PLAYO

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roDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                          Gaps
                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                              POLY-PRO.
12 X 4 AA REPEAT OF A-A-P-[AVI].
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67.5; DB 1; Length 231;
Pred. No. 3.8;
1; Mismatches 13; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                   A48C9C5498D8E797 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 GAAPAGGAYQSGPAFGGAAPAGGAYQSGPAFGGAAPAVGGAY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDAPAGGAVPGGAVPGGAVP-----GGFGPLLDGWY 38
             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Cuticiin 2 precursor.
231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BR3A_HUMAN STANDARD; PRT; 423 AA 001851; Q15318; Q14986; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                        POTENTIAL.
CUTICLIN 2.
POLY-GLY.
PRT;
                                                                                    SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-95021520; PubMed-7935621;
                                                                                                                                                                                                                                                                                                                                                                                                                  20833 MW;
                                                                                                                                                                                                                                                                  EMBL; X74838; CAA52832.1; -. PIR; S37108; S37108.
                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 40.5%;
Conservative
STANDARD;
                                                                                                                                                                                                                                                                                Cuticle; Signal; Repeat.
                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                          218
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 17; Conserv
CUT2_CAEEL
P34682;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
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255
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Inucleic Acids Res. 20:4919-4925(1922).

Inucleic Acids Res. Any Play a Role In Determining OR Maintaining OR M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE#Retina;
MEDLINE-95348789; PubMed-7623109;
MEDLINE-95348789; PubMed-7623109;
Miang M., Zhou, L.-J., Macke J.P., Yoshioka T., Hendry S.H., Eddy R.L.,
Shows T.B., Nathans J.;
"The Brn-3 family of POU-domain factors: primary structure, binding
specificity, and expression in subsets of retinal ganglion cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Croce C.M., Israel M.A., Theil T., Moroy T., Depinho R.A., Alt F.W., "A novel POU homeodomain gene specifically expressed in cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94052142; PubMed-8234287;
Bhargava A.K., Li Z., Welssman S.M.;
Bhargara A.K., Li Z., Welssman S.M.;
"Differential expression of four members of the POU family of
proteins in activated and phorbol 12-myristate 13-acetate-treated
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (OCT-T1)
(Homeobox/POU|domain protein RDC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 90:10260-10264(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93027214; PubMed-1357630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U10063; AAA57161.1; -.
EMBL; U10062; AAA57161.1; JOINED.
EMBL; [L20433] AAA6565.1; -.
EMBL; K64624; CAA45907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatosensory neurons.";
J. Neurosci. 15:4762-4785(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PD00010; Homeobox; 1.
; PD000583; POU_domain; 1.
SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001356; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 85-423 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:9218; POU4F1.
                                                                                                                                                                                   POU4F1 OR BRN3A OR RDC1.
                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jurkat T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSFAC; TO1876;
FRANSFAC; TO4463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 601632
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421 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OST-PTP).
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DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTPO_RAT
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SEQUENCE OF 286-401 FROW N.A.

STRAIN-T6 / TW1; TISSUE-Testis;

MEDINE-90221898; bubwed-1970171;

M.Goldsborough A., Ashworth A., Willison K.;

d. Goldsborough A., Ashworth A., Willison K.;

"Cloning and sequencing of Poul-boxes expressed in mouse testis.";

"Cloning and sequencing of Poul-boxes expressed in mouse testis.";

"Le conting and sequencing of Poul-boxes expressed in mouse testis.";

"Cloning and sequencing of Poul-boxes expressed in mouse testis.";

"The IDEA ROBBLE TRANSCRIPTION FACTOR WHICH MAY PLAY A ROLE IN DETERMINING OR MAINTAINING

"THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A SUBSET OF NEURONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING

"THE IDEATITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS."

"THE IDEATITIES OF A SMALL SUBSET OF VISUAL SYSTEM AND PRECIPCITY: BRAIN, PERIPHERAL SENSORY NERVOUS SYSTEM AND RETINA. IN THE ADULT NERVOUS SYSTEM BRN-3.0 PREDOMINATES IN THE MEDIAL HABBNULA, SUPERFICIAL GRAY OF THE SUPERIOR COLLICULUS, RED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-9215319; Pubmed-8162704;
MEDLINE-9215319; Pubmed-8162704;
Theil T., Zechner U., Klett C., Adolph S., Moeroey T.;
"Chromosomal localization and sequences of the murine Brn-3 family of developmental control genes.";
Cytogenet. Cell Genet. 66:267-271(1994).
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
SMART; SM00352; POU; 1.
PROSITE: PS00025; HOMEOBOX_1; 1.
PROSITE: PS00465; POU_2; 1.
PROSITE: PS00465; POU_2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (BRN-3.0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 1; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                            A -> R (IN REF. 3).

AER -> GS (IN REF. 3).

AQR -> PS (IN REF. 3).

B3AE4732E1309F34 CRC64;
                                                                                                                                                                      A -> R (IN REF. 1).

GAG -> ARR (IN REF. 3).

MISSING (IN REF. 2).

MISSING (IN REF. 3).
                                                                                                                                                                                                                       GP -> AA (IN REF. 3).
GP -> PR (IN REF. 3).
GP -> AA (IN REF. 3).
                                                                                                                                                             TS -> H (IN REF. 3)
                                                                                                                                                                                                                                                        G -> A (IN REF. 3).
A -> S (IN REF. 2).
MISSING (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                              24.6%; Scor.
56.0%; Pred. No. , ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA.
                                                                                       POU-IV BOX.
                                                                                                  POLY-HIS.
GLY-RICH.
                                                                                                                           ALA-RICH.
                                                                                                                                                 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    153 GGCPGGGGPGGGPGG--GGGGP 175
                                                                                                                                                                                                                                                                                                                                                                                                      8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                               42939 MW;
                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                              123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BR3A_MOUSE
                                                                                                                                               DNA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                      DOMAIN
                                                                                                             DOMAIN
                                                                                    DOMAIN
                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
BR3A_MOUSE
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NUCLEUS, MESENCEPHALIC NUCLEUS OF THE TRIGEMINAL GANGLION, NUCLEUS AMBIGUUS, INFERIOR OLIVARY NUCLEUS, AND PERIPHERAL SENSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Osteotesticular protein tyrosine phosphatase precursor (EC 3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Osteosarcoma;
MEDLINE-95074080; PubMed-7527035;
MEDLINE-95074080; PubMed-7527035;
Mario LJ., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R., Dixon J.E.;
"Identification of a hormonally regulated protein tyrosine phosphatase associated with bone and testicular differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                      -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42781 MW; 34EC99D789EBE939 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                             -! - SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1711 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 65.5; E
58.3%; Pred. No. 10;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POU-IV BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-HIS.
GLY-RICH.
ALA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POU.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                  PIR: $09237; $09237.

HSSP; P10037; 1AU7.

HSSP; P10037; 1AU7.

MGD; MGI:102525; Poudf1.

InterPro; IPR00135; Poudf1.

Ffam; PF00157; Pouglann.

Pfam; PF00157; Pouglann.

Pfam; PF00157; Pouglann.

PF0008; PF0008; POUDOMAIN.

PF0DDm; PD00010; Homeobox; 1.

PFNDFR; SM0038; POUGlanni; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEOMAIN; 1.

PROSITE; PS00045; POUJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 DGPGGGGGPGGGGPGGG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 DAPAGGAVP-GGAVPGGAVPGGFG 31
                                                                                                                                                                                                                                                                                                                                                                        EMBL; S69350; AAB30577.2; -. EMBL; X51959; CAA36218.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                        CLASS-4 SUBFAMILY
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187292 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
       PIR; A94441; HMIVHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMA_IAME2
                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                CARBOHYD
                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                      SEQUENCE
                                          CARBOHYD
                                                           CARBOHYD
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HEMA_IAME2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIDDRAR REPRESENTATION OF THE PROPERTY OF THE 
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                                                                HOL. Chem. 269:30659-30667(1994).
FUNCTION: MAY FUNCTION IN SIGNALING PATHWAYS DURING BONE
REMODELING, AS WELL AS SERVE A BROADER ROLE IN CELL INTERACTIONS
ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS. OPTIMAL PH FOR
                                                                                                                                                                                                                                                                                                                                                     INDUCTION: BY PARATHYROID HORMONE AND CYCLIC AMP ANALOGS.
PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 2 PROFEIN-TYROSINE PHOSPHATASE DOMAINS. SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE PHOSPHATASE 1. PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR0070U; FALS.
SMART; SM00060; FN3; 6.
SMART; SM00194; PTPC; 1.
SMART; SM001021; PTPC; 1.
PROSITE; PS000383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000340; DS_phosphatase.
InterPro: IPR003961; FN.III.
InterPro: IPR003962; FN.III.repeat.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; TYT_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan: PF00041; fn3; 7. Pfan: PF00102; 7. Pfan: PF00102; 7. Phosphatase; 1. PRINTS; PR00104; FNTYPHIASE. PRINTS; PR00700; PRTYPHPHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L36884; AAA63911.1; -. HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                     EPITHELIUM.
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CARBOHYD
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-1- FUNCTION HERAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-1- SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMACGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sledgh M.J., Both G.W., Brownlee G.G., Bender V.J., Moss B.A.;
The haemagglutinin gene of influenza A virus: nucleotide sequence
analysis of cloned DNA copies.";
(In) Laver G., Air G. (eds.);
Structure and variation in influenza virus, pp.69-79, Elsevier,
                                                                                                                                                              POTENTIAL)
                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ORATIRRGDAPAGGAVPGGAVPGGFGPLLDG-WYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 00, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAl chain;
Hemagglutinin HA2 chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

24.1%; Source Construction 38.5%; Pred. No. 37;

Matches 20; Conservative 10; Mismatches 19; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
NCBL_TaxID=11439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF04D2D1A47A18A0 CRC64;
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutlain; 1.
PRINTS; PR00329; HEMAGGLUTN12.
Prodom; P0000225; Hemagglutn; 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEMAGGLUTININ HAI CHAIN. HEMAGGLUTININ HAZ CHAIN.
N-LINKED (N-LINKED (N-LINK
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RESULT 14
HS71_CANAL
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                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snutch T.P., Heschl M.F.P., Balllie D.L.; "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                          POTENTIAL)
                                                      POTENTIAL)
                              POTENTIAL)
                                                                                                                                               51;
                                                                    (POTENTIAL)
                                                                                POTENTIAL)
                                                                                                                    Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s 64:241-255(1988).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 640;
                                                                                                                                        10; Indels
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                                                                                           1D9313AB3C380CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                                 Score 64.5; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                  (GLCNAC.
                                                                                                        23.7%; Scur. 20.2%; Pred. No. 1,, 20.2%; Pred. No. 1,, ...
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Last annotation update)
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Pred. No. 19;
2; Mismatches
  N-LINKED
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                                                                                                                                                                   2 RATIRRGDAPAGGAV-----PGGAVPG-----
                                                                                                                                                                                                                                              340 PEKRIRGLFGALAGFIENGWEGMIDGWYG 368
                                                                                                                                                                                                                      24 -----GAVPG----GFGPLLDGWYG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-88297155; PubMed-2841196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGAVPGGAVPGGAVPGGFGPLLD 35
                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
                                                                                           63264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                          Heat shock 70 kDa protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M18540; AAA28078.1; -.
PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.3%;
                                                                                                             Query Match
Best Local Similarity 20.29
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                      HSP-1 OR HSP70A.
Caenorhabditis elegans.
                                                                                           566 AA;
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                     RESULT 13
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Excles P., Sentandreu M., Florza M.V., Sentandreu R.;

"Cloning of a DNA fragment encoding part of a 70-kDa heat shock protein of Candida albicans.";

FEMS Microbiol. Lett. 128:95-10(1995).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

H.M., Bromuro C.B.;

Cassone A.C., la Valle R.L., Crisanti A.C., Muller H.M. Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases

SEQUENCE FROM N.A. STRAIN=ATCC 20955;

NCBI_TaxID=5476;

FROM N.A. PubMed=7744244;

OF 1-243 FROM

SEQUENCE OF 1-243 MEDLINE=95262895;

Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.

01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)

01-NOV-1995 01-NOV-1995

HS71_CANAL P41797:

Heat shock protein SSA1. SSA1 OR HSP70. Candida albicans (Yeast).

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                                                                                and for commercial
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLATION (BY SIMILARITY).
A -> G (IN REF. 2).
634743E4D6DAD9D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 19;
2; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                     PRINTS: PR00301; HEATSHCCK70.

ProDom; PD000089; HSp70, 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS00329; HSP70_3; 1.

Heat shock; ATP-binding; Multigene family; Acetylation.

INIT_MET 0 0 BY SIMILARITY.

MOD_RES 1 1 ACETYLARITY.

SEQUENCE 655 AA; 70192 MW; 634743E4D6DAD9D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GDAPAG-GAVPG-GAVPGGRAVPGGFGPLLDGWYGVDVSDSTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%; Score 64.5;
                                                                                                                                                                                                     EMBL; S78163; AAB34280.1; -. HSSP; P19120; 3HSC
                                                                                                                                                                                                                                          COMPLUYEAST-2DPAGE; P41797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%;
                                                                                                                                                                                                                                                                             InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                             EMBL; Z30210; CAA82929.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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AGGA-PPGAAPGGAAGGAGGPIE 637

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                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
                                                                                                                                                                                                                                                                                                                                           SPIICING.; GEOFICE SECTIONS STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND -!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY. -!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-92241859; PubMed-1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                           AEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-91104868; PubMed-1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:9677-9683(1990).
                                                                                                                                                               SEQUENCE OF 781-864 FROM N.A.
MEDLINE-88330868; PubMed-2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN CERTAIN ISOFORMS).
MISSING (IN CERTAIN ISOFORMS).
456894BB09E79FD4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOINED.
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308
809
864 AA;
                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                      splicing.
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SIGNAL
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557 GLGPGVGGVPGGVGG-LPGGVGP--GGVTGIGTGPGT 592 Search completed: May 7, 2003, 16:48:02 Job time: 10.9523 secs 셤

7

Gaps

3,

2; Mismatches 17; Indels

Pred. No. 25;

8 GDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDST 46

17; Conservative

Matches

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Local Similarity

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prn proteins. Bor Bordetella bronchi B. bronchiseptica B. bronchiseptica F647 monocional an Pem3 monocional an Pem4 monocional an

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Elastin-like pepti

us-09-855-754b-7.rag

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B. bronchiseptica strain I-1 pertactin outer membrane protein region I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
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                   AAE16183
AAE16188
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AAE17141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16186 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000US-206969P
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(INSP ) INST PASTEUR
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AAE16186
 B. bronchiseptica
Bordetella paraper
Bordetella paraper
Bordetella nitigen
B. bronchiseptica
Bordetella pertuss
Bordetella pertuss
B. bronchiseptica
B. bronchiseptica
Pertactin antigen
                                                                                                                     7, 2003, 16:31:28 ; Search time 26.4991 Seconds (without alignments) 256.453 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa1980.DAT:*
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                                                                                                                                                                                             US-09-855-754B-7
272
1 QRATIRRGDAPAGGAVPGGA.....PLLDGWXGVDVSDSTVDLAQ
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               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAR25578
AAE16185
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Gapop 10.0 , Gapext 0.5
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Minimum DB seq Maximum DB seq

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Perfect score:

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Scoring table:

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    575..612
/note= "contains 9 direct repeats of Pro-Gln-Pro"
712..714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acellular vaccine for immunisation against whooping cough comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                      Length 51;
                                                                                                                                                                                                                                                                                                                                                                    1 QRATIRKGDAPAGGAVPGGAVPGGAVPGGRGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                     1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                    100.0%; Score 272; DB 23;
100.0%; Pred. No. 2.3e-24;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR25578 standard; Protein; 922 AA.
Claim 26; Fig 1b; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35..643
/label= P70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella parapertussis.
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/note= "m4
266..285
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hes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-250033/30.
N-PSDB; AAQ26509.
                                                                                                                                                                                                                                                        51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding-site
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                                                                                                                                                                                                                                                                                      Query Match
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Matches
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AAR25578
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Claim 1; Fig 1; 20pp; English

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                        recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the bamHi site of cosmid pHC79. The cosmids were screened with a 1.8kb claif fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70.000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Perferred fragments include amino acids Pro577 to Prof12 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                     Length 922;
                                                                                                                                                                                                                                                                                                                                                                        51
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                                                                                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGAVPGGAVPGGRVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                     100.0%; Score 272; DB 13;
100.0%; Pred. No. 4.2e-23;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; antibiotic; antibacterial; p.70.
                cosmid library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16185 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; AAD26442.
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                     922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16185;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                        Best
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Gaps

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Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                         WPI; 1991-325214/44.
N-PSDB; AAQ14320.
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
AAE16189
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used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                    Length 922
                                                                                                                                                                                                                                                                                       254 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 304
                                                                                                                                                                                                                                                                   1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                                                                                                              Query Match 100.0%; Score 272; DB 23; Best Local Similarity 100.0%; Pred. No. 4.2e-23; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          AAR14321 standard; Protein; 922 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WELL ) WELLCOME FOUNDATION LTD.
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/label-_repeat
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'label= repeat
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label- repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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'label- re
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/label= re
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/label- re
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'label= r
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/label= re
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|abel= r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin antigen P.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clare JJ, Romanos MA;
                                                                                                                                                               922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-1992
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR14321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                       Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. bronchiseptica strain prnl pertactin outer membrane protein region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                 The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                           Score 263; DB 12; Length 9
Pred. No. 4.5e-22;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ORATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suiso-maclous N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16189 standard; peptide; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1b; 47pp; English.
Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                           96.78;
96.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE16189;
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Indels

Pred. No. 1.4e-19; 3; Mismatches 1

Length 910;

DB 23;

Score 241.5;

88.8%; 83.9%;

Query Match 88.8 Best Local Similarity 83.9 Matches 47; Conservative

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The present invention relates to Bordetella bronchiseptica pertactin (couter membrane protein) or their fragments. Pertactin (FRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fulids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. pertussis pertactin outer membrane protein, p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                               protein; vaccine; Bordetella infection;
antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                               Gaps
                                                                                                                                                        51
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                                                                                                                                                  QRATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis pertactin outer membrane protein, p.69.
                                                                                                Length
                                                                                         Score 241.5; DB 23; Length
Pred. No. 8.2e-21;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            254..309
'note= "Pertactin region I"
                                                                                                                                                                                                                                                                                                                                                                                        therapy; antibiotic; antibacterial; p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                      AAE16184 standard; Protein; 910 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                            PRN: outer membrane
                                                                                         88.8%;
83.9%;
                                                                        Query Match
Best Local Similarity 83.9%,
A7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                   (first entry)
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568..609
/note= "Po
                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-097639/13.
                                                             56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-097639/
N-PSDB; AAD26441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2
                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                            Pertactin;
                                                             Seguence
                                                                                                                                                                                                                                                                                     AAE16184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                         AAE1618
                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                          Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides derived from Bordetella pertussis pertactin, usefu
a vaccine against infections caused by Bordetella strains, and othe
infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                 1 QRATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 241.5; DB 23;
Pred. No. 1.4e-19;
3; Mismatches 1;
                                                                                                                                                                                              Bordetella pertussis pertactin (Prn1) protein.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
597..604
/note= "Conserved region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is B. pertussis prn1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 35-38; 52pp; English.
                                                                                                     AAE17146 standard; Protein; 910 AA.
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83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000EP-0202309
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 83.9
Matches 47; Conservative
                                                                                                                                                                                                                                                                                     Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-139897/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910 AA;
                                                                                                                                                                                                                                                            immune response.
                                                                                                                                                                                                                                                                                                                                                                            WO200200695-A2.
                                                                                                                                                                 18-APR-2002
                                                                                                                                                                                                                                            diphtheria;
                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002.
                                                                                                                                     AAE17146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mooi FR;
                                                                                                                                                                                                                                                                                                                   Key
Region
                                                                          RESULT 7
                                                                                       AAE17146
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RESULT 8

910 AA;

Sequence

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WO200190143-A2.

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    bronchiseptica strain prn4 pertactin outer membrane protein region I.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

    B. bronchiseptica strain I-2 pertactin outer membrane protein region I.

                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORATIRRGDAPAGGAVPGGAVPGGRVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 241; DB 23; Length 5
Pred. No. 8.6e-21;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16187 standard; peptide; 46 AA.
AAE16192 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 88.6%;
l Similarity 88.2%;
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000; 2000US-206969P
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPI; 2002-097639/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200190143-A2.
                                                                                                                                   6-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-NOV-2001
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                                                                   AAE16192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local
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Couter membrane protein or their fragments. Pertactin (PRN) is used as waccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques in affinity chromatographic columns. Pertactin is useful as antiques an infinity chromatographic columns. Pertactin is useful as antiques and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                         The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.5%; Score 232.5; DB 23; Length 46; 90.2%; Pred. No. 7.4e-20; live 0; Mismatches 0; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                               Claim 26; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14320 standard; Protein; 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266..270
/label= repeat
271..275
/label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= repeat
584..586
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                                                       23-MAY-2001; :001WO-EP06457
                                                                                   25-MAY 2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570..572
/label= re
574..576
/label= re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.5
Best Local Similarity 90.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin antigen P.68.
                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                        WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR14320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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/label= repeat 587..589 /label= repeat

599..601 /label= repeat

Peptide Peptide

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outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                             The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kb which is associated with protection of pigliets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                   obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in plgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ORATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                   encoding a Bordetella bronchiseptica protein - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.5%; Score 232.5; DB 13; 90.2%; Pred. No. 1.5e-18; 1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; PRN; outer membrane protein; v
therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16183 standard; Protein; 911
                                                                                                                                                                                                                                                               Claim 1; Fig 1; 28pp; English.
                                                              91GB-0006568
                                92WO-GB00561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-EP06457.
                                                                                          (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                   WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200190143-A2
                               27-MAR-1992;
                                                              27-MAR-1991;
 15-OCT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                         Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE16183;
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                                                                                                                                                                                                                                                                                                                                                                                        Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                               Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 232.5;
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Disclosure; Fig 1B; 38pp; English

(WELL) WELLCOME FOUNDATION LID

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WPI; 1991-325214/44.

N-PSDB; AAQ14319

90GB-0007416 91WO-GB00487

28-MAR-1991; 02-APR-1990;

17-0CT-1991

WO9115571-A.

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AAR26503 standard; Protein; 911

RESULT 11

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12-MAR-1993 (first entry)

AAR26503;

prn proteins

Bordetalla bronchiseptica

Protein

Region Region

Query Match Best Local Similarity 90.2%; Matches 46; Conservative

911 AA;

Sequence

1989).

'label= RGD_tripeptide 701..703 /label- RGD_tripeptide

W09217587-A.

..262

Peptide

Peptide

570..589 /label- Repeat_region 266..279 /label- Repeat_region Location/Qualifiers 35..632 /label= P.68

ä

Gaps

for

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigons in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigons to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68. B. bronchiseptica strain I-3 pertactin outer membrane protein region I. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I. Gaps Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods ŝ Length 911; 51 1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ DB 23; Score 232.5; I Pred. No. 1.5e-0; Mismatches Disclosure; Page 28; 47pp; English Š AAE16188 standard; peptide; 56 85.5%; 90.2%; 23-MAY-2001; 2001WO-EP06457 (first entry) Bordetella bronchiseptica, Query Match Best Local Similarity 90.2 Matches 46; Conservative 911 AA; WO200190143-A2 26-MAR-2002 29-NOV-2001. Seguence AAE16188; RESULT 13 AAE16188

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Sequence
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vacchne. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens
                                                                                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                           Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Fig 1b; 47pp; English.
25-MAY-2000; 2000US-206969P
                                                                                 (INSP ) INST PASTEUR,
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to iden'tify antibodies to Bordetella in materials such as human or other animal itsusue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative or quantitative or guantitative or percentage. Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain prn3 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                  5;
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2
                                                                                                                                                                                                                                                                       1 ORATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 228.5; DB 23; Length 56; 80.4%; Pred. No. 2.6e-19; 1ve 3; Mismatches 3; Indels 5
                                                                                                                                                                                  Length
                                                                                                                                                                                                                  Indels
                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                    ..
..
                                                                                                                                                                           Score 228.5; DB 2.
Pred. No. 2.6e-19;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guiso-maclouf N, Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1b; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                              standard; peptide; 56
                                                                                                                                                                              84.0%;
80.4%;
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tes 45; Conserv
                                                                                                                                            56 AA;
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. bronchiseptica strain prn2 pertactin outer membrane protein region I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
1 QRATIRRGDAPAGGAVPGGAV-----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                         AAE16190 standard; peptide; 61 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1b; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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0 61 61 Search completed: May 7, 2003, 16:47:02 Job time: 37.4991 secs

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CITY: ...
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY, AGENT INFORMATION:
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET UNBER: Popov-2
TELEPHANE: (703) 243-6410
INFORMATION FOR ESE IN NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: AMINO 
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN
FEAST
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ADDRESSEE Milen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITT: ARLINGTON
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                                US-09-249-585A-3
PCT-US94-01149-32
US-08-453-848-15
US-08-169-027-15
US-09-169-027-21
US-09-169-027-21
US-08-562-311-4
US-09-562-311-4
US-09-702-572-6
US-09-702-572-6
US-09-702-572-6
US-08-548-076-6
US-09-702-572-6
US-08-542-051-32
US-08-542-051-32
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US-08-542-051-18
US-08-397-633A-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
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272
1 QRAITRRGDARAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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5-08-804-227C-14

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-09-247-806-2
-08-425-069-4
-08-317-844B-4
5-08-556-978B-61
5-09-247-806-10
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.08-529-190B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                            Run on:
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DB 4; Length 922;

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APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRATIRRGDAPAGGAVPGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                         Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.5; DB 2; Length 745;
Pred. No. 0.0012;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOUTHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILTURE NUMBER: US/No////
                                                                                                                                                                                                                                                                                                                                                                       Score 231.5; DB 4;
Pred. No. 3.3e-20;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: BIRCH, STEWART, KOLASCH & BIRCH 8110 GATEHOUSE RD. SUITE 500E
APPLICATION NUMBER: US/08/460,269C
                                                    NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REPERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
TELEPHONE: (703) 241-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 GGAGPGGAGPGGAGPGGAGP---GGYG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GDAPAGGAVPGGAVPGGFGPLLDGWYG 39
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/09/010,928B
22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09010928B Patent No. 5994099 GENERAL INFORMATION:
                                                                                                                                                                    243-6410
                                                                                                                                                                                                                               LENGTH: 910 amino acids TYPE: amino acid
                                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerald M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NOTICE TO REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%;
Best Local Similarity 65.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                             85.1%;
82.1%;
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  TELEFAX: (703) 243-
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.1
Best Local Similarity 82.1
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy Jr., Ge
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                      US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                            ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 232.5; DB 4 Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37,067 REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lebovitz, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                         Sequence 4, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                           APPLICANT: CLARE, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.5%;
90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Best Local Similarity 90.2%;
Matches 46; Conservative
                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          · TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                       STATE: VA
COUNTRY: USA
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US-08-460-269C-2
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APPLICANT: Lewis, Randolph V
APPLICANT: HAYSALI, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                    Length 907;
                                                                                                                                                                                                                                                      Score by, _-
Pred. No. 0.0067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: BIRCH, STEWART, KOLASCH & BIRCH F: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                      Score 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VIRGINIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-804-227C-14; Sequence 14, Application US/08804227C; Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                               163 GGAGPGGAGPGGAGPGGAGP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                      8 GDAPAGGAVPGGAVPGGEGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
               NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 29977
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                    32.7%;
72.0%;
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78.9%;
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECÜLE TYPE: protein
US-09-010-9288-9
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE
                                                                                                                                                                                                         US-09-010-928B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-010-928B-9
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CITY: FA
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                      Sequence 2, Application US/09010928B
Patent No. 5994099
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94.5; DB 2; Length 870;
Pred. No. 0.0014;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 GATEHOUSE RD. SUITE 500E CITY: FALLS CHURCH STATE: VIRGINIA
                                                                                                                                                                                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 GATEHOUSE RD. SUITE 500E CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 GGAGPGGAGPGGAGPGGAGP---GGYG 397
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APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                 CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 870 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.77
Best Local Similarity 65.6
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-928B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                22042
             JS-09-010-928B-2
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Query Match 25.0%; Score 68; DB 2; Length 4550; Best Local Similarity 48.5%; Pred. No. 15; Matches 16; Conservative 1; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68; DB 2
Pred. No. 15;
1; Mismatches
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ZUPILITY 46285
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macintosh
SOFTWARE: MICROSOFT WORD 7.0
SOFTWARE: MICROSOFT WORD 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                         X-8231
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STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTATION UNDRER: 35,784
REFERENCE/DOCKET UNDRER: X-82:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08804198 Patent No. 5945320
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ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/POCKET NUMBER: P91.
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 48.5%;
Matches 16; Conservative 1
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-804-227C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: peptide US-08-804-198-2
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                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                           amino acid
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STATE:
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhaftoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                     APPLICANT: DeHOff, Bradley S.
APPLICANT: Kulstoss, Stuart A.
APPLICANT: ROSteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
AILLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
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SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-8231
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
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ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MOTITER: IBM COMPATIBLE
"MOTITER: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4545 annho acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0%;
Best Local Similarity 48.5%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                               INDIANAPOLIS
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
SY: unknown
                                                                                                                                                                                                                                                                                                                                                                                               RY: USA
46285
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Gaps
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           COMPOUR: IBM PC compatible
COMPEDIATION SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SUBSTRANTE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: LO461/7008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.6%; Score 67; DB 56.0%; Pred. No. 1.3; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Van Amsterdam, John R. REGISTATION NUMBER: 40,212 REFERENCE/DOCKET NUMBER: 10461/7008 TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/430,85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 GGGPGGGGGGGGG--GGGGP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75-09-430-854-8
; Sequence 8, Application US/09430854
; Patent No. 6271019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             : 420 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.0°
Matches | 14; Conservative
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-206-537-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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STREET: bor
TTV: Boston
                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOS
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Sequence 8, Application US/09206537

Sequence 8, Application US/09206537

GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Oculie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Box Smet, Charles
APPLICANT: House, Sophie
CORRESPONDENCE SIGNERMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf. Cro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-FOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                 APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
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Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/845,998
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                             US-08-845-998-8
Sequence 8, Application US/08845998
Patent No. 5873892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.6%;
Best Local Similarity 56.0%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-845-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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STREET: buc
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02210
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COMPUTER READABLE FORM:

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TITLE OF INVENTION:
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                                                                                                                                                                       Gaps
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GENERAL INFORMATION:
APPLICANT: Levis, Randolph V
APPLICANT: Hypashi, Cheryl Y
APPLICANT: Hypashi, Cheryl Y
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                     5
                                                                                                                                     Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
CITY: FALLS CHURCH
                                                                                                                                                                   0; Mismatches
                                                                                                                                   Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  150 GGGPGGGGGGGGGGG--GGGGP 172
                                                                                                                                                                                                   8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURDAY Jr., Gerald M
REGISTRATION NUMBER: 28977
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRRACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                Query Match
Best Local Similarity 56.0%;
Matches 14; Conservative
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68.8%;
                               : 420 amino acids amino acid
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PGGYGPGGSGPGGYGP 16
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 PGGAVPGGAVPGGFGP 32
                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-430-854-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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Best Local Similarity
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               SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                            LENGTH:
TYPE: an
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OLMSTED, ELIZABETH A.

MAURO, LAURA J. DAVIS, ALAN R. DIXON, JACK E.

APPLICANT: APPLICANT: APPLICANT:

Sequence 2, Application US/08342930 Patent No. 5821084 GENERAL INFORMATION: APPLICANT: OLMSTED, ELIZABETH A.

RESULT 15 US-08-342-930-2

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Gaps
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OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRATIREGDAPAGGAVPGGAVPGGAVPGGFGPLLDG-WYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                   19;
                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.1%; Score 65.5; 38.5%; Pred. No. 9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 7, 2003, 16:56:57 Job time: 11.5185 secs
                                                         E: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  1711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                           CORRESPONDENCE ADDRESS:
                             NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 20; Conserva
                                                                                     Palo Alto
                                                                                                                  USA
                                                      ADDRESSEE:
STREET: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-342-930-2
                                                                                     CITY: F
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7, 2003, 16:53:34 ; Search time 15.2913 Seconds (without alignments) 306.927 Million cell updates/sec
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1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                             US-09-855-754B-7
                                                                                                         Мау
                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                    Scoring table:
                                                                  OM protein
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/2/pubpaa/PCS07_PUBCOMB.pep:*

Published_Applications_AA:* : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:

Database :

Description	Sequence 7, Appli Sequence 6, Appli Sequence 10, Appli Sequence 11, Appli Sequence 13, Appli Sequence 9, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 194, Appli Sequence 2, Appli
SUMMARIES	US-09-855-754-7 US-09-855-754-5 US-09-855-754-10 US-09-855-754-10 US-09-855-754-18 US-09-855-754-18 US-09-855-754-14 US-09-855-754-14 US-09-812-754-11 US-09-812-754-11 US-09-812-754-11 US-09-812-382-3 US-09-812-382-3 US-09-813-384-60 US-09-811-384-60 US-09-811-31A-60 US-09-811-31A-60 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9 US-09-811-31A-9
DB	
a Query Match Length DB	9229 9229 946 946 946 946 946 946 946 946 946 94
8 Query Match	100.0 100.0 891.4 891.4 885.5 887.5 87.5
Score	2 4 4 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Result No.	126480012641111111111111111111111111111111111

Sequence 10, Appl Sequence 14, Appl Sequence 14, Appl	Sequence 13, Appl Sequence 58, Appl Sequence 13, Appl Sequence 58, Appl Sequence 37, Appl	Sequence 37, Appl Sequence 34, Appl Sequence 34, Appl Sequence 31, Appl Sequence 25, Appl	358 65, 1 112, 1	21, 21, 95, 91,
10 US-09-861-597-10 9 US-10-235-674-14 10 US-09-263-689-14 9 US-09-820-843A-18	10 US-09-837-969A-13 10 US-09-837-969A-58 10 US-09-841-321A-13 10 US-09-841-321A-58 10 US-09-837-969A-37	10 US-09-841-321A-37 10 US-09-837-969A-34 10 US-09-841-321A-34 9 US-09-883-343A-31 10 US-09-888-260-25	10 US-09-864-761-35807 10 US-09-782-980-15 10 US-09-909-743-6 10 US-09-891-216-12 10 US-09-891-216-15 10 US-08-891-216-15	10 US-09-837-9587-21 10 US-09-841-321A-21 10 US-09-815-837-95 10 US-09-815-837-91 0 US-10-185-991-2 9 US-09-992-238-13
714 262 262 256	111 111 111 111 782	782 2003 2003 60 65	357 574 934 117	166 166 233 252 572 572
2.2.2.2 2.2.2.2 2.2.2.2 2.2.2.2	23.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	0.0.0.8.8. 0.0.0.8.8.	0.0.0.0.0.0 0.0.0.0.0.0 0.0.0.0.0.0	444400
63.5 63.5 63.5	62222 62233 6233 633 633 633 633 633 633	62.5 62.5 62.5 62.5 62.5	22222	61 61 61 61 61 61 61
20 21 22 23	24 25 27 27	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	# # # # # # # # # # # # # # # # # # #	044444 0112643

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GGISO-MACLOUE, NICOLE
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: BORDETELLA PARPERTUGSIS, AND BORDETELLA
TITLE OF INVERTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVERTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-855-754-6

Sequence 6, Application US/09855754

Publication No. US20020192237A1

GENERAL INFORMATION

APPLICANT: BODISAUX-EUDE, CAROLINE

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 272; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-7
                          Sequence 7, Application US/09855754
Publication No. US20020192237A1
                                                                               GENERAL INFORMATION:
-09-855-754-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7
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NUMBER OF SEC ID NOS: 24
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Best Local 8
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BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BROWHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 922;
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VENTION: POLYMORPHISMS OF
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100.0%; Score 272; DB 9;
Best Local Similarity 100.0%; Pred. No. 5.5e-21;
Matches 5j; Conservative 0; Mismatches 0;
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Pred. No. 1.6e-18;
3; Mismatches 0
                                                                                                                                       CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754-6
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TITLE OF INVENTION: POLYPEPTIDES CY
TITLE OF INVENTION: REGIONS OF PER
TITLE OF INVENTION: BORDETELLA PAR
TITLE OF INVENTION: BRONCHISEPTICY
TITLE OF INVENTION: BRONCHISEPTICY
TITLE OF INVENTION: INMUNICENIC CY
FILE REFERENCE: 03495-0206-00000
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US-09-855-754-5
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85.7%;
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Best Local Similarity 85.7
Matches 48; Conservative
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                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver.
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TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: PRECIOUS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRAPAPERUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISPEPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 5.9e-19;
3; Mismatches 3;
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Pred. No. 5.7e-19;
3; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/855,754
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-10
                      CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/206,969
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-13
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PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 88.2%;
Matches 45; Conservative
                                                                       PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 56
                                                                                                                                                                                                                                                                                                                            st Similarity 83.9%; 47; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYBEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PELING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSOFTWARE: PATENTING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                   Length 56;
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73.8%; Pred. No. 2.7e-17;
Live 3; Mismatches 3;
                                                   DB 9;
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Pred. No. 1.3e-17;
3; Mismatches 3;
                                              Score 228.5; DB 9
Pred. No. 1.3e-17;
2; Mismatches 4
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US-09-855-754-12
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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80.4%;
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80.4%;
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Best Local Similarity 80.4
Matches 45; Conservative
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Best Local Similarity 73.8
Matches 45; Conservative
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SOFTWARE: PatentIn Ver
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Best Local Similarity
Matches 45; Conserv
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US-09-855-754-12
  US-09-855-754-9
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LENGTH: 56
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LENGTH: 61
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPORTINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERFACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                            Length 46;
                                                                                                                                                                                                                                                                             21
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                                                                                                                                                                                                                                                  1 ORATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                 .2e-18;
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Pred. No. 7.9e-17;
----heq 0;
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                                                                                                                                                       Score 232.5; I
Pred. No. 4.2e.
0; Mismatches
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                                                                                   ) ORGANISM: Bordetella bronchiseptica US-09-855-754-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                          85.5%;
90.2%;
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90.2%;
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 90.2
Matches 46; Conservative
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                        46;
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                 SEQ ID NO 8
LENGTH: 46
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                                                                  TYPE: PRT
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ITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
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TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
FILE REFERENCE: BERL-020/04US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/841,321A, CURRENT FILING DATE: 2001-04-30 PRIOR APPLICATION NUMBER: US 09/258,723 PRIOR FILING DATE: 1990-02-26 PRIOR PLING DATE: 1998-05-29 PRIOR FILING DATE: 1998-05-29 PRIOR FILING DATE: 1998-05-29 PRIOR FILING DATE: 1998-02-27 NUMBER OF SEQ ID NOS: 65 NUMBER OF SEQ ID NOS: 65 SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5; DE Pred. No. 1.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69.5;
Pred. No. 1.3
                                      CURRENT APPLICATION NUMBER: US/09/837,969A CURRENT FILING DATE: 2001-06-19
                                                        CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/258,723
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
PRIOR PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 65
SSOFWARE: Patentin version 3.0
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RGDAPAGGAVPGGAVPGGAVPG----GFG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 RGDSP-GVGVPGVGVPGKGVPGVGFPGFG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 RGDAPAGGAVPGGAVPGGAVPG----GFG 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-841-321A-60
; Sequence 60, Application US/09841321A
; Patent No. US20020116069A1
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ilarity 58.6%;
Conservative
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Best Local Similarity 58.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                       FILE REFERENCE: BERL-020/03US
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
LOCATION: (1)..(111)
CTHER INFORMATION: Synthetic
US-09-837-969A-60
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; LOCATION: (1)..(11)
; OTHER INFORMATION: Synthetic
US-09-841-321A-60
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Best Local Similarity
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US-09-837-969A-9
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--- PGGAVPGGFGPLLDGWYGVDVSDSTVDLA 50
                 0; Gaps
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Sequence 6, Application US/09812382
Sequence 10.25001003450501
Sequence 6. Application US/09812382
Sequence 6. Application US-009812382
SEREAL INFORMATION:
TITLE OF INVENTION: Fusion Peptides Isolatable by Phase Transition
FILE REFERENCE: 4176-101
CURRENT APPLICATION NUMBER: US/09/812,382
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR APPLICATION NUMBER: US 60/190,659
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CALILOLI, Ashutosh
TITLE OF INVENTION: Fusion Peptides Isolatable by Phase Transition
FILE REFERENCE: 4176-101
CURRENT APPLICATION NUMBER: US/09/812,382
CURRENT FILING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
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Pred. No. 0.99;
0; Mismatches
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Pred. No. 0.14
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 GAGVPGAGVPGGGVPGGGVP 402
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Patent No. US20010034050A1
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60.0%;
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 60.09
Matches 15; Conservative
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Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: ELP[V5A2G3-90]
US-09-812-382-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: ELP[V5A2G3-10]
US-09-812-382-3
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US-09-837-969A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 450
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ò 셤 Gaps

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Gaps

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GENERAL INFORMATION:

APPLICANT: UTTY, Dan

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/837,969A

CURRENT APPLICATION NUMBER: US/09/837,969A

CURRENT PELLIG DATE: 1999-02-26

PRIOR PILLING DATE: 1999-02-26

PRIOR FILLING DATE: 1998-02-27

PRIOR FILLING DATE: 1998-02-27

PRIOR FILLING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATCHTION NUMBER: US 60/076297

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATCHTION OF SEQ ID NOS: 65

SOFTWARE: PATCHTION OF SEQ ID NOS: 65

SEQ ID NO 9

LENGTH: 48

TYPE: PRT

ORGANICH: ARTHIFICIAL SEQUENCE

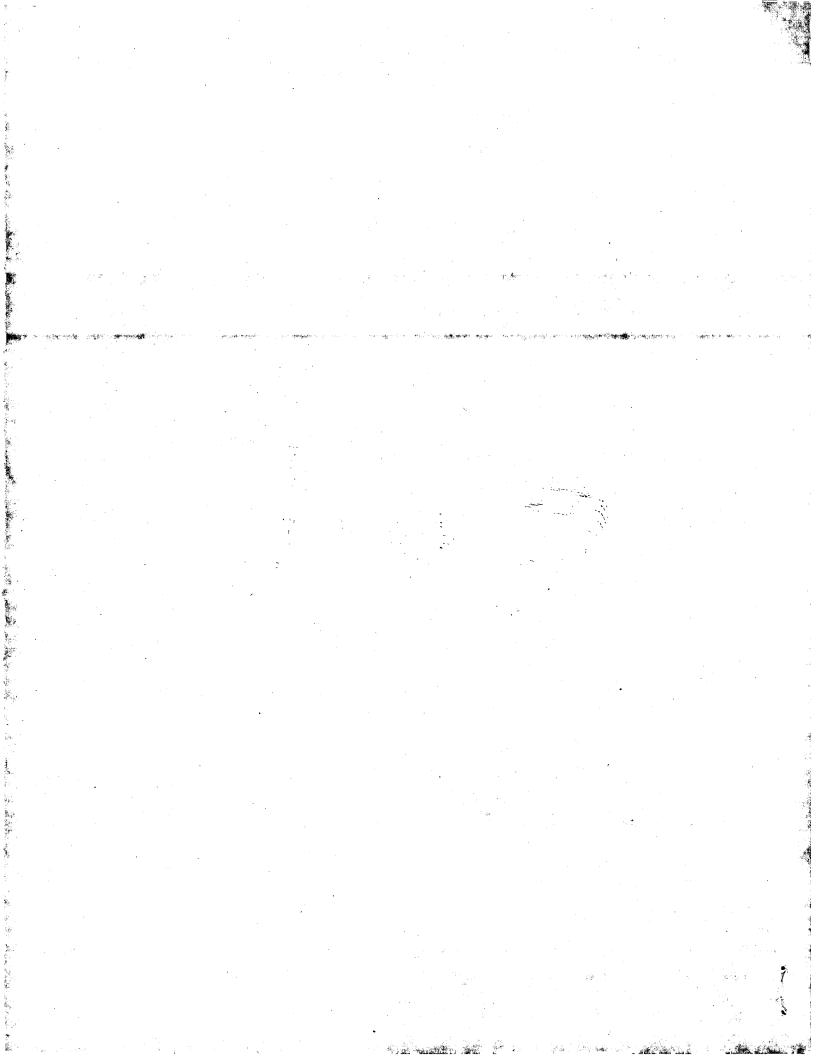
FRATURE:

LCCATION: (1)..(48)

COTHER INDERMATION: Synthetic

US-09-837-969A-9
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24.6%; Score 67; DB 10; Length 48; Best Local Similarity 68.0%; Pred. No. 1.2; Matches 17; Conservative 0; Mismatches 4; Indels
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein 7, 2003, 16:41:02; Search time 9.55707 Seconds (without alignments) 513.008 Million cell updates/sec May Run on:

Title:

Perfect score:

US-09-855-754B-7 272 1 QRATIRRGDAPAGGAVPGGA......PLLDGWYGVDVSDSTVDLAQ Sequence:

51

BLOSUM62 Scoring table:

283224 seqs, 96134422 residues Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	pertactin - Bordet	E	outer membrane pro	probable serine-th	ATP-dependent RNA	MFS18 protein - ma	elastin precursor	major merozoite su	dnaK-type molecula	major merozoite su	heat shock protein	glycine-rich prote		hypothetical prote	O)	hypothetical prote			sporozoite surface	glycine-rich cell	octamer binding tr	proteinase do (EC	hypothetical prote	elastin - bovine (hypothetical prote		protein-tyrosine-p	conserved hypothet	himothotion
SUMMAKIES	OI OI	S15204	A47675	A32560	T35389	T45677	S25103	EAMS	A28121	A49242	A45532	PC7036	JQ1063	T24865	T29167	T03166	A85217	T04441	S37108	A45560	T09262	159234	AG3328	T30743	I45885	C95291	T49890	A55148	B75476	20120
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ø	Query Match	100	85.5		30.5	29.8	28.7		25.9	25.9	25.9	25.6	25.4	25.4	25.2	25.2	25.0	25.0	24.8	24.8	•	24.6	24.4	24.3	24.1	24.1		24.1	•	,
	Score	272	232.5	231.5	83	81	78	74	70.5	70.5	70.5	69.5	69	69	68.5	68.5	68	68	67.5	67.5	67	67	66.5	99	'n.	65.5	5.	65.5	65	١
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NAD-dependent form hypothetical prote	<pre>molybdenum cofacto hemagglutinin prec dnaK-type molecula</pre>	hypothetical prote dnaK-type molecula elastin precursor	DNA repair protein hypothetical prote spidroin 2, dragii	CREB-binding prote hypothetical prote	<pre>IgB-binding prote! hypothetical prote hemagglutinin prec</pre>
C98152 AI3135	A84169 HMIVHM HHKW7A	T21394 S51712 EART	B70804 T29299 A44112	T13828 T22572	A54889 T15155 HMIVTN
000	7 - 1 - 5	777	777	77	777
114	278 566 640	640 656 864	480 589 627	3190 215	262 471 565
23.7	23.7 23.7 23.7	23.7 23.7 23.7	23.5 23.5 23.5	23.5	23.3 23.3 3.3 3.3
64.5	6.64 5.64 5.67 5.67	64.5 64.5 64.5	4 4 4	- 64 63.5	633.5 53.55
30	2 E E	35 37	38 39 40	4 4 2 2	4 4 4. 6 4 7.

ALIGNMENTS

RESULT 1 S15204 Partactin - Bordetella parapertussis N;Alternate names: outer membrane protein P70 C;Species: Bordetella parapertussis C;Species: Bordetella parapertussis C;Date: 07;Apr.1994 #sequence_revision 07-Apr.1994 #text_change 08-Oct-1999 C;Accession: S15204; S14659 R;Li, L.J.; Dougan, G; Novotny, P; Charles, I.G. Mol. Microbiol. 5; A00-417, 1991
A; Title: P:70 per tactin, an outer-membrane protein from Bordetella parapertussis: clo A; Reference number: S15204; MUD:91251771; PMID:2041476 A; Reference number: S15204 A; Molecule type: DNA A; Residues: 1-922 < LIDA A; Residues: 1-922 < LIDA A; Cross-references: FMRL: X4447. NID: A39761. DIDN: CAA34410 1. DID: A30762
C;Genetics: A;Gene: prn C;Keywords: membrane protein
Query Match 100.0%; Score 272; DB 2; Length 922; Best Local Similarity 100.0%; Pred. No. 3.6e-21; Associated by the state of the s

RESULT 2

68K Outer membrane protein P.68 pertactin - Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C; Accession: A47675 R; Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Fairweather, N.F.; Novotny, P.; Pairweather, C.; Charles, I.G. J.; Fairweather, N.F.; Novotny, P.; Pairweather, I.G. J.; Fairweather, N.F.; Novotny, P.; Pairweather, I.G. J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Pairweather, I.G. J.; Pairweathe

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A;Accession: A47675 A;Status: preliminary A;Molecule'type: incleic acid A;Residues: 1-911 (LLI) A;Cross-references: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397 A;Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

2; Query Match 85.5%; Score 232.5; DB 2; Length 911; Best Local Similarity 90.2%; Pred. No. 5.3e-17; Matches 46; Conservative 0; Mismatches 0; Indels 5

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Gaps

1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFQPLLDGWYGVDVSDSTVDLAQ 51

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NAIternate names: tropoelastin
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999 .
C;Accession: A5771
R;Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A;Filte: Use of an intron length polymorphism to localize the tropoelastin gene to 1
A;Reference number: A55721; MUID:95130069; PMID:7829060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; extracellular matrix; glycoprotein; hydroxylysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Zea mars (maize)
C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 29-Oct-1999
C; Accession: S25103
S; Withaht, S.Y.; Suner, M.M.; Bell, P.J.; Vaudin, M.; Greenland, A.J.
S; Withaht, S.Y.; Suner, M.M.; Bell, P.J.; Vaudin, M.; Greenland, A.J.
A; Reference number: S25103
A; Recession: S25103
A; Status: preliminary
A; Status: preliminary
A; Status: Pype: man, A
A; Residues: 1-128 < VMRLA
A; Residues: 1-128 < VMRLA
A; Residues: EMBL:X67324; NID:922646; PIDN:CAA47738.1; PID:922647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-860 <WYD>
A; Cross-references: GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74; DB 1; Length 860;
Pred. No. 3.1;
3; Mismatches 11; Indels
                                                                                                                                                                                                                              Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128
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                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: cultivar Columbia; BAC clone F14P22 C; Genetics:
A; Map position: 3
A; Introns: 239/3; 267/3; 348/3; 404/3; 442/3
A; Note: F14P22.160
C; Superfamily: ATP-dependent RNA helicase DBP1
                                                                                                                                                                                                                                                                                                                                            1 ORATIRRGDAPA---GGAVPGGAVPG---GAVPGGFGPLLDGWYG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Naperfamily: elastin
C;Keywords: alternative splicing; extracellular matrix;
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-660/Product: elastin #status predicted <MAT>
F;850-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATIRRGDAPAGGAVPG----GAVPG----GAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
0.18;
                                                                                                                                                                                                                              Score 81; DB 2, Pred. No. 0.42; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GDAPAGGAVPGGAVPGGAVPG----GFGPLLDGW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 78;
Pred. No.
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Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.7%;
Best Local Similarity 44.1%;
Matches 15; Conservative
A; Cross-references: EMBL: AL137082
                                                                                                                                                                                                                           29.8%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elastin precursor - mouse
                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
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R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K., submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
A;Stecession: T45677
A;Status: preliminary
                                                                                                                                                                                                                                                               P.; Morriss
                                                                                                                                                                                                                                             R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morris: Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P. A;Reference number: A32560; WUID:89264462; PMID:2542937
A;Accession: A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T35389
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL079348; PIDN:CAB45488.1; GSPDB:GN00070; SCOEDB:SC66T3.32c
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NiAlternate names: protein F14P22.160
C:Species: Arabidopsis thaliana (mouse-ar cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
                                                                                                                                                                            Species: Bordetella pertussis
Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross_references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A;Note: it is uncertain whether Met-1 or Met-3 is the initiator
C;Keywords: membrane protein
F;134/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable serine-threonine protein kinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence revision N5-Now-1000
     254 QRATIRRGDAPA----GGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                              outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 231.5; DB 2;
Pred. No. 6.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RGDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain A3(2) C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: SCOEDB:SC66T3.32c
C; Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.1%;
Best Local Similarity 82.1%;
Matches 46; Conservative
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nes 16; Conservative
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A; Accession: T35389
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A; Residues: 1-783 <MUR>
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A; Residues: 1-646 <DAN>
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Indels 23;

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R:Dally, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Blochem. Parasitlol. 36, 289-288, 1989
A:Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: cloni
A:Reference number: A45531; MUID:90014982; PMID:2797064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ride Oliveira, D.B.; Seurinck, J.; Inze, D.; Van Montagu, M.; Botterman, J. Plant Cell 2, 427-438, 1990
Plant Cell 2, 427-438, 1990
A; Title: Differential expression of five Arabidopsis genes encoding glycine-rich prot
A; Reference number: JQ1060; MUID:93044485; PMID:2152168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine-rich protein 4 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jul-2000
C;Accession: JQ1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rhizopus nigricans
C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
X;Residues: 1-112 <DEO:
A;Cross-references: GB:S47413; NID:g259448; PIDN:AAB24076.1; PID:g259449
A;Experimental source: strain C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TIRRGDAPA-----GAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Accession: PC7036
R. Cernila, B.; Cresnar, B.; Breskvar, K.
Blochem. Blophys, Res. Commun. 265, 494-498, 1999
A.Fille: Induction of Hsp70 in the fungus Rhizopus nigricans. A; Reference number: JC7132; MUID:20025372; PMID:10558896
A. Status: preliminary
A. Molecule type: mRNA
                                                                                                                                                                A; Accession: A45531
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 454-1094 <DAL>
A; Cross-references: GB.J03975; NID:g160081; PID:g160082
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                A; Cross-references: GB:J04668; NID:g160492; PID:g160493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heat shock protein 70 - Rhizopus nigricans (fragment)
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Pred. No. 6.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 25.9%; Score 70.5; D
Best Local Similarity 44.1%; Pred. No. 15;
Matches 26; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.4%; Score 69; DB Best Local Similarity 48.4%; Pred. No. 1.4; Matches 15; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDAPAGGAVPG -- GAVPGGAVPGGFGPLLDG 36
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A, Cross-references: GB:AF188289
C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 GGMPGGGGMPGGGAPGG-FPGG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GDAPAGGAVPGGAVPGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%;
59.1%;
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Matches 13; Conservative
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dnax-type molecular chaperone hsp70 - Plasmodium cynomolgi
C;Species: Plasmodium cynomolgi
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A49242
R;Eckert, V; Sanchez, L.; Cochrane, A.; Enea, V
Exp. Parasitol. 75, 323-338, 1992
A;Title: Plasmodium cynomolgi: the hsp 70 gene.
A;Reference number: A49242; MUID:93050041; PMID:1426134
A;Recession: A49242
A;Status: preliminary
A;Molecule type: nucleic acid
A;Rocession: 1-686 <ECKA
A;Rocession: 1-686 <ECKA
A;Ross-references: CB:M90978; NID:q160349; PIDN:AAA29625.1; PID:q160350
A;Note: sequence extracted from NCBI backbone (NCBIN:118975, NCBIP:118976)
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Plasmodium yoelii
C.Species: Plasmodium yoelii
C.Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C.Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C.Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
R.Lewis, A.P.
Mol. Blochem. Parasitol. 36, 271-282, 1989
Mol. Blochem. Parasitol. 36, 271-282, 1989
A.Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface
A.Recession: A45532
A.Status: preliminary
                                                                                                                                                                                                                                                                  er
                                                                                 Cispecies: Plasmodium yoelii
Cispecies: Plasmodium yoelii
Cispecies: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
Cispecies: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
Cispecies: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
Francession: A28121
A:Title: The 3' portion of the gene for a Plasmodium yoelii merozoite surface antigen (A:Reference number: A28121; MUID:88124889; PMID:2448778
A:Reference number: A28121
A:Moccession: A28121
A:Residues: 1-680 A384
A:Cross-references: GB:J03612; NID:g160678; PID:g160679
A:Cross-references: Strain 17XL
A:Rotes: the authors translated the codon GTA for residue 429 as Leu
C;Superfamily: major merozoite surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TIRRGDAPA-----GGAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 686;
                                                       major merozoite surface antigen - Plasmodium yoelii (fragment)
C;Species: Plasmodium yoelii
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #184+ Abana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.5; DB 2;
Pred. No. 5.7;
4; Mismatches 8;
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Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 26; Conserv
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A; Residues: 1-1772 <LEW>
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Matches
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RESULT 8
A28121
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A;Experimental source: strain Bristol N2; clone T28H11
                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281120; PIDN:CAB03349.1; GSPDB:GN00021; CESP:T12DB.8
A;Experimental source: clone T12DB
                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <4012>
A;Residues: 1-422 <4012>
A;Coss-references: EMBL:283241; PIDN:CAB05818.1; GSPDB:GN00021; CESP:T12D8.8
A;Experimental source: clone T25C8
                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T24865; T25273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Ppothetical protein T28H11.5 - Caenorhabditis elegans
| Species: Caenorhabditis elegans
| Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 21-Jan-2000
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probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
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A;Introns: 88/1; 372/1
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Nelson, J.; Wohldmann, P.
submitted to the EMBL Data Library, July 1996
A; Description: The sequence of C. elegans cosmid T28H11.
A; Reference number: 220582
A; Accession: T29167
hypothetical protein T12D8.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 STWTAVGAPGGGASALGAAPPAGSMSGGGGGATSGYFGV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ATIRRGDAPAGGA-VPGGAVPGGAVPGGFGPLLDGWYGV 40
                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, December 1996
A;Reference number: Z20008
A;Accession: T25273
                                                                                          R.McMurray, A. submitted to the EMBL Data Library, October 1996 A.Reference number: 219944
A.Recession: T24865
A.Accession: T24865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69; DB 2
Pred. No. 5.1;
1; Mismatches
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Pred. No. 5.6;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 35/2; 157/2; 228/3; 375/1
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ilarity 41.0%;
Conservative 6
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Best Local Similarity 50.0%;
Matches 13; Conservative
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Best Local Similarity
Matches 16; Conserv
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A; Residues: 1-405 <NEL>
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                                                                                                                                                                                                                                                                                                                       R; Gardner, A.
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03166
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Accession: T0316
A;Accession: T0
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database :

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Q10265 schizosacch
P16770 human cytom
035984 mus musculu
P23118 strongyloce
P11133 influenza a
P26139 influenza a
P26139 influenza a
P10209 herpes simp
Q01877 pucchia yr
P47845 oryotolagus
Q10707 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li.J., Dougan G., Novotny P., Charles I.G.;
Pp.70 pertactin, an outer-membrane protein from Bordetella
parapertussis: cloning, nucleotide sequence and surface expression in
Bscherichia coli.*;
Mol. Microbiol. 5:409-417(1991).
-! FUNCTION, A GGGLUTINGEN THAT BINDS TO EURARYOTIC CELLS; A PROCESS
MEDIATED BY THE R.-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
-! SUBUNIT: MONOMER.
-! SUBUNIT: MONOMER.
-! DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-! MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.95.
PERTACTIN (P.70).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordețella parapertussis.
Bacteria: Proteobacteria: beta subdivision: Alcaligenaceae;
Bordețella.
                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTINEAMLY.
OUTET | membrane; Signal; Virulence; Repeat.
SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                              ALIGNMENTS
                                      PBX2_MOUSE
BIND_STRFN
HEMA_IAZH2
                                                                                                  HEMA_IAEN7
HEMA_IAZCO
HEMA_IAVI7
                                                                                                                                                         UL25_HSV11
HS71_PUCGR
LEG3_RABIT
                                                                                                                                                                                                                     YK98_MYCTU
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EMBL; A26124| CAA01786.1; --
EMBL; A19182| CAA01454.1; --
PIR; S15204; S15204.
PIR; S14659; S14659.
InterPro; IPR003992; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CN2591;
MEDLINE-91251771; PubMed-2041476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03212; Pertactin; 1.
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647
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P24328;
  PERT_BORPA
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  003035 bordeterro
P32439 zea mays (m
P54320 mus musculu
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rattus norv
mycobacteri
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bos taurus
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                                                                                                                             7, 2003, 16:31:49; Search time 4.9523 Seconds (without alignments) 427.133 Million cell updates/sec
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                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                      US-09-855-754B-7
272
1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                112892 seqs, 41476328 residues
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PERT_BORPE
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CUT2_CAEEL
BR3A_HUMAN
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PTPO_RAT
HEMA_IAME2
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HS71_CANAL
ELS_RAT
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SPD2_NEPCL
LEG3_RAT
HEMA_IATKP
ELS_BOVIN
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Maximum Match 100%
Listing first 45 summaries
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3_CANFA
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.;
"Molecular coloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                             (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
            LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nuclectide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
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                                                                                                                                 922;
                                                                                                                                                                                              254 QRATIRRGDAPAGGAVPGGAVPGGRQFLDGWYGVDVSDSTVDLAQ 304
                                                                                                                                                                                   1 QRATIRRGDAPAGGAVPGGAVPGGRGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                       Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                 Length
                                                                                                                               ; Score 272; DB 1;
; Pred. No. 7.3e-20;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CN2992;
MEDLINE-89264462; PubMed-2542937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1527510;
                                                                                                       95178 MW;
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100.0%;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                STANDARD;
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REVISIONS TO 264 AND 332.
MEDLINE=92407514; Pubmed=
                                                                                                      922 AA;
                                                                                                                                            Similarity
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                                                    271
276
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575
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P14283;
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Gen. Microbiol. 138:1697-1705(1992).

BEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

SUBGELLULAR LOCATION: Outer membrane.

SUBCELLULAR LOCATION: Outer membrane.

DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.

MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
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5 x 5 AA TANDEM REPEATS OF G-G-A-V-P.
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ADHESION TO VARIOUS EUKARYOTIC CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P. A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 7.6e-17;
3; Mismatches 1
                                                                                                                                                                                                                                                                                    PERTACTIN (P.69).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA
                                                                                                                                                                                              Outer membrane; Signal; Virulence; Repeat.
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                    InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam. PF03112; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTINFAMLY.
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83.9%;
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262
PIR; A32560; A32560.
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286
579
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Q03035;
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EMBL; X54815; CAA38584.1; -.

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EMBL; J04560; AAA22980.1; ALT_SEQ

;

GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on:

May 7, 2003, 16:38:52; Search time 26.0647 Seconds

(without alignments)

1: sp_archea:*
2: sp_bacteria:*
3: sp_bacteria:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mnemal:*
8: sp_organial:*
10: sp_plage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_vertebrate:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_archia:*
16: sp_bacteriap:*
17: sp_archeap:*

SPTREMBL_21:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		٠.
		dР					
Result No.	Score	Query Match	Query Watch Length DB	DB	ID	Description	
-	27.2	000	!	<u>.</u>			
1	7/7	7.00		7	CARDEO	Uskodo pordetella	
~	272	100.0		7	Q9K5G8	09k5g8 bordetella	
m	272	100.0		~	Q9K5I0	09k5i0 bordetella	
4	272	100.0		0	09AHP1	Ogahol hordetella	
s	272	100.0		~	ОЭКЛУЗ		
Q	259.5	95.4	216	~	Q9KJY4		
7	241.5	88.8	387	~	Q9S3M9		
80	241.5	88.8	910	~	Q9S6N1		
6	241	98.6		7	Q93L99		
10	241	98.6		~	6M9S6D		
11	241	88.6		~	0N9S60	_	
12	239	87.9		7	093705		
13	237.5	87.3		~	069257		
14	237	87.1	181	7	Q9ALQ1	09alq1 bordetella	
15	235	86.4		~	Q8RSU0		
16	232.5	85.5		7	098546		

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Gaps

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Length 158; Indels

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 51; Conservative 0; Mismatches 0;

159 A.A.

PRT;

PRELIMINARY;

Q9K5G8 Q9K5G8;

RESULT 2 Q9K5G8

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Q985h8 bordetella Q985h bordetella Q985h bordetella Q985h bordetella Q985h2 bordetella Q9a1q5 bordetella Q9a1q5 bordetella Q9472 bordetella Q945q3 bordetella Q945q3 bordetella Q985q3 bordetella Q985q3 bordetella Q985q3 bordetella Q945q4 bordetella Q945q4 bordetella Q945q4 bordetella Q945q4 bordetella Q945q4 bordetella	· · · · · · · · · · · · · · · · · · ·	ALIGNMENTS RT; 158 AA. ated) t sequence update) t annotation update)	(Alcaligenes bronchisepticus). beta subdivision; Alcaligenaceae; 0899896; kegions of Pertactin in Bordetella pronchiseptica."; 7(2000)
Q9K5H8 Q9K5H4 Q9K5H0 Q9K5H2 Q9ALQ3 Q9ALQ3 Q9ALQ3 Q9ALQ2 Q9K5G3 Q9K5G3	0953M8 088143 098143 093L98 093L98 09ALP6 09ALP6 09NHW3 09NHW4 09NHW3 09NHW3 09NHW3 09CA11 09CA11	ALIGN PRT; Created) Last sec Last and	(Alcaligeno beta subdi 10899896; Regions of Regions of Ppertussis, 17(2000).
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Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156769; AAF82393.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                     154 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 204
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus), astetraia, proteobacteria; beta subdivision; Alcaligenaceae; Bordetella.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UT-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
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211 AA; 20946 MW; E751FFA1510D99A4 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (Fragment).
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ilarity 100.0%; Pred. No. 2e-21;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e-21;
tive 0; Mismatches 0;
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                                                                                                                                                                                                bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
Embz. AF298589; AAK16690.1; ...
InterPro; IPR003992; pertactin.
PRINTS; PR01482; PERTACTIN.
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179 AA; 17270 MW;
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   Pertactin (Fragment).
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                                                                                                                                                                                                                   Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (P.68) (Fragment).
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MEDLINE-20359389; PubMed=10899896;
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"Polymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends
and evidence for vaccine-driven evolution.";
Infect. Immun. 66:670-675(1998).
EMBL; AJ133784; CAB40080.1; -.
InterPro; IPR00392; pertactin.
InterPro; IPR00399; pertactin.
InterPro; IPR004899; pertactin._vir.
InterPro; IPR004899; pertactin._vir.
InterPro; IPR004899; Pertactin._vir.
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MEDINE-98114370; PubMed=9453625;
MOOI F.R., VanOirschot H., Heuvelman K., vanderHeide H., Gaastra W.,
Willems R.R.J.;
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   3acteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                      van Oirschot H.F.L.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                     910 AA; 93495 MW; AF38246F8D82E03D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last anno
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PRINTS; PR01484; PRTACTNFAMLY.
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Best Local Similarity
Matches 47; Conserv
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Matches 45;
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MEDLINE-99345256; PubMed-10418915;
MEDLINE-99345256; PubMed-10418915;
MEDLINE-99345256; PubMed-10418915;
Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;
Intranasal murine model of Borderella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular vaccine.";
Vaccine 17:2651-2660(1999).
EMBL: AJ006134; CAA06896.1; -.
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                                                                                   Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
"Variability in the pertactin genes of Bordetella bronchiseptica
ancholates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
Subnitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS6768; AFF82392.1; -.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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95.4%; Score 259.5; DB 2; Length
Best Local Similarity 91.1%; Pred. No. 4.3e-20;
Matches 51; Conservative 0; Mismatches 0; Indels
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35 >387 PERTACTIN.
387 387
387 AA; 38714 MW; 61195D45D347A1EB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Pertactin precursor (Fragment).
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Best Local Similarity
Matches 47; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                        SEQUENCE FROM N.A.
                           NCBI_TaxID-518;
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               Bordetella
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SEQUENCE
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SEQUENCE
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Weber C., Boursaux-Eude C., Njamkepo E., Guiso N.;
Polymorphism of Bordetella pertussis isolates circulating the last
ten years in France, a country using the same effective whole-cell
"Polymorphism of pertussis";
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                                                                               Bordețella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                             vaccine since more than thirty years.";
Submitted (MAY 2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ309315; CAC48161.1;
NON.TER 3382 382
                                                                                                                                                                                                                                                                                                                                                                                      382 AA; 38333 MW; 2803BDA9581AC8E6 CRC64;
Last sequence update)
Last annotation update)
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Pertactin (Fragment).
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PRN OR PRN6.
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"Polymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends
and evidence for vaccine-driven evolution.";
Infect. Immun. 66:670-675(1998).
EMBL, Ali33245; CAB39891.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertact.
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                                                                                                                                                                                                                                                                                                                                                Mooi F.R., He Q., Van Oirschot H., Mertsola J.; "Variation in the Bordetella pertussis virulence factors pertuss toxin and pertactin in vaccine strains and clinical isolates in
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                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERTACTIN.
7AE0F69C1B305E52 CRC64;
                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect. Immun. 67:3133-3134(1999).
EMBL; AJ011015; CAA09460.1; .
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact.in.vir.
InterPro; IPR04899; Pertact.sup.
Pfam; PR03122; Pertact.in. 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTIN.
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35 905 Pi
905 AA; 93071 MW;
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Pfam; PF03212; Pertactin; 1.
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Matches 45; Conservative
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                                                                                                                                               Bordetella pertussis.
                                                                                                   Pertactin precursor,
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NCBI_TaxID=520;
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Q9S6N0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weber C., Boursaux-Eude C., Nicole G.;
"Polymorphism of Bordetella pertussis isolates circulating the last ten years in France, a country using the same effective whole-cell vaccine since more than thirty years.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ318056; CAC67458.1; ...
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                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID-520;
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Bordetella.
Bordetella.
NCBL_TaxID=520;
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77.0%; Pred. No. 4.9e-18;
ive 3; Mismatches 1; Indels
                                                                                     Score 241; DB 2; Length 90
Pred. No. 1.8e-17;
3; Mismatches 3; Indels
                                                                                                                                                                            1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DRINTS; PRO1484; PERTACTIN.
PRINTS; PRO1484; PRTACTNFAMLY.
SEQUENCE 905 AA; 93114 MW; 74B155EDB61059B4 CRC64;
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167 AA; 15826 MW; E136B4CF809565F0 CRC64;
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Last annotation update)
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                                                                                     88.6%;
88.2%;
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Best Local Similarity 77.03
Matches 47; Conservative
                                                                                  Query Match 88.6
Best Local Similarity 88.2
Matches 45; Conservative
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01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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van Loo I.H., Mool F.R.;
"Changes in the Bordetella pertussis population in the first 20 years after the introduction of vaccination.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430832; CAD23609.1;
SEQUENCE 912 AA; 93680 MW; 7F417BA66B732EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                         1 QRATIRRGDAPAGGAVPGGAV------PGGFGPLLDGWYGVDVSDSTVDLA 50
                                                                                                           Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                       Length 912;
                                                                                                                                                                                                                                                                                      86.4%; Score 235; DB 2; Length 91
75.4%; Pred. No. 7.9e-17;
Live 3; Mismatches 2; Indels
                            Created)
Last sequence update)
Last annotation update)
  912 AA.
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    PRT;
                          01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
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  FRELIMINARY;
                                                                                             Bordetella pertussis.
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Job time: 29.0647 secs
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=520;
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                                                                  Pertactin.
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                                                                            Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;
Tiranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular
vaccine."; 12651-2660(1999).

Li Vaccine."; 12651-2660(1999).

EMBL; AJ132095; CAA06694.1; ---
REMBL; AJ132095; CAA06694.1; ---
REMBL; AJ132095; CAA066012.2; ---
REMBL; AJ132095; Pertactin."

InterPro; IPR004999; Pertactin..

InterPro; IPR004999; Pertactin..

InterPro; IPR004999; Pertactin..

InterPro; PR004999; Pertactin..

InterPro; PR00489; Pertactin..

RINTS; PR01482; PERTACTIN.

RINTS; PR01484; PRTACTURAMIX.

SIGNAL

I 34 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                         DB 2; Length 907;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001). EMB: ARG38442.1. .. InterPro; IPR003992; Pertactin. PRINTS: PR01482; PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 237; DB 2; Length 18
Pred. No. 8.7e-18;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                        Score 237.5; DB 2; Length
Pred. No. 4.3e-17;
3; Mismatches 2; Indels
van Oirschot H.F.L.M., Mool F.R.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 PERTACTIN.
3A7D05F4094420EA CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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MEDLINE-21117018; PubMed-11179374;
                                                                  MEDLINE-99345256; PubMed-10418915;
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82.1%;
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86.3%;
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Matches 44; Conservative
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234 76.0 234 76.0 228.34 76.0 228.5 74.2 228.5 74.2 212 58.8		91.59 91.59	Bordetella bronchiseptica. W0200190143-A2. 29-NOV-2001. 23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P. (INSP) INST PASTEUR. Guiso-maclouf N, Boursaux-eude C; WPI; 2002-097639/13. Polypeptides containing polymorphisms of pertactin in Bordetella species, useful iterating infections caused by Bordetella
		RESG AAE1 XX XX XX XX XX XX XX XX XX XX XX	\$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$ \$\$
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. protein - protein search, using sw model ton: May 7, 2003, 16:31:28; Search time 29.0971 Seconds (without alignments) 256.453 Million cell updates/sec	Title: US-09-855-754B-9 Perfect score: 308 Sequence: 1 ORATIRRGDAPAGGGVPGGAPVLDGWYGVDVSGSTVELAQ 56 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 908470 seqs, 133250620 residues Total number of hits satisfying chosen parameters: 908470 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Maximum DB seq length: 2000000000 Maximum DB seq length: 2000000000	Database: A_Geneseq_101002:* i: \$1D52/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 2: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 3: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 4: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 5: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 6: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 7: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 8: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 9: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 10: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 11: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 12: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 13: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 14: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 15: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 16: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 17: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 18: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 18: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 19: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 10: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 11: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 12: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 13: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 14: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 15: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 16: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 17: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 18: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 19: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 20: \$51D52/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* 21: \$51D52/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* 22: \$51D52/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*	## Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. ## SUMMARIES Query Score Match Length DB ID Description

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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens an infinity chromatographic columns. Pertactin is useful as antiquens animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                           The present invention relates to Bordetella bronchiseptica
Claim 26; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Gaps
                              ;
         Length 56;
                              Indels
      100.0%; Score 308; DB 23;
100.0%; Pred. No. 9.7e-25;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.0
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1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 g ŝ

AAE16191 RESULT

AAE16191 standard; peptide; 56 AA.

AAE16191;

26-MAR-2002 (first entry)

B. bronchiseptica strain prn3 pertactin outer membrane protein region I.

Pertactin, PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

Disclosure; Fig 1b; 47pp; English.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Disclosure; Fig 1b; 47pp; English.

Couter membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fullds, such as human or other animal body fluids, including human sera, and to determine the concentration of ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of The present invention relates to Bordetella bronchiseptica pertactin

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B. bronchiseptica strain prn1 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
                                                                            Gaps
Bordetella in a material. The present sequence is B. bronchiseptica
pertactin outer membrane protein region I.
                                                                                              1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGGGPVLDGWYGVDVSGSTVELAQ 56
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                                                    Length 56
                                                                          2; Indels
                                                   Score 291; DB 23;
Pred. No. 5.4e-23;
1; Mismatches 2;
                                                                                                                                                                                                                                                                               therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                           AAE16189 standard; peptide; 56 AA.
                                                     94.5%;
94.6%;
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                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica.
                                                                                                                                                                                                                        (first entry)
                                                                          53; Conservative
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                                                     Query Match
Best Local Similarity
                               56 AA;
                                                                                                                                                                                                                                                                                                                          WO200190143-A2
                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                  29-NOV-2001.
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Matches
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ö (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for traating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica Gaps present invention relates to Bordetella bronchiseptica pertactin 1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 ö Length 56; Score 281; DB 23; Length 5 Pred. No. 5.7e-22; 1; Mismatches 3; Indels Pred. No. 5.7e 1; Mismatches 91.2%; Query Match 91.2 Best Local Similarity 92.9 Matches 52; Conservative 56 AA; Sequence The ò

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Pertactin; pinl; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides derived from Bordetella pertussis pertactin, useful a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                     Bordetella pertussis pertactin (Prn1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 35-38; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEWE-) NEDERLANDEN MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000EP-0202309.
                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001; 2001WO-NL00493
                18-APR-2002 (first entry)
                                                                                                                                                                         Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-139897/18.
                                                                                                                                                                                                                                                                                         WO200200695-A2
                                                                                                                                                                                                                                                                                                                              03-JAN-2002.
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                                                                                                                                                                                                               Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal cells, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. pertussis pertactin outer membrane protein, p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                         Pertactin; PRN: outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                     Bordetella pertussis pertactin outer membrane protein, p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 910;
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Pred. No. 7.7e-21;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                   Location/Qualiflers
254..309
/note= "Pertactin region I"
568..609
                                              AAE16184 standard; Protein; 910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N, Boursaux-eude C;
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92.9%;
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                                                                                                                              (first entry)
                                                                                                                                                                                                                                                              Bordetella pertussis.
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Best Local Similarity
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                                                                                                                              26-MAR-2002
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                                                                                       AAE16184;
                                                                                                                                                                                                                                                                                                       Key
Region
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          RESULT 4
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useful as

Location/Qualifiers 597..604 /note= "Conserved region"

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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Pril). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polio and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is B. pertussis pril protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. bronchiseptica strain prn2 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
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                                                                                                                                                                                                                                                                                                                                                                                                        1 QRATIRREDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                   Length 910;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                 91.2%; Score 281; DB 23;
92.9%; Pred. No. 7.7e-21;
11ve 1; Mismatches 3;
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Best Local Similarity 92.9
Matches 52; Conservative
                                                                                                                                                                                                                                                                    910 AA;
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AAE16190
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Indels

Conservative

52;

Matches

AAE17146 standard; Protein; 910 AA.

AAE17146;

AAE17146 ID AAE1 XX AC AAE1

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                                                                                                                                                                                                                                                                                                                                                                                                                           Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The persent sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. bronchiseptica strain prn4 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic.compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
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Pred. No. 1.1e-21;
1; Mismatches 2; Indels 5;
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                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1b; 47pp; English.
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86.9%;
                                                              23-MAY-2001; 2001WO-EP06457.
                                                                                                       25-MAY-2000; 2000US-206969P
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                                                                                                                                                  (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                       WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200190143-A2.
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                 29-NOV-2001
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Best Local S
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquent to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
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                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ.56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pertactin outer membrane protein region I
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   Boursaux-eude C;
                                                                                                                                                                                                                                                                                          Disclosure; Fig 1b; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE17153 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001; 2001WO-NL00493
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                                                                    WPI; 2002-097639/13.
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Guiso-maclouf N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PeM3 monoclonal antibody specific for region 1 of pertactin.
                                                                                                                                                                                                                                                                                                     Length 45;
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                                                                                                                                                                                                                                                                                                                                                                           3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDV
                                                                                                                                                                                                                                                                                                  Score 234; DB 23;
Pred. No. 3.1e-17;
0; Mismatches 3;
                                                                                                                                                                                                      sequence is a monoclonal antibody specifiused for epitope mapping and vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Flg 2a; 52pp; English.
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/note= "Epitope"
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Local Similarity 93.3%;
hes 42; Conservative
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                                                                                                                                                                                                                                                                45 AA;
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Example
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caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region 1 of pertactin used for epitope mapping and vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PeM4 monoclonal antibody specific for region 1 of pertactin.
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                                                                                                                                                               Length 45;
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Pred. No. 3.1e-17;
0; Mismatches 3;
                                                                                                                                                         Score 234; DB 23;
Pred. No. 3.1e-17;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE17155 standard; Protein; 45 AA.
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/note= "Epitope"
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                                                                                                                                                            76.0%;
93.3%;
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                                                                                                                                                                                                           Conservative
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Best Local Similarity 93.3
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-139897/18.
                                                                                                                                                                                  Local Similarity
les 42; Conserv
                                                                                                        45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AA;
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                                                                                                        Sequence
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polio and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present used for epitope mapping and vaccination.
                                                                            Pertactin; prnl; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides derived from Bordetella pertussis pertactin, useful a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                              PeM70 monoclonal antibody specific for region 1 of pertactin
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2a; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                     (NEWE-) NEDERLANDEN MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000EP-0202309.
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                 (first entry)
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les 42; Conserv
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                 18-APR-2002
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                                                                                                                                                                      Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polic and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region I of pertactin used for epitope mapping and vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                                                                                                                                                                                            Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
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                                                                                                                                                                                                 PeM68 monoclonal antibody specific for region 1 of pertactin.
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Pred. No. 3.1e-17;
0; Mismatches 3; Indels
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 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDV 47
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                                                                                                       AAE17156 standard; Protein; 45
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93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2001; 2001WO-NL00493
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                                                                                                                                                                   18-APR-2002 (first entry)
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Best Local Similarity 93.33
Matches 42; Conservative
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                              PeM71 monoclonal antibody specific for region 1 of pertactin.
Score 234; DB 23; Length 45;
Pred. No. 3.1e-17;
0; Mismatches 3; Indels
                                                                                                              3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDV 47
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                                                                                                                                                                                                                                          AAE17158 standard; Protein; 45
76.0%;
llarity 93.3%;
Conservative (
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. barapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, pollo and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections seaused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region 1 of pertactin used for epitope mapping and vaccination.
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                                                                                                                                                                                   New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 234; DB 23; Length 45;
Pred. No. 3.1e-17;
0; Mismatches 3; Indels
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                                                             (NEWE-) NEDERLANDEN MIN WELZIJN
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93.3%;
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Matches 42; Conservative
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                                                                                                     MOO1 FR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polico and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region I of pertactin used for epitope mapping and vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
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Pred. No. 3.1e-17;
0; Mismatches 3;
             Location/Qualiflers
31..35
/note= "Epitope"
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/note= "Epitope"
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93.3%;
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Best Local 8
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.

Sequence

Gaps 5; Query Match

Query Match

74.2%; Score 228.5; DB 23; Length 51;
Best Local Similarity 80.4%; Pred. No. 1.3e-16;
Matches 45; Conservative 2; Mismatches 4; Indels 5

1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 ò qq

Search completed: May 7, 2003, 16:47:03 Job time: 30.0971 secs

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1 QRATIRRGDAPAGGGVPGGA.....PVLDGWYGVDVSGSTVELAQ
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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US-09-010-928B-2
US-09-010-928B-2
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US-09-010-928B-2
US-09-047-806-9
US-09-247-806-9
US-09-247-806-10
US-09-247-806-2
US-09-010-928B-7
US-09-010-928B-7
US-09-010-928B-7
US-08-256-978B-18
US-08-256-978B-18
US-08-56-978B-18
US-08-56-978B-7
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                     US-09-855-754B-9
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Match
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228.5
212
120.5
116
116
91.5
90.5
90.5
90.5
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86.5
86.5
77
77
77
77
74
                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                       Run on:
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                    Sedineuce Sedine
                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON STATE: VA COUNTRY: USA ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                  US-08-458-298-52
US-08-556-978B-46
US-08-963-168C-9
US-08-963-11-4
US-08-257-073-7
US-08-257-073-7
US-08-541-139-114
US-08-542-051-33
US-08-542-051-32
US-08-542-051-33
US-08-542-051-18
US-08-542-051-18
US-08-542-051-18
US-08-397-633A-78
US-08-397-633A-78
US-08-397-633A-78
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Best Local Similarity 91.1%; Pred. No. 5.6e-22;
Matches 51; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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Gaps
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APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TIRRGDAP------AGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 907;
                                                                                                                                                                                                                                                                                                                                                                                          Score 212; DB 4; Length 911;
Pred. No. 1.6e-15;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 120.5; DB 2
Pred. No. 1.7e-05;
1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: BIRCH, STEWART, KOLASCH & BIRCH 8110 GATEHOUSE RD. SUITE 500E
                                                         NAME: LEBOVIEZ, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/460,269C
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09010928B
Patent No. 5994099
GENERAL INFORMATION:
                                                                                                                                                                                                                                              LENGTH: 911 amino acids
                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murphy Jr., Gerald M REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.1%;
Best Local Similarity 48.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 68.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 amino acids amino acids
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.8
Best Local Similarity 75.0
Matches 42; Conservative
                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-09-010-928B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8110 GATEHOU
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STAT
ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Patent No. 6197548

GENERAL INFORMATION:

APPLICANT: CLARE, JEFFREY J.

TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                  ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 922;
                                                                                                                                                                                                                                                Zelano & Branigan, P.C. vd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branis
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 228.5; DB 4;
Pred. No. 2.5e-17;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: Millen, White, Ze
STREET: 2200 Clarendon Blvd.
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                           Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION: APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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Best Local Similarity 80.4%;
Matches 45; Conservative
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                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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         RESULT 2
US-08-460-269C-6
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TRANSFORMED CELL
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TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CEL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.7%; Score 91.5; DB 1; Length 595; 41.5%; Pred. No. 0.016; 1ive 3; Mismatches 25; Indels
                                                                                                                                                                                                                                                       Score 116; DB 2; Length 870;
                                                                                                                                                                                                                                                                                                                                                                     702 GGAGGSGVGPGGSGPGGSGPGGSGPGCSGPGGSGS 747
                                                                                                                                                                                                                                                                                                                                         8 GDAPAGGGV-PGGAVPGGFDPGGFGPGGFGP--VLDGWYGVDVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/425,069
FILLING DATE: U9-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CIIY: Falls Church
                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MULPHY JI., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/POCKET NUMBER: 1447-106P
FELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08425069
Patent No. 5728810
NAME: MULPBY JT., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 144.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERICSICS:
LENGTH: 870 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis, Randolph V.
Xu, Ming
Hinman, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                     37.7%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22045
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.5'
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                    protein
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                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                        Local Similarity
hes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lewis,
                                                                                                                                                                               MOLECULE TYPE:
US-09-010-928B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-425-069-4
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                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                          Best Local
Matches
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                                          Patent No. 5994099
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 GGAGGSGGVGPGGSGPGGYGPGGYGPGGSGPGGYGPGGSGS 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GDAPAGGGV-PGGAVPGGFDPGGFGPGGFGP--VLDGWYGVDVSGS 50
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                         SEE: BIRCH, STEWART, KOLASCH & BIRCH: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: BIRCH, STEWART, KOLASCH & BIRCH: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 116;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/010,928B FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
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                       Sequence 28, Application US/09010928B
Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09010928B
Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                        VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2;
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  22042
  JS-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                             COUNTRY:
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STATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: GARSON, Jean-Pierre
APPLICANT: GARSON, Jean-Pierre
APPLICANT: GARGON, Jean-Pierre
TITLE OF INVENTION: COMBETT ON DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILLING DATE: 1999-02-11
EBALLER APPLICATION NUMBER: FR 98/01614
EBALLER FILLING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GSAAAAAAGPGQQGPGGYGPGGYGP---GQQGPSGPGSAAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPAX: 302-773-0164
                                                                                                             APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-556-978B-61
; Sequence 61, Application US/08556978B
; Patent No. 6268169
                                                                                                                                                                                                08/077,600
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Patent No. 6280747
                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,60
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXMETHY
REGISTRATION NUMBER: 33,692
COMPATIBLE OPERATING SYSTEM: MICROSOFF SOFTWARE: MICROSOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.4%;
Best Local Similarity 43.8%;
Matches 21; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.4%;
Best Local Similarity 43.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     : 119 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Nephila clavipes US-09-247-806-9
                                                                                       CURRENT. APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-556-978B-60
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US-09-247-806-9
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: COTALINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF INVENTION: COTALINING THE ISOLATED DNA, AND PRODUCTS THEREOF
CORRESPONDENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/ACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60, Application US/08556978B
Patent No. 6268169
GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.016;
25;
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MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                           Sequence 4, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MUTPhy Jr., Gerald M
REGISTRATION UNMER: 28,977
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 241-1300
(703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.7%;
Best Local Similarity 41.5%;
Matches 22; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Virginia
: U.S.A.
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US-08-556-978B-60
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Score 90.5; DB 4; Length 714; Pred. No. 0.025; Mismatches 22; Indels
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                                                                                                                              8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Voulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Hoon, Thlerry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Van Baren, Nicolas
APPLICANT: Coulle, Pierre G.
APPLICANT: De Smet, Charles
Lucas, Sophie
APPLICANT: Boon, Thiery
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 90; DB 2;
Pred. No. 0.016;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: | Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                            Sequence 8, Application US/08845998
Patent No. 5879692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09206537
Patent No. 6130052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Van Amsterdam, John F
REGISTRATION NUMBER: 40,211
REFERENCE/JOCKET NUMBER: LÉ
FELECOMMUNICÀTION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%;
                       29.4%;
illarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 420 amino acids
amino acid
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                Query Match
Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                      RESULT 13
US-08-845-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-206-537-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PHILLIPPE, Michel
APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Claude
TITLE ON: INVENTION: COSMETIC ON BERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: LANALOG
FILE REPERENCE: 6388-0365-0
CURRENT PAPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:protein US-09-247-806-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                   E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                          E: DISKETTE, 3.50 INCH
IBM PC COMPATIBLE
SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD FOR WINDOWS 95
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR-9389-A
                                                                                                                                                        STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-
TELECOMMUNICATION INFORMATION:
TELECHHUNE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-247-806-10
Sequence 10, Application US/09247806
; Patent No. 6280747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                      NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS: ADDRESSEE: E. I. DU STREET: 1007 MARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-556-978B-61
                                                                                                                                                                                                                     COMPUTER READABLE FORM MEDIUM TYPE: DISKET
                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
APPLICANT: FAHNESTC
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                       WILMINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                    19898
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 GGGPGGGGPGGGGGGGGGGGGGG 179
                                                                        NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION: 1FFORMATION:
TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 7, 2003, 16:56:58
Job time: 10.3447 secs
        APPLICATION NUMBER: 08/845,998
                                                                                                                                                                           TELEFAX: (617720-2441
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.2
Best Local Similarity 60.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-430-854-8
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                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
                                            E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPHONE: (617)720-341
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 GGGGGGGGGGGGGGGGGGGGGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGP 37
                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 420 amino acids
amino acid
GY: linear
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                   Boston
                                                                                                                             RY: US
02210
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                    FILING DATE
                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                       STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-206-537-8
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RESULT 15

1. Sequence 8, Application US/09430854

1. APPLICANT: Outlie, Pierre G. APPLICANT: De Smet, Charles APPLICANT: De Smet, Charles APPLICANT: Deon, Thierry Trille OF INVENTION: LEUKEMIA ASSOCIATED GENES OUNTESPONDENCE ADDRESS: 16

1. CORRESPONDENCE ADDRESS: 16

1. STREET: 600 Atlantic Avenue CITY: Boston All Carential Evenue COUNTRY: US

2. ZIATE: MA

COUNTRY: US

2. ZIATE: MA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,854

CLASSIFICATION: PRIOR APPLICATION DATA:

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Sequence 9, Appl. Sequence 194, App. Sequence 60, Appl. Sequence 119, App. Sequence 14, Appl. Sequence 14, Appl. Sequence 15, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 37, Appl. Sequence 34, Appl. Sequence 34, Appl. Sequence 34, Appl. Sequence 34, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 17, Appl. Sequence 16, Appl. Sequence 21, Appl.
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOUGSAUX-EUDE, CAROLINE
APPLICANT: BOUGSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: BOLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VET. 2.1
SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 56;
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0 US-09-841-321A-9

US-0708-770-194

US-09-837-966A-60

US-09-841-321A-60

US-09-841-321A-60

US-10-235-674-14

US-10-263-689-14

US-09-919-172-41

US-09-919-172-41

US-09-964-761-35807

US-09-964-761-35807

US-09-888-260-25

US-09-817-969A-37

US-09-841-321A-37

US-09-934-323-2

US-09-934-323-2

US-09-934-323-3

US-09-934-323-3

US-09-944-321-3

US-09-944-321-3

US-09-987-969A-34

US-09-987-969A-34

US-09-987-969A-34

US-09-987-969A-34

US-09-987-969A-34

US-09-987-969A-34

US-09-987-969A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-759-010-4
US-09-837-969A-21
US-09-841-321A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-855-754-12
Sequence 12, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
  US-09-855-754-9
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Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 6012, Ap
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                                                                                                                                                                          (without alignments)
306.927 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                   1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ
                                                                                                                                                     ; Search time 16.7905 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / cgn2_6/ptodata/2/puppaa/USOB_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/NCG_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO9_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/puppaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 US-09-855-754-9
9 US-09-855-754-10
9 US-09-855-754-11
9 US-09-855-754-11
9 US-09-855-754-13
1 US-09-855-754-7
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1 US-09-855-754-6
0S-09-855-754-6
0S-09-855-754-6
0S-09-855-754-6
0S-09-855-754-6
0S-09-855-754-6
0S-09-861-597-10
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                     7, 2003, 16:53:34
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Maximum DB seq length: 200000000
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Match Length
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of

Total number

Database

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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Gaps

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79.5 78

87.5

278.5 274.5 224.5 228.5 228.5 212 212 90.5 88

Score

Result

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CURRENT APPLICATION NUMBER: US/09/855,754
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US-09-855-754-13
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US-09-855-754-5
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND ENCHESEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYPETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPETICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
GURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-06-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTION VOICE: 21
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                                     BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 291; DB 9;
Pred. No. 2.6e-22;
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORL
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AN
TITLE OF INVENTION: BROKHISEPPICA, THEIR USE IN
TITLE OF INVENTION: BROKHISEPPICA, THEIR USE IN
TITLE OF INVENTION: LAMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARRE: PATENTIN Ver. 2.1
SEQ ID NO 12
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT CORGANISM: Bordetella bronchiseptica US-09-855-754-10
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US-09-855-754-12
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92.9%;
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l Similarity 94.6%;
53; Conservative
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Best Local Similarity
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US-09-855-754-11
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US-09-855-754-10
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LENGIH: 56
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Best Local
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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91.1%; Pred. No. 1.7e-19;
iive 1; Mismatches 4;
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Pred. No. 4.8e-21;
1; Mismatches 2;
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PRIOR APPLICATION NUMBER: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 61
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                                                                                                                                                                                                             ); TYPE: PRT
() ORGANISM: Bordetella bronchiseptica
US-09-855-754-11
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella pertussis
US-09-855-754-5
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86.9%;
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Best Local Similarity 91.1
Matches 51; Conservative
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Best Local Similarity 86.9
Matches 53; Conservative
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us-09-855-754b-9.rapb

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SEQ ID NO 4
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          SEQ ID NO 6
LENGTH: 922
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                                                         TYPE: PRT
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Best Local
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFEELA PERTUGSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISREPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Publication to. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLIONE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TILLE OF INVENTION: 1000000
CURRENT APPLICANTON NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                  Length 51;
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Pred. No. 9.5e-19;
1; Mismatches 1
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION UNDER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 13
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 51
                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                             ch 82.6%;
1 Similarity 87.5%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Matches 49; Conserv
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Matches
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APPLICANT: BOUGREAUX BUDE, CAROLINE
APPLICANT: BOUGREAUX BUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRETACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PETTE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PETTE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT PELLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 8
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APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIES OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: INMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 020206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                     Length 922;
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                                                                                                 DB 9;
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ilarity 75.0%; Pred. No. 1.4e-14;
Conservative 2; Mismatches 2
                                                                                              Score 228.5; DB 9
Pred. No. 5.3e-15;
                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Bordetella bronchiseptica
US-09-855-754-8
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US-09-855-754-4
ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                                                                 74.2%;
80.4%;
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                                                                                                                                                             45; Conservative
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                                                                                                                    Best Local Similarity
Matches 45; Conserv
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Length 714;

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450
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US-09-861-597-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
Query Match
                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
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PEPLICANT: ARRADDEAU, Jean-Pierre

TITLE OF INVENTION: CENETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN TITLE OF INVENTION: ANALOG PILE REPERRENCE: 6388-0355-0

CURRENT APPLICATION NUMBER: US/09/861,597

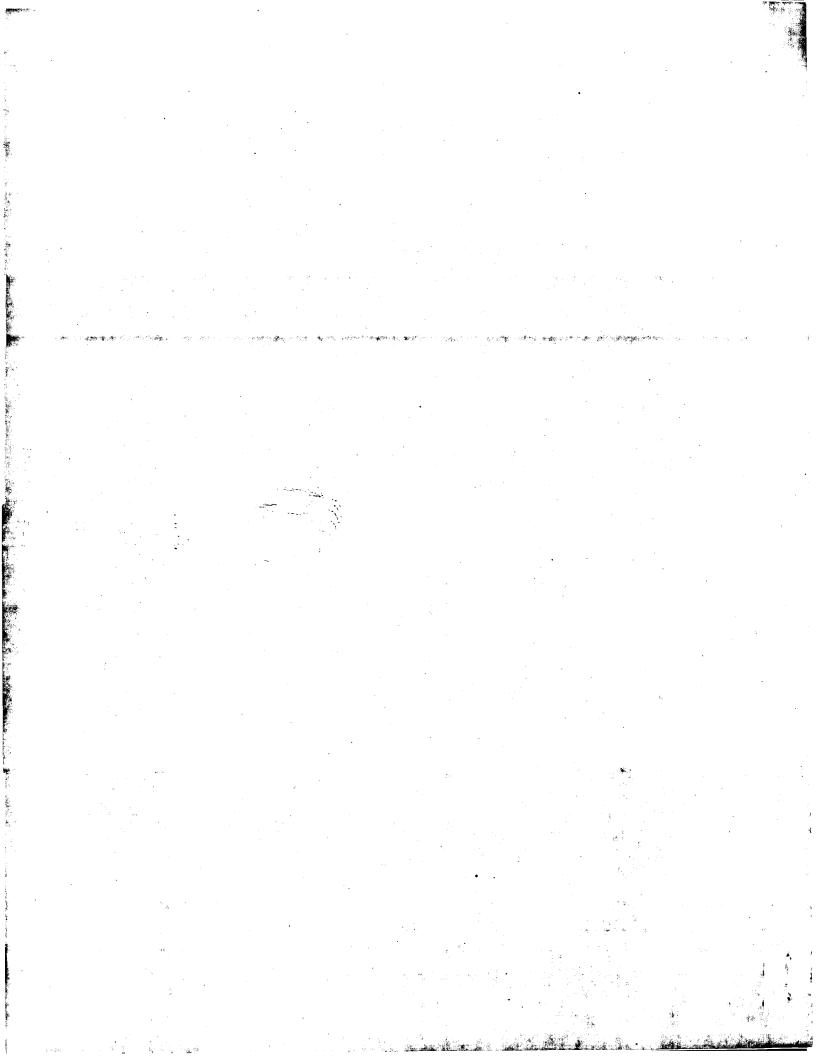
CURRENT FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                         APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: GRASON, Jean-Claude
APPLICANT: ARRADDRAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ARABLOG
FILE REPERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                               1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:protein 35-09-861-597-10
                Length 911;
                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GQQGPSGPGSAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.033;
                Score 212; DB 9;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GSAAAAAAGPGQGPGGYGPGQQGPGGYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09861597
Patent No. US20020064539A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 9, Application US/09861597
Patent No. US20020064539A1
GENERAL INFORMATION:
                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                68.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 29.4%;
1 Similarity 43.8%;
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-02-1
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Nephila clavipes
US-09-861-597-9
                                                       42; Conservative
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Best Local Similarity
                Query Match
Best Local Similarity
Matches 42; Conserv
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US-09-861-597-10
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LENGTH: 714
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US-09-861-597-9
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APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
                                                Gaps
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chilkoti, Ashutosh
TITLE OF INVENTION:
FILE REFERENCE: 4176-101
FILE REFERENCE: 4176-101
CURRENT APPLICATION NUMBER: US/09/812,382
CURRENT FILING DATE: 2001-03-20
PRIOR PAPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                             3;
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                                                                                                                                  601 GSAAAAAGPGQGFGGYGPGQQGPGGYGP---GQQGPSGPGSAAAAA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
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                                                                                         8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 APAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
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Score 90.5; DB 10;
Pred. No. 0.18;
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Pred. No. 0.2;
1; Mismatches 20
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Pred. No. 0.26
3; Mismatches
                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/247,806
; PRIOR FLILING DATE: 1999-02-11
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
                                                                                                                                                                                                                                            Sequence 6, Application US/09812382
Patent No. US20010034050A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09861597 Patent No. US20020064539A1
29.4%;
ilarity 43.8%;
Conservative 2
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Best Local Similarity 43.5%;
Matches 20; Conservative
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APPLICANT: PHILLIPPE, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Nephila clavipes US-09-861-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
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US-09-812-382-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 24; Conserv
                         Similarity
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RESULT 15
RESULT 15
SEQUENCE 1381. Application US/09925300
SEQUENCE 1381. Application US/09925300
SEQUENCE 1381. Application US/09925300
SEQUENCE 1381. Application US/09925300
SEQUENCE INVENTION:
APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
APPLICANT: CALCATION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIOL 08-10
CURRENT APPLICATION NUMBER: DC7001-08-10
FRIOR APPLICATION NUMBER: PC7000/05988
PRIOR APPLICATION NUMBER: PC7000/05988
PROOR PILING DATE: 1909-03-10
PROOR PILING DATE: 1909-03-10
SOTTWARE: PARCET: 1999-03-12
SOTTWARE: PARCET: 1999-03-12
SOTTWARE: PARCET: 1999-03-12
SOTTWARE: PARCET: 1999-03-12
SOTTWARE: STITE
OCCATION: (507)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: STITE
LOCATION: (507)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: STITE
LOCATION: (502)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: STITE
LOCATION: (502)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COURTY MATCH: STITE
LOCATION: (502)
OTHER LOCATION: (502)
OTHER LOCATION: (502)
OTHER LOCATION: (502)
SOTHWARE CRAIS: STITE
LOCATION: (502)
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OTHER LOCATION: (502)
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OTHER LOCATION: (503)
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OTHER LOCATION: (504)
SOTHWARE CRAIS: STITE
LOCATION: (504)
OTHER LOCATION: (504
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q

Search completed: May 7, 2003, 17:30:49 Job time: 18.7905 secs



GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

7, 2003, 16:41:02; Search time 10.494 Seconds (without alignments) 513.008 Million cell updates/sec Run on:

US-09-855-754B-9 308

1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ Title: Perfect score: Sequence:

26

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	outer membrane pro	pertactin - Bordet	68K outer membrane	probable serine-th	glycine-rich cell	spidroin 2, dragli	elastin precursor	hypothetical prote	octamer binding tr	ATP-dependent RNA	probable cell wall	hypothetical prote	heat shock protein	dnaK-type molecula	hypothetical prote			fibrillin-2 precur	hypothetical prote	dnaK-type molecula	RNA helicase RH11	ATP-dependent RNA	elastin precursor	probable immediate	dnaK-type molecula	elastin precursor	leukophysin - huma	MFS18 protein - ma	dnaK-type molecula
ID	A32560	S15204	A47675	T35389	T09262	A44112	EAMS	B86181	159234	T45677	T40618	T15126	PC7036	S41372	H84217	A31994	KRHUO	A54105	T24865	A49242	T51742	T45671	EART	T03166	S51712	A26601	G01226	\$25103	A54507
DB	~	~	~	~	~	7	Н	~	7	~	~	7	7	7	~	~	Н	~	~	~	7	~	-	~	~	~	7	~	~
Length	910	922	911	783	16	627	860	200	420	646	273	259	641	645	133	561	593	2918	422	686	224	603	864	1300	929	784	235	128	198
Query Match	88.0							29.5	29.5	29.1	27.6	27.3	26.8	26.8	26.6	26.6	26.6	26.6	26.5	26.3	26.1	26.1	26.1	26.1	26.0	26.0	25.8	25.5	25.3
Score	271	228.5	212	106	95.5	91.5	91	90	90	89.5	82	84	82.5	82.5	82	82	83	æ	81.5	81	80.5	80.5	80.5	80.5	80	80	79.5	• 1	78
Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	59
	Query Score Match Length DB ID	Ouery Score Match Length DB ID 271 88.0 910 2 A32560	Score Match Length DB ID Description 271 88.0 910 2 A32560 outer member 228.5 74.2 922 2 515204	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T09262	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 627 2 A44112	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 212 68.8 911 2 A47675 106 34.4 781 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 106 34.4 78 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS 90 29.2 420 2 15924	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T9262 91.5 29.7 667 2 A44112 91 29.5 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 200 2 B86181 99.5 99.1 646 2 T45677	Score Match Length DB ID 228.5 74.2 92.2 \$15204 212 68.8 911 2 A47675 106 34.4 765 2 T35389 95.5 31.0 76 2 T35389 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS 90 29.2 200 2 B86181 99.5 29.1 642 2 T55234 89.5 29.1 6 273 2 T45677	Ouery Score Match Length DB ID 228.5 74.2 92.2 515204 212 68.8 911 2 A47675 106 34.4 763 2 135389 95.5 31.0 76 27 2 A44112 91 59.5 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 420 2 159234 89.5 29.1 646 2 145677 84 27.3 259 2 115126	Ouery 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T92862 95.5 31.0 76 2 T92862 91.5 29.7 867 2 A44112 91 29.5 860 2 B86181 90 29.2 200 2 B86181 90 29.2 420 2 159234 89.5 27.6 273 2 T45618 84 27.3 274 6518 82.5 26.8 641 2 PC7036	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 420 2 T45677 89.5 29.1 646 2 T45677 84 27.3 2 T40618 82.5 26.8 645 2 S41372	Ouery Score Match Length DB ID 228.5 74.2 910 2 A32560 212 68.8 911 2 A47675 106 34.4 765 2 T95262 91.5 29.7 627 2 A44112 91 29.5 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 420 2 159234 89.5 29.1 646 2 T45677 85 27.6 27.3 27668 82.5 26.8 641 2 PC7036 82.5 26.6 133 2 H84217	Ouery 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T92862 91.5 29.7 6 2 T92862 91.5 29.7 860 1 B86181 90 29.2 200 2 B86181 90 29.2 200 2 B86181 90 29.2 200 2 B86181 89.5 29.1 646 2 T45677 85 27.6 273 2 T46618 84 27.3 25.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.6 561 2 A31991	Ouery Score Match Length DB ID 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 627 2 A44112 90 29.2 200 2 B86181 90 29.2 200 2 B86181 90 29.2 420 2 T45677 89.5 29.1 646 2 T45677 89.5 20.1 646 2 T45677 84 27.3 2 T40618 84 27.3 2 S9 2 T15126 82.5 26.8 641 2 PC7036 82.5 26.8 645 2 S41372 82.26.6 593 1 KRHUO	Ouery Score Match Length DB ID 228.5 74.2 912 2 815204 212 68.8 911 2 A47675 106 814 76 2 175504 91.5 29.7 627 2 A44112 91 29.5 31.0 76 2 179262 91.5 29.7 627 2 A44112 90 29.2 200 2 186181 99 29.2 200 2 186181 89 5 27.6 27 426 2 175234 89 5 27.6 27 2 44618 84 27.3 259 1 15126 82 56.8 641 2 PC7036 82 26.6 133 2 H84217 82 26.6 551 2 A31994 82 26.6 2918 2 A54100	Ouery 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T9262 91.5 29.7 867 2 A44112 90 29.2 200 2 B86181 89.5 29.1 646 2 T45677 85 27.6 273 2 T40618 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 A31972 82.6 531 2 A84217 82 26.6 561 2 A31994 82 26.6 561 2 A54105 81.5 26.5 2918 2 A54105	Ouery 271 88.0 910 2 A32560 228.5 74.2 92.2 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 T35389 95.5 31.0 76 2 T09262 91.5 29.7 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 200 2 B86181 89.5 29.1 646 2 T45677 85 27.6 273 2 T40618 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.6 593 1 KRHUO 82 26.6 593 1 KRHUO 81.5 26.5 26.8 2 A54105 81.5 26.5 26.8 2 A54105 81.5 26.5 26.5 2 A492465	Ouery Score Match Length DB ID 228.5 74.2 92.2 \$15204 212 68.8 911 2 A47675 106 34.4 765 2 15204 95.5 31.0 76 2 79368 91.5 29.7 627 2 A44112 90 29.2 200 159282 90 29.2 420 2 159234 99.5 29.1 646 2 745677 84 27.3 259 2 745677 82 26.8 645 2 740618 82.5 26.8 641 2 PC7036 82 26.6 591 1 KRHUO 82 26.6 591 2 A54105 81.5 26.6 2918 2 A54105 81.5 26.5 24 2 2 724865 81.5 26.1 224 2 751742	Ouery 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 783 2 S15204 95.5 31.0 76 2 T09262 91.5 29.7 860 1 EAMS 90 29.2 200 2 B86181 90 29.2 200 2 B86181 90 29.2 420 2 159234 89.5 29.1 646 2 T45677 85 27.6 273 2 T4618 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 A31974 82 26.6 561 2 A31974 82 26.6 561 2 A31974 83 26.6 561 2 A31974 84 26.5 2918 2 A54105 81 26.5 2918 2 A54105 81 26.3 686 2 A49242 80.5 26.1 603 2 T54142	Ouery 271 88.0 910 2 A32560 228.5 74.2 92.2 2 S15204 212 68.8 911 2 A47675 106 34.4 78.3 2 T35389 95.5 31.0 76 2 T35389 90 29.2 200 2 B86181 90 29.2 200 2 B86181 90 29.2 200 2 B86181 89.5 29.1 646 2 T45677 85 27.6 273 2 T40618 82.5 26.8 641 2 PC7036 82.5 26.8 641 2 PC7036 82.5 26.6 591 1 KRHUO 82 26.6 591 2 A31994 82 26.6 591 2 A31994 82 26.6 591 2 T4865 81.5 26.6 2422 2 T24865 81.5 26.7 242 2 T5142 80.5 26.1 244 2 T5142	Ouery Score Match Length DB ID 271 88.0 910 2 815204 212 68.8 911 2 A47675 106 31.4 76 2 15204 95.5 31.0 76 2 175389 95.5 31.0 76 2 175389 90 29.2 200 2 B86181 90 29.2 420 2 159234 89.5 29.1 627 2 A44112 89.5 29.1 627 2 175267 88.2 26.8 645 2 17527 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175126 82.5 26.8 645 2 175136 82.5 26.8 645 2 175136 82.5 26.8 645 2 175136 82.5 26.8 251 2 A54105 82.5 26.8 251 2 A54105 82.5 26.8 251 2 A54105 82.5 26.1 224 2 175142 80.5 26.1 1300 2 145671 80.5 26.1 1300 2 103166	Ouery 271 88.0 910 2 A32560 228.5 74.2 922 2 S15204 212 68.8 911 2 A47675 106 34.4 763 2 S15204 95.5 31.0 76 2 T09262 91.5 29.7 6 2 T09262 90 29.2 2 00 2 B86181 91 29.5 860 1 FAMS 85 27.6 273 2 T40618 85 27.6 273 2 T40618 86 27.6 273 2 T40618 87 26.8 641 2 FC7036 82 26.6 561 2 A31972 88 26.6 561 2 A31974 89 26.6 561 2 A54105 81 26.5 2018 2 A54105 81 26.3 686 2 A4242 80.5 26.1 603 2 T24865 80.5 26.1 804 1 EART 80.5 26.1 804 2 T51742 80.5 26.1 804 2 E31766 80.5 26.1 864 2 E31766	Ouery 271 88.0 910 2.83560 228.5 74.2 92.2 215204 212 68.8 911 2 A47675 106 34.4 78.3 2 735289 95.5 31.0 76 2 735289 90 29.2 200 2 886181 90 29.2 200 2 886181 90 29.2 200 2 886181 89.5 29.1 646 2 745677 85 27.6 273 2 740618 82.5 26.8 641 2 2 87372 82.5 26.8 641 2 87372 82.5 26.6 593 1 KRHUU 82.5 26.6 593 2 724865 81.5 26.5 274865 81.5 26.5 274865 80.5 26.1 224 2 75174 80.5 26.1 1300 2 703166 80.5 26.1 300 2 703166 80.5 26.0 556 2 551712	Ouery Score Match Length DB ID 271 88.0 910 2 815204 228.5 74.2 922 2 815204 31.6 68.8 911 2 A47675 106 81.6 91.2 2 735389 95.5 31.0 76 2 735389 90.5 31.0 76 2 735389 90.29.2 200.0 186181 90.29.2 200.0 186181 90.29.2 200.0 186181 80.5 20.1 64.0 2 745677 82 20.6 27.6 2 745677 82 20.8 64.1 2 745677 82 20.6 64.1 2 745178 82 20.6 133 2 484217 82 20.6 593 1 KRHUO 82 20.6 593 2 A49142 81.5 20.6 593 2 A49142 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 1300 2 703166 80.5 20.1 20.2 2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2	Ouery 271 88.0 910 2 A32560 28.5 74.2 922 2 S15204 28.5 74.2 922 2 S15204 28.6 34.7 783 2 T35389 95.5 31.0 76 2 T35389 91.5 29.7 627 2 A44112 91.5 29.7 627 2 A44112 90. 29.2 2 20.2 B86181 90. 29.2 2 20.2 B86181 90. 29.2 2 T09262 91.5 29.1 646 2 T45677 91.5 29.1 646 2 T45677 92.2 2 T40618 92.2 2 T40618 92.2 2 T40618 92.2 2 T40618 93.3 2 T40618 94.2 2 T40618 95.5 20.1 100.0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

glycine-rich prote	protein R09B5.8 (1	hypothetical prote	lactose-binding le	transcription fact	hypothetical prote	. polyketide hydroxy	dnaK-type molecula	dnaK-type molecula	hypothetical prote	hypothetical prote	hypothetical glyci		myosin-IA - Acanth	hypothetical prote	glycine-rich prote
501821	G88949	T00799	A49688	A49642	T29299	T35608	S11456	JC4610	A97443	AC2661	A70812	T20801	T32734	T22078	T49890
-	N	~	7	7	N	~	7	7	7	7	7	~	~	~	7
252	82	201	294	420	589	627	650	651	699	699	749	1126	1215	112	185
25.3	25.2	25.2	24.8	24.8	24.8	24.8	24.8	24.8	24.8	24.8	24.8	- 24.8	24.8	24.7	24.7
78	77.5	77.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	92	9/
30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A32560 A10 A10	A, Accession: A32560 A. Molecule type: DNA A. Mote: 11 is unjectain whether Met-1 or Met-3 is the initiator C. Keywords: membrane protein C. Keywords: membrane protein F; 1-34/Domain: signal sequence #status predicted <sig> F; 35-910/Product: outer membrane protein P6.9 #status predicted <mat> Query Match B8.0%; Score 271; DB 2; Length 910; Best Local Similarity 91.1%; Pred: No. 1.16-18; Matches 51; Conservative 1; Mismatches 4; Indels 0: Gaps</mat></sig>	Qy 1 QRATIREGDAPAGGGVPGGAVPGGFDPGGFGPVLDGWYGVDVSGSTVELAQ 56
# # 00000# # # # # # # # # # # # # # #		<i>ਨ</i> ਬ

Partactin Bordetella parapertussis
N:Alternate names: outer membrane protein P70
C;Species: Bordetella parapertussis
C;Date: 07.Apr.1994 #sequence_revision 07-Apr.1994 #text_change 08-Oct.1999
C;Accession: S15204; S14659
R;Li, Lu. J. Dougah, G; Novotny, P.; Charles, I.G.
Mol. Microbiol. 5; 409-417, 1991
A;Reference number: S15204; MuID:91251771; PMID:2041476
A;Accession: S15204
A;Molecule type: DNA
A;Molecule type: DNA
A;Accession: S15204
A;Molecule type: DNA
A;Accession: S15204
A;Molecule type: DNA
A;Accession: S15204
C;Genetics: CG:Genetics: EMBL:X54547; NID:939761; PIDN:CAA38419.1; PID:939762

A;Gene: prn C;Keywords: membrane protein

Gaps 2, Query Match 74.2%; Score 228.5; DB 2; Length 922; Best Local Similarity 80.4%; Pred. No. 1.4e-14; Matches 45; Conservative 2; Mismatches 4; Indels 5;

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QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56

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Gaps

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A44112
Spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
Spidroin 2, dragline silk fibroin, dragline
Nalternen enames: silk fibroin, dragline
Nalternen enames: silk fibroin, dragline
C; Species: Nephila clavipes
C; Species: Nephila clavipes
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Mar-1998
C; Accession: A44112; S27824
S; Hinman, M.B.; Lewis, R.V.
J; Biol. Chem. 257, 19320-19324, 1992
A; Title: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavip
A; Reference number: A44112; MUD: 92406876; PMID: 1527052
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-627 cHINA
A; Residue cextracted from NCBI backbone (NCBIP: 113893)
A; Rilmann M.B; Lewis; R.V.
Submitted to the EMBL Data Library, May 1992
A; Rescription: Isolation of a clone encoding a second dragline silk fibroin: Nephila
A; Rescription: 527824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine F;127/Domain: signal sequence #status predicted <MAT>
F;28-860/Product: elastin #status predicted <MAT>
F;88-0-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the tropoelastin gene to
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N'Alternate names: tropedastin
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA
                                                                                                                                               Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
                                                                                                                                                                                                                                Indels
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A;Title: Use of an intron length polymorphism to localize A;Reference number: A55721; MUID:95130069; PMID:7829060
A;Cross-references: EMBL:L47748; NID:91350525; PID:91350526
C;Genetics:
A;Gene: EMB31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91.5; DB 2;
Pred. No. 0.15;
3; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 91; DB 1;
Pred. No. 0.23;
                                                                                                                                                       ;
                                                                                                                                                   Score 95.5; DB 2 Pred. No. 0.0084;
                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                      8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFG 36
                                                                                                                                                                                                                                                                                                                                                 9 GPGPGGPGGPGGWGPG---PGGFGPGGFG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.7%;
Best Local Similarity 41.5%;
Matches 22; Conservative
                                                                                                                                                           31:0%;
nilarity 65.5%;
Conservative (
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A, Molecule type: MRNA
A, Residues: 19'627 <HLZ>
A, CLOSS-references: EMBL:M92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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A; Residues: 1-860 <WYD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: elastin
                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A5572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 5
                                                                                                                                                                                                                                                19;
                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                  obx outer membrane protein P.68 pertactin - Bordetella bronchiseptica (Species: Bordetella bronchiseptica C.5pecies: Bordetella bronchiseptica C.5pecies: Bordetella bronchiseptica C.5pecession: A47675 #sequence_revision 18-Nov-1994 #text_change 08-oct-1999 C;Accession: A47675 Novotny, P.; Dougan, G.; Charles, I.G. J. Gen. Microbiol. 138, 1697-1705, 1992 A;Tille: Cloning, nucleotide sequence and heterologous expression of the protective outed A;Reference number: A47675; MUID:92407514; PMID:1527510 A;Aconcents: CN7531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A; Reference number: 221576
A; Residues: 1-783 < WURS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AL079348; PIDN: CAB45488.1; GSPDB: GN00070; SCOEDB: SC6673.32c A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Status: preliminary
A; Molecule type: nucleic acid
A; Molecule type: nucleic type: nucle
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c;Species: Picea glauca (white spruce)
c;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable serine-threonine protein kinase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 212; DB 2; Length 911;
Pred. No. 5.3e-13;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
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R; Dong, J.Z.; Dunstan, D.I.
submitted to the EMBL Data Library, June 1996
A; Description: Gene expression during somatic embryogenesis.
A; Reference number: Z16588
A; Reference number: Li6588
A; Accession: T09262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PAGGG----VPGGAVPGGFDPGGFGPGFGPVLDGWYGVDVSGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.4%; Score 106; DB 2;
ilarity 54.5%; Pred. No. 0.0076;
Conservative 1; Mismatches 15
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A;Molecule type: mRNA
A;Residues: 1-76 <DON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 68.8%;
1 Similarity 75.0%;
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A47675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
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T09262
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Matches
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C;Accession: T45677 T. Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, Submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23011
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A; Residues: 1.273 <LIXD>
A; CTOSS - references: EMBL:AL034563; PIDN:CAA22526.1; GSPDB:GN00067; SPDB:SPBC660.06
A; Experimental source: strain 972h-; cosmid c660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cell wall protein - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
                                                                                                                    N;Alternate names: protein F14P22.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04_Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T20B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T15126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-dependent RNA helicase-like protein - Arabidopsis thaliana N;Alternate names; protein F14P22.160
                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia; BAC clone F14P22 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Accession: T40618
R. Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, December 1998
A. Reference number: Z21941
A. Accession: T40618
A. Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5; DB
Pred. No. 0.25;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 GGFGGG--PGGFEGGPGGFGGGFGGGLGGFGG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.29
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3
A;Introns: 239/3; 267/3; 348/3; 404/3; 442/3
Note: F14P22.160
C;Superfamily: ATP-dependent RNA helicase DBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYYGPGGYGTVPNQGYGPGVASA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- FGPGGFGPVLDGWYGVDVSGS 50
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homology
                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-646 <DAN>
A; Cross-references: EMBL: AL137082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.1%;
31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.33
Matches 26; Conservative
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C;Superfamily: WW repeat
F;8-48/Domain: WW repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SPDB: SPBC660.06
                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                     A; Accession: T45677
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Matches
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                                                                                                                                                                                                 hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B86181
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosoma l of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: neliminary; translated from GB/EMBL/DDBJ
A;Stoss-references: GB:L20433; NID:g418015; PIDN:AAA65605.1; PID:g418016
B;Stoperfamily: unassigned homeobox proteins; homeobox homology; POU domain homology
C;Steywords: DNA binding; homeobox; nucleus; transcription regulation
F;268-338/Domain: POU domain homology <POU>
F;358-318/Domain: homeobox homology <HOX>
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A;Residues: 1-200 <STO>
A;Cross-references: GB:AE005172; NID:g7211985; PIDN:AAF40456.1; GSPDB:GN00141
C;Genetics:
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       Gaps
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                                            2 RATIRRGDAPAGGGVPG----GAVPGGFD----PGGFGPFGPVLDGWYGVDVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 90; DB 2; Length 420;
Pred. No. 0.15;
0; Mismatches 12; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: glycine-rich cell wall structural protein 1
  20;
  Mismatches
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llarity 36.1%;
Conservative
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llarity 60.0%;
Conservative
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  Conservative
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A; Status: preliminary
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Best Local Simi
Matches 18;
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23;
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Best Local Si
Matches 22;
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4

Gaps -----GG 29

33;

Indels

15; DB 2;

Length 646;

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Gaps

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Length 273;

DB 2;

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Cipecies: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: Ha4217
C;NG, WO.Y; Rennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                           //A; Molecule type: protein
A; Residues: 4-10;137-143;158-164;221-227;329-335;362-368;388-394;425-431;573-579;609-
                                             A;Cross-references: EMBL:229379; NID:g443914; PIDN:CAA82570.1; PID:g443915
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                               C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein C;Superfamily: heat shock protein 70
C;Keywords: ATP; cytosol; heat shock; molecular chaperone; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE004437; NID:q10580192; PIDN:AAG19108.1; GSPDB:GN00138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Vng0597h [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82.5; DB 2;
Pred. No. 1.2;
1; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 2;
Pred. No. 0.29;
3; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7, 2003, 16:55:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 26.8%;
Best Local Similarity 48.9%;
Matches 22; Conservative
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42.68;
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Best Local Similarity 42.6
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: H84217
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-133 <STO>
           A; Residues: 1-645 <TIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: May
Job time: 11.494 secs
                                                                                                                     A; Accession: S71636
                                                                                                                                                                                                                                                                 A; Gene: HSA1; HSP72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: VNG0597H
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                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946988; PIDN:AAB52890.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone T2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: State of the control of control of
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C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
C;Accession: Pc7036
R;Cernila, B; Cresnar, B.; Breskvar, K.
Biochem. Biophys. Res. Commun. 265; 494-498, 1999
A;Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
A;Reference number: JC7132; MUID:20025372; PMID:10558896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Pichla angusta
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Apr-2000
C; Accession: S41372; S71640; S71636
R; Diesel, A.A.; Roggenkamp, R.R.
submitted to the EMBL Data Library, January 1994
A; Description: HSP70 genes of the yeast Hansenula polymorpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GDAPAGGGVPGGAVPGGFDPGGFGP----GGFGPVLDGWYGVDVSG 49
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R;Beck, C.; Wamsley, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T20B6.
A;Reference number: Z18297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat shock protein 70 - Rhizopus nigricans (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                           A;Accession: T15126
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:T20B6.3
A;Map position: 3
A;Introns: 9/2; 231/1
C;Superfamily: Phaseolus glycine-rich protein 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 82.5; D
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AF188289
C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 GGMPGGGGMPGGGAPGGF-PGG 629
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68.2%;
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Best Local Similarity 68.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 44.7
Matches 21; Conservative
                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-259 <BEC>
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A; Residues: 1-641 <CER>
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A; Status: preliminary
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3;

OM protein - protein search, using sw model

May 7, 2003, 16:31:49 ; Search time 5.43782 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-9 308 1 QRATIRRGDAPAGGGVPGGA.....PVLDGWYGVDVSGSTVELAQ 56 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:	Description	P14283 bordetella	_		P46804 nephila cla	_	Q01851 homo sapien	P17208 mus musculu	P53421 pichia angu		P35556 homo sapien		_		Q99372 rattus norv	P41797 candida alb	P07916 gallus gall						Q01877 puccinia gr	P38486 cants famil	P42534 streptomyce		P09789 petunia hyb	P21522 schistocerc	Q01546 homo sapien	P04985 bos taurus	P27483 arabidopsis	P08699 rattus norv	bos t	P35908 homo sapien
	GI .	PERT_BORPE	PERT_BORPA	PERT_BORBR	SPD2_NEPCL	ELS_MOUSE	BR3A_HUMAN	BR3A_MOUSE	HS71_PICAN	K1CJ_HUMAN	FBN2_HUMAN	DDX9_MOUSE	HS70_PLACB	HS70_BLAEM	ELS_RAT	HS71_CANAL	ELS_CHICK	DDX9_HUMAN	K2C1_HUMAN	MF18_MAIZE	HS70_SCHJA	GRP1_PHAVU	HS71_PUCGR	LEG3_CANFA	HYDL_STRCO	HS7C_BOVIN	GRP1_PETHY	ROA1_SCHAM	K220_HUMAN			LEG3_RAT	K1CJ_BOVIN	K22E_HUMAN
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ery.	Match	7.	4.2	œ.		.5		7.8	8.	9.	9.	٠. ت	m		7.	0.	0.	8.	. و		<u>س</u>	<u>س</u>	5.3	4.8	4.8	œ.		'n.	5.	₹.	?	0.	0.	6.
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į	score	281	228.5	212	91.5	91	90	85.5	82.5	82	82	81.5	81	80.5	80.5	80	œ	79.5	79	78.5	78	78	78	76.5	76.5	76.5	_	75.5	75.5	75	74.5	74	74	73.5
Result	Q	1	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	59	30	31	32	33

P37705 daucus caro P12035 homo sapten 092125 xenopus lae P87047 paracoccidi 061555 mus musculu P47953 cricetulus P19013 homo sapten 092804 homo sapten 09473 brachydanio P10599 accartamoceb P10591 saccharomyc 053553 mycobacteri
GRP3_DAUCA K2C2_HUMAN K2C2_HUMAN HS70_PARBR FBN2_MOUSE LEG3_CRILO K2C4_HUMAN RB5C_HUMAN RB5C_HUMAN RSC_ACACA HS71_KBSTT
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195 629 512 649 2907 244 534 534 592 649 1168
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72.5 72.5 72.5 71.5 71.5 71.5 71.5 70.5
488 33 33 33 34 4 4 4 4 4 4 4 4 4 4 4 4

RESULT 1 PERT_BORNE TO 1-724 1-1994 (Rel. 13, Created) TO 1-724 1-1994 (Rel. 13, Last sequence update) BY BOTOGETH DEFENCE (Outer membrane protein p. 69) (P.93). TO 1-724 1-1994 (Rel. 13, Last sequence update) BY BOTOGETH DEFENCE (Outer membrane protein p. 69) (P.93). TO 20 BOTOGETH DEFENCE (Outer membrane protein p. 69) (P.93). TO 20 BOTOGETH DEFENCE (OUTER PROPER OF PROTEINS OF
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EMBL; X54815; CAA38584.1; -.
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Q03035;
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Li L.J., Dougan G., Novotny P., Charles I.G.;
Pp. Operaction, an outer-membrane protein from Bordetella
parapertussis: cloning, nucleotide sequence and surface expression in
Bscherichia coli.;
Mol. Microbiol. 5:409-417(1991).
IMOL. MICROBIOL. 5:409-417(1991).
MOL. MICROBIOL. SEQUENCE PERRACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLUTAR LOCATION: Outer membrane.
-i- DISBASE: MAY CONTRIBUTE TO THE DISBASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 QRATIRRGDAPAGGAVPGGAVPGGRVPGGFGPGFGPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                                                                                                                         X 5 AA TANDEM REPEATS OF G-G-A-V-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
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X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 281; DB 1; Length ye. Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                                                                                                                                                                 PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                     Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                IPR003991; pertactin_vir
     InterPro; IPR003992; pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93452 MW;
                                                                                 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
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                             InterPro; IPR003991; pertacti
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 92.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 52; Conserv
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P24328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERT_BORPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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-i- FUNCITON: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBGINIT: MONOMER.
-i- SUBCELGIARA LOCATION: Outer membrane.
-i- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 QRATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 228.5; DB 1
Pred. No. 8.6e-14;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                PERTACTIN (P.70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                                                       Outer membrane; Signal; Virulence; Repeat.
SIGNAL 1 34 POTENTIAL.
PIR; S15204; S15204.
PIR; S14659; S14659.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.
Pfan; PF03212; Pertactin.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92407514; PubMed-1527510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.4 nes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290
270
275
280
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603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575
922 AA;
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chromosome 7
                                                                                                                                                                                                                                                                                                                                      ELS_MOUSE
P54320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                       SEQUENCE
                                                                                                                   REPEAT
REPEAT
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                 RESULT 5
ELS_MOUSE
                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Included in the control of a clone encoding a second dragline silk fibroin.

Nephila clavipes dragline silk is a two-protein fiber.",

J. BAOL Chem. 267:19324 (1992).

-I- FUNCTION: Spiders major ampullate silk possesses unique characteristics of strength and elasticity. Fibroin consists of pseudocristaline regions of antiparallel beta-sheet interspersed with elastic amorphous segments.

-I- SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 1, OF THE DRAGLINE SILK.

-I- SUBURIT: MAJOR SUBUNIT, WITH SPIDROIN 1, OF THE DRAGLINE SILK.

-I- SUBCELLULAR LOCATION: Extracellular.

-I- DOWAIN: Highly repetitive protein characterized by regions of polyalanine and glycine-rich repeating units.

-I- SIMILARITY: BELONGS TO THE SILK FIBROIN FAMILY.
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                    CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Chellcerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
                                                                                                                                                                                                                                                                              Score 212; DB 1; Length 911;
Pred. No. 2.7e-12;
2; Mismatches 2; Indels 10;
                                                                                                                                                                                                                                3 (APPROXIMATE).
7 x 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spidroin 2 (Dragline silk fibroin 2) (Fragment).
Nephila clavipes (Orb spider).
                                                                                                                            PERTACTIN (P.68).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                       627 AA.
                                                                                            Signal; Virulence; Repeat.
EMBL; A19180; CAA01453.1; -.
PIR; A47675; A47675.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                           LINES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92406876; Pubmed=1527052;
Hinman M.B., Lewis R.V.;
                                                       PEGN; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                        93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M92913; AAA29381.1; -. Silk; Repeat.
                                                                                                                                                                                                                                                                              ch 68.8%;
1 Similarity 75.0%;
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                               911
712
911
262
                                                                                                                                                                                    701
266
266
271
276
570
911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCBI_TaxID-6915;
                                                                                             Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                     SPD2_NEPCL
P46804;
                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                           CHAIN
PROPEP
SITE
                                                                                                       SIGNAL
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 23:125-131(1994).
-I- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH WUST EXPAND RAPIDLY AND RECOVER COMPLETELY.
-I- SUBBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
-I- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-I- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C: TISSUE-Lung;
MEDINE-95130069; PubMed-7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoclastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 627;
APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                      CB9B63779B2C594B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCOBESAAELEDD7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein; Repeat; Signal; Connective tissue.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; DB 1;
0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-1996 (Rel. 34, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.15
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELASTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95317; Eln.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                      35.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      54184 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U08210; AAA80155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41...
-hos 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                         516
627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                860 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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EMBL; L20433; AAA65605.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Croce C.M., Israel M.A., Theil T., Morcy T., Depinho R.A., Alt F.W.;

T a novel DOU homeodomain gene specifically expressed in cells of the developing mammalian nervous system.";

INUCLEIC Acids Res. 20:4919-4925(1992).

THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A SUBSET OF NEURONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING CHECKONAL STAGES.

THE IDENTIFIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

THE DEVELOPMENTAL STAGES.

THE DEVELOPMENTAL STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95348789; PubMed-7623109; Xiang M., Zhou L.-J., Macke J.P., Yoshioka T., Hendry S.H., Eddy R.L., Shows T.B., Nathans J., Shows T.B., Nathans J. T.B., The Brn-3 family of POJ-domain factors: primary structure, binding specificity, and expression in subsets of retinal ganglion cells and
                                                        Gaps
                                                                                                                                MEDLINE-94052142; PubMed-8234287;
Bhargava A.K., Li Z., Weissman S.M.;
"Differential expression of four members of the POU family of proteins in activated and phorbol 12-myristate 13-acetate-treated Jurkat T cells.";
                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                    BR3A_HUMAN STANDARD; PRT; 423 AA.
601851; 015318; 014986;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Dast annotation update)
16-JUN-2002 (Rel. 41, Dast annotation update)
17-JUN-2002 (Rel. 41, Dast annotation update)
18-JUN-2002 (Rel. 41, Dast annotation update)
                                                     .;
8
                                                                                                     2 RATIRRGDAPAGGGVPG----GAVPGGFD----PGGFGPGGFGPVLDGWYGVDVSGS
DB 1; Length 860;
                                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 90:10260-10264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                     6; Mismatches
  Score 91;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somatosensory neurons.";
J. Neurosci. 15:4762-4785(1995).
  29.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 85-423 FROM N.A.
                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASS-4 SUBFAMILY
  Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue-Retina;
                                                                                                                                                                                                                                         RESULT 6
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MEDLINE-94215319; PubMed-8162704;
Theil T., Zechner U., Klett C., Adolph S., Moeroey T.;
"Chromosomal localization and sequences of the murine Brn-3 family of developmental control genes.";
Cytogenet. Cell Genet. 66:267-271(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00027; HOMEGBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
PROSITE; PS50071; HOMEGBOX_2; 1.
TRANSCRIE; PS50071; HOMEGBOX_2; 1.
TRANSCRIPT; PS50071; HOMEGBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (BRN-3.0).
POU4F1 OR BRN3A OR BRN3 OR BRN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3AE4732E1309F34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TS -> H (IN REF. 3).
A -> R (IN REF. 1).
GAG -> ARR (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 3).
GP -> AA (IN REF. 3).
GP -> PR (IN REF. 3).
GP -> AA (IN REF. 3).
GP -> AA (IN REF. 3).
G -> A (IN REF. 3).
A -> S (IN REF. 3).
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AER -> GS (IN REF.
AQR -> PS (IN REF.
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ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POU-IV BOX.
POLY-HIS.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 GGGPGGGGPGGGGGGGGGGGGGG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALA-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMEOBOX
                                                                                                                                                                                                               PRINTS; PRO0028; POUDOMAIN.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000018; POU_domain; 1.
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU domain.
Pfam; PF00166; homeobox; 1.
Pfam; PF00157; pou; 1.
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EMBL; X64624; CAA45907.1;
                                        TRANSFAC; T01876; -.
TRANSFAC; T04463; -.
Genew; HGNC:9218; POU4F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.2
Best Local Similarity 60.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                      P10037;
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                                                                                                         MIM; 601632;
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P17208;
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Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID-4905;
       15-JUL-1999 (Rel. 38, Last annotation update)
Heat-shock protein 70 1 (HSP72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 229379; CAA82570.1; -. HSSP; P19120; 3HSC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR001023; Hsp70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K1CJ_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: BRAIN, PERIPHERAL SENSORY NERVOUS SYSTEM AND
RETINA. IN THE ADULT NERVOUS SYSTEM BRN-3. O PREDOMINATES IN THE
MEDIAL HABENULA, SUPERFICIAL GRAY OF THE SUPERIOR COLLICULGS, RED
NUCLEUS, MESENCEPHALIC NUCLEUS OF THE TRIGEMINAL GANGLION, NUCLEUS
AMBIGUUS, INFERIOR OLIVARY NUCLEUS, AND PERIPHERAL SENSORY
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00035; POU_1; 1.
PROSITE; PS00461; POU_2; 1.
PROSITE; PS50071; HOMEODOX, 2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Pred. No. 0.38;
0; Mismatches 10;
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(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
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ALA-RICH.
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HSSP; P10037; 1A07.
HGD; MGI:102525; Poud.f1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
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roDom; PD000583; POU_domain; 1.
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[2]
SEQUENCE OF 286-401 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S69350; AAB30577.2; -. EMBL; X51959; CAA36218.1; -.
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Pfam; PF00157; pou; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00389; HOX; 1
SMART; SM00352; POU: 1
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100
130
205
265
357
421 AA;
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HS71_PICAN
ID HS71_PICAN
AC P53421;
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01-0CT-1996
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44 KB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Saccharomycetes;
                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
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                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                              STRAIN-ATCC |34438;
MEDLINE-96437974; PubMed-8840502;
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MEDLINE-94117870; PubMed-7507152;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compton J.G., Bale S.J.; Preferential sites in keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                               Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides the C-terminal V2 subdomain due to variable numbers and sizes of glycine loops.";
                          MEDLINE-88122104; PubMed=2448602; Darmon M.T., Semat A., Darmon M.T., Vasseur M.; Selected according "Sequence of a cDMA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothmagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.; "Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                                 Microsequences of 145 proteins recorded in the two-dimensional gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Gludice G., Pearson R., Fuchs Syder A.J., Yu Q.-C., and the XIO genes of patients with "Genetic mutations in the XI and XIO genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                             MEDLINE-97386600; PubMed-1381287; Cheng J., Syder A.J., Yu Q.-C., Letai A., Paller A.S., Fuchs E. "The genetic basis of epidermolytic hyperkeratosis: a disorder of differentiation-specific epidermal keratin genes."; cell 70:811-819(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126
                                                                                                                                                                 10
                                                                                                                                                                                                                                                         Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E. Vandekerckhove J.;
                                                                                                                                                                "Exons I and VII of the gene (Rer10) encoding human keratin
undergo structural rearrangements within repeats.";
Gene 116:245-251(1992).
                                                                                                                                         Ikachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                                                                              protein database of normal human epidermal keratinocytes."
Electrophoresis 13:960-969(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am. J. Hum. Genet. 54:179-190(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   flisease severity.";
J. Clin. Invest. 93:1533-1542(1994).
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MEDLINE-94117868; PubMed-7507150;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92141228; PubMed-1371013;
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                                                                                                                                                                                                                                              MEDLINE-93162043; PubMed-1286667;
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                                                                                                                 SEQUENCE OF 197-593 FROM N.A. MEDLINE-92339897; Pubmed-1378806;
                                                                                        Mol. Biol. Rep. 12:277-283(1987)
                                                                                                                                                                                                                    SEQUENCE OF 180-184 AND 577-589.
              OF 130-593 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 257:1128-1130(1992).
                                                                                                                                                                                                                                  TISSUE-Keratinocytes;
                                                                                                                                                                                                                                                                                                                                      VARIANT EHK HIS-156.
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                                                                                                                                                        Kisselev L.L.;
                                                                                expression."
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     [2]
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C -1- POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN
THE GLY-RICH REGION (POSITIONS 490-50).
TCHTHYOSIFORM BRYTHHOODENA, (BCIE)); A HERBUITARY SKIN DISORDER
CHARACTERIZED BY BLISTERING AND AMARKED THIOKENING OF THE STRATUM
CORNEGM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH
CONTINISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL
DOMINNAT, BUT MOST CASES ARE SPORADIC.
COMMINISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL
CONTININISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL
CONTININISH AND HYPERKERATOSES CHANCAL CONTINICAL AND HISTOLOGIC FEATURES OF
CONTININISH AND AND ADDIVIDUAL SUBJECTIVICAL AND HISTOLOGIC FEATURES OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I
McMillan J.R.,
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-! SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

-!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN POSITIONS 513 TO 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOTH EPIDERMOLYTIC HYPERKERATOSIS AND ICHTHYOSIS BULLOSA OF
                                                                                                                  "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and clinical mosaicism in a type of epidermal nevus."; New Engl. J. Med. 331:1408-1415(1994).
McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan ,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suga Y., Duncan K.O., Heald P.W., Roop D.R.;
Ah novel helix termination mutation in Keratin 10 in annul
epidermolytic ichthyosis, a variant of bullous congenital
ichthyosiform erythroderma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Invest. Dermatol. 111:1220-1223(1998).
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MEDLINE-99072665; Pubmed-9856845;
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MEDLINE=95059228; PubMed=7526210;
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Aarhus/Ghent-2DPAGE; 7405; IEF
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Nature 352:330-334(1991).
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                                                                                                                                            VARIANTS CCA HIS-1114.
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Lee B., Godfrey M., Vitale E., Horl H., Mattel M.-G., Sarfarazl M., Tsipouras P., Ranirez F., Hollister D.;
"Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saplens (Human).
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure and expression of fibrillin-2, a novel microfibrillar component preferentially located in elastic matrices."; Cell Biol. 124:855-863(1994).
                           InterPro: IPR001664; IF.
InterPro: IPR002957; Keratin_I.
Promons: filament; 1.
PRINTS; PR001248; TYPEHERATIN.
PROSTE; PS00226; IF; 1.
Intermediate filament; Colled coll; Keratin; Disease mutation;
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MEDLINE-94165150; Pubmed-8120105;
Zhang H., Apfelroth S.D., Hu W., Davis B.C., Sanguineti C.,
Bonadio J., Mecham R.P., Ramirez F.;
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R -> H (IN EHK).

/FTId-vAR_003827.

R -> C (IN EHK).
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/FIId=VAR_010506.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrillin 2 precursor.
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5; Mismatches
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l Similarity 44.7%;
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MIM; 148080;
MIM; 113800;
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P35556;
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Kisiclow P., Miazek A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: UNWINDS DOUBLE-STRANDED DNA AND RNA IN A 3' TO 5'
DIRECTION. GENERATES MULTIPLE SECONDARY STRUCTURES THAT INFLUENCE
RNA-BINDING PROTEINS. MAY PLAY A ROLE IN X-LINKED GENE EXPRESSION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDX9.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDX9_MOUSE STANDARD, PRT; 1380 AA.
070133; 035931; 054703;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP-dependent RNA helicase A (Nuclear DNA helicase II) (NDH II)
(DEAD-box protein 9) (MHEL-5).
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35.5%; Pred
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STRAIN-129/Sv;
MEDLINE-98149984; Pubmed-9480750;
      [2]
SEQUENCE OF 386-919 FROM N.A.
STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     helicase A.";
Genomics 47:365-371(1998).
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hes 22;
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DISGULFID
DISGUL
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DDX9_MOUSE
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948720;
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HS70_BLAEM
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                       SIMILARITY: CONTAINS 2 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Cytoplasmic antigen) (74.6 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eckert V., Sanchez L., Cochrane A.H., Enea V.;
*Plasmodium cynomoligi: the hsp 70 gene.";
Exp. Parasitol. 75:33-328 (1992).
-1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN THE ASEXUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00699; DEAM, ATP.
PROSITE; PS00699; DEAM, ATP.
HellCase; NA-binding; DNA-binding; Repeat; Nuclear protein;
DOMAIN 3 71 DRBM 1.
DOMAIN 182 254 DRBM 2.
NP_BIND 413 420 ATP (POTENTIAL).
SITE 513 516 DEAM BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81.5; DB 1; Length 1380;
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-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium cynomolgi (strain Berok).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AGGGVPGGAVPGGFDPGGFGPGGFG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                -> A (IN REF. 1; AAC05301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
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-> V (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                          InterPro: IPR001410; DEAD.
InterPro: IPR001464; DEAH Dox.
InterPro: IPR001155; DS. RBD.
InterPro: IPR0011650; Helicase_C.
                                                                                                                                                                                                                                         Pfam: PF00035; dsrm; 2.
Pfam: PF00035; dsrm; 2.
SMART; SM00487; DEXDC; 1.
SMART; SM00358; DSRM; 2.
SMART; SM00490; HELICC; 1.
                                                                                                                                              EMBL; U91922; AAC05725.1; -.
                                                                                                                                                        EMBL; AF023530; AAC05301.1;
EMBL; U92080; AAB72087.1; -.
MGD; MGI:108177; Ddx9.
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Q05746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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HS70_PLACB
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               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           EMBL outstation
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MEDLINE-95129910; PubMed-7828923;
Stefani R.M.; Gomes S.L.;
"A unique intron-containing hsp70 gene induced by heat shock and during sporulation in the aquatic fungus Blastocladiella emersonil.";
Gene 152:19-26(1995).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukarýota; Fungi; Chytridiomycota; Blastocladiales; Blastocladiaceae;
Blastócladiella.
NCBL_TaxID-4308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA TANDEM REPEATS OF
   the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FF31F448FFCBF286 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Heat shock 70 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                649 AA.
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS0136; HSP70_3; 1.
ATP-binding; Heat shock; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74602 MW;
                                                                                                                                                                                                                                                      EMBL; M90978; AAA29625.1; -. PIR; A49242.
HSSP; P08109; 1CKR.
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                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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HSSP; P19120; 3HSC.
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the European
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Best Local Simi
Matches 23;
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REPEAT
SEQUENCE
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HS71_CANAL P41797;
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SIGNAL
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Best Local
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HS71_CANAL
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-i- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-i- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-i- SUBDNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER

INTO AN EXTENSIBLE 3D NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING. MEDILINE-9241865; Pubmed-1572637; PlearCe R.A., Alatawi A., Deak S.B., Boyd C.D.; Flements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-3104068; Pubmed-1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 781-864 FROM N.A.
MEDLINE-88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilopase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                        Length 649;
                                                                                                                                                                                                                                  Indels
                                                                                                                                               70833 MW; 152D5CF67B924A8D CRC64;
                                                                                                                                                                                                                                                                                                   splicing.
-1- PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                             12 AGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVE 53
                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                        Score 80.5; Di
Pred. No. 1.6;
                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               864 AA
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             PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
                                                                                                                                                                                          26.1%;
42.9%;
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                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Pfam; PF00012; HSP70; 1.
                                                                                                                                               649 AA;
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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M86364; 7
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                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 ELS_RAT
Q99372;
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                                                                                                                                                                                                                                       Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-243 FROM N.A.
MEDLINE-99256995; PubMed=7744244;
Eroles P., Sentandreu M., Elorza M.V., Sentandreu R.;
"Cloning of a DNA fragment encoding part of a 70-kDa heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein of Candida albicans.";
FEMS Microbiol. Lett. 128:95-100(1995).
-1- SUBCELLUTAR LOCATION: CYtoplasmic Cap similarity).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           Length 864;
                                                                                                                                                                                                                                                    MISSING (IN CERTAIN ISOFORMS)
MISSING (IN CERTAIN ISOFORMS)
MISSING (IN CERTAIN ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; ATP-binding; Multigene family; Acetylation.
HINT_MET 0 0 BY SIMILARITY.
EMBL; M86371; AAA42271.1; JOINED.
EMBL; M86376; AAA42272.1; -
EMBL; M86375; AAA42272.1; JOINED.
EMBL; M86375; AAA42272.1; JOINED.
EMBL; M86375; AAA42272.1; JOINED.
Structural protein; Connective tissue; Repeat; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                           456894BB09E79FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Heat shock protein SSAI.
                                                                                                                                                                                                                                                                                                                                                                       Score 80.5; F
                                                                                                                                                                                                      BY SIMILARITY ELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GDAPAGGGVPGGAVPGGFDPGGFGPGG 34
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                                                                                                                                                                                                                                                                                                                                             72786 MW;
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ProDom; PD000089; Hsp70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                 26.1%;
63.0%;
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Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSA1 OR HSP70.
Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 63.0
17; Conservative
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864
307
308
823
                                                                                                                                                                                                                                                                                                                                             864 AA;
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STRAIN=ATCC 20955;
Cassone A.C., la V.
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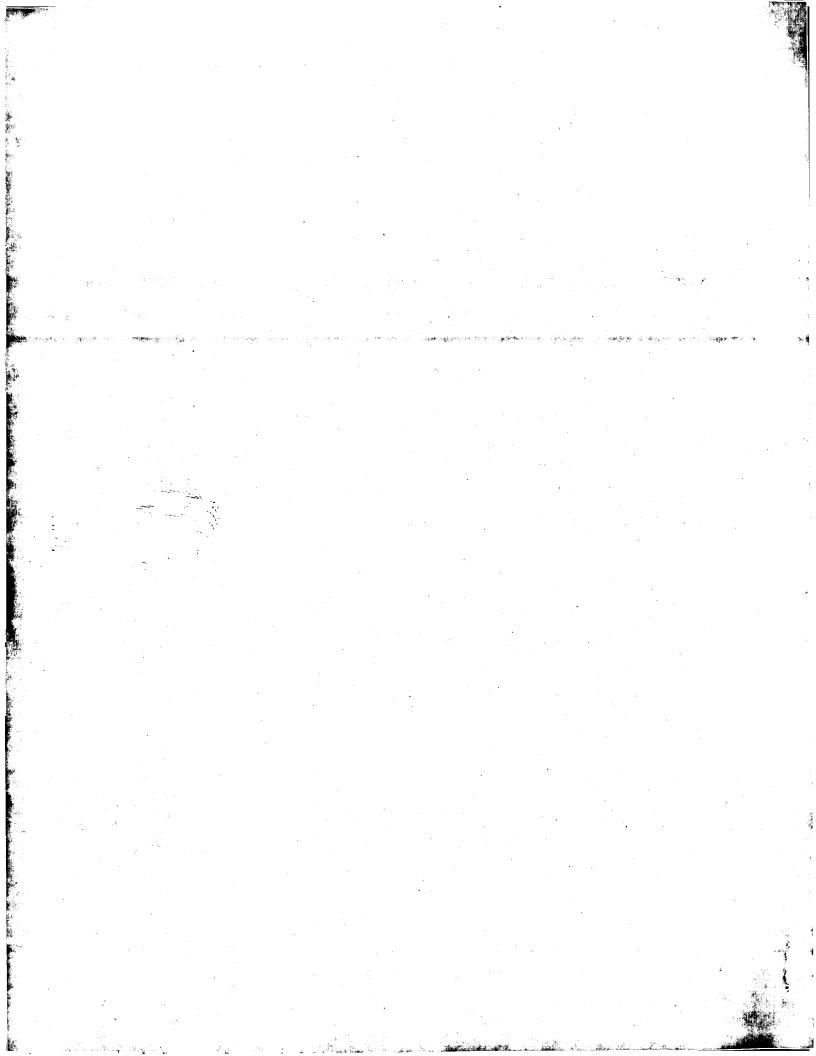
us-09-855-754b-9.rsp

Query Match 26.0%; Score 80; DB 1; Length 655; Best Local Similarity 50.0%; Pred. No. 1.8; Matches 24; Conservative 1; Mismatches 13; Indels ACETYLATION (BY SIMILARITY). A -> G (IN REF. 2). ; 634743E4D6DAD9D5 CRC64; 1 1 1 175 175 A 655 AA; 70192 MW; MOD_RES CONFLICT SEQUENCE FT ŏ

10; Gaps

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Search completed: May 7, 2003, 16:48:04 Job time : 7.43782 secs



Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number Minimum DB 8 Maximum DB 8

Database

Searched:

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995600 bordetella

995600 bordetella

995596 bordetella

99596 bordetella

99500 bordetella

99500 bordetella

99500 bordetella

99500 bordetella

99550 bordetella

99550 bordetella

99550 bordetella

99500 bordetella

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99100 bordetella

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canis famil
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Q9biu8 a
Q95ig9 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus). Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella. NCBL_TaxID-518;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (E.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 308; DB 2;
100.0%; Pred. No. 7.4e-24;
11ve 0; Mismatches 0;
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09K5G6
09K5G8
09K5I0
09KJY3
09KJY3
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09ALQ3
093ST1
09KJY2
09L4E2
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Q9NHW3
Q44359
Q9NHW2
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Q9BIU8
Q95LG9
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09nhw1
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160
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              2254.5
2284.5
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212
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SEQUENCE
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Q9K5G2
ID Q9K5G2
AC Q9K5G2;
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403.166 Million cell updates/sec
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1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ
                                                                                                 7, 2003, 16:38:52 ; Search time 28.6201 Seconds
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09alp4
069259
009alp6
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069257
0983m9
0986n1
088143
0931x8
0931x8
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09s3m8
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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O88143
Q9AIX8
Q93L98
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069259
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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
sp_bacteriap:*
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sp_invertebrate:*
sp_mammal:*
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sp_bacteria:*
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Gaps

308 308 301 291 290.5 290.5

Score

Result No.

287 281 281 278.5 276 276

274.5 268.5 260.5 255.5

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NCBI_TaxID=518;
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL, AJ250094; CAB76448.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Pred. No. 3.8e-23;
0; Mismatches 1; Indels
                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
Embl. AROO7276; AAG38452.1;
InterPro; IPRO03992; pertactin.
PRINTS; PRO1482; PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA; 15435 MW; 7FACB18F1FD0507E CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%; Score 308; DB 2; Local Similarity 100.0%; Pred. No. 7.5e-24; es 56; Conservative 0; Mismatches 0;
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01-AUG-1998 (TrEMBLrel. 07, Created)
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                                                                                                                                                                                                                                                                                                               MEDLINE-20359389; PubMed-10899896;
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98.2%;
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nes 55; Conservative
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159 AA;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                  Bordetella.
NCBI_TaxID=518;
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SEQUENCE
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Q9ALP4;
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Q9ALP4
ID Q9ALF
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069259
ID 06929
AC 06929
DT 01-A
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MEDLINE-21931812; PubMed-11500425;

PEY N.K., Neal S., Harrison T.G., Miller E., Matthews R., George R.C.;

"Genotypic Variation in the Bordetella pertussis Virulence Factors
"Genotypic variation in the Bordetella pertussis Virulence Factors
pertactin and Pertussis Toxin in Historical and Recent Clinical
Isolates in the United Kindom.";

Infect. Immun. 69:5520-5528(2001).

EMBL; AJ0061362; CAA06898.2;

EMBL; AJ001362; CAA06475.1;

EMBL; AJ001392; CAA07477.1;

EMBL; AF346485; AAY2093.1;

InterPro; IPR003992; pertactin.

InterPro; IPR004899; Pertact.—vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Polymorphism in the Bordetella pertussis virulence factors P.69/pertactin and pertussis toxin in The Netherlands: temporal trends and evidence for vaccine-driven evolution.";
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=287, AND ALIS61;
MEDLINE-99345256; PubMed-10418915;
BOUTSBUX-ENDE C., Thiberge S., Carletti G., Guiso N.;
"Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98114370; PubMed-9453625;
Mool F.R., Vanoirschot H., Heuvelman K., vanderHeide H., Gaastra W.
Willems R.R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 910;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-DIN precursor (Pertactin outer membrane protein).
PRN OR PRN3 OR PRN3.
Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERTACTIN.
9035EE1F07A52BC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Pertactin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.5%; Score 291; DB 2; Le Best Local Similarity 94.6%; Pred. No. 2.2e-21; Matches 53; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 66:670-675(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine 17:2651-2660(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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910
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910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                             Bordetella.
NCBI_TaxID-520;
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EMBL; AJ066122; CAA66894.1; --
EMBL; AJ132095; CAA10566.1; --
EMBL; AJ066169; CAA10566.1; --
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.
Interpro; IPR004899; Pertact_sup.
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CHAIN 35 907 PI
SEQUENCE 907 AA; 93298 MW;
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PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03212; Pertactin; 1
                                                                                                                                                                                                                                                                                                                                                                                          Vaccine 17:2651-2660(1999)
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                           Pertactin precursor.
PRN OR PRN6.
                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                NCBI_TaxID=520;
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                                                                                                    Bordetella.
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Best Local 3
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SIGNAL
CHAIN
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Q9S3M9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.3%; Score 290.5; DB 2; Length 195; Best Local Similarity 78.9%; Pred. No. 5.3e-22; Matches 56; Conservative 0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                               94.3%; Score 290.5; DB 2; Length 184; 78.9%; Pred. No. 5e-22; Live 0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMEL; AOVO7272; AAG38448.1; -. InterPro; IPR003992; Pertactin. PONUTER 195 PROIARCTIN.
NON_TER 195 195 195 SEQUENCE 195 AA; 18724 MW; 7409C189267C2D71 CRC64;
                                                    Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007274; AAG38450.1;
InterPro; IPR003992; pertactin.
PRINTS; PR01482; PERTACTIN.
                                                                                                                                                       195 195
195 AA: 18724 MW: 7409C189267C2D71 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                           STRAIN-ST. LOUIS;
MEDLINE-21117018; Pubmed-11179374;
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STRAIN-MBORD901;
MEDLINE-21117018; Pubmed-11179374;
                                                                                                                                                                                                                              1 Similarity 78.9 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertactin (Fragment).
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                                                                                                                                                                                                                Query Match
Best Local (
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069257
ID 06929
AC 06929
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STRAIN-CZ;
MEDLINE-99345256; PubMed-10418915;
MEDLINE-99345256; PubMed-10418915;
Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;
Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular vaccine.";
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"Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                    Bordetella pertussis.
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                    Boursaux-Eude C., Guiso N.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                           van Oirschot H.F.L.M., Mool F.R.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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PERTACTIN.
3A7D05F4094420EA CRC64;
07, Created)
07, Last sequence update)
21, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Vaccine 17:2651-2660(1999)
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Signal. SIGNAL

DR FT FT SO

Matches

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Mool F.R., VanOirschot H., Heuvelman K., Vanderheide H.G., Gaastra W., Willems R.J., "Polymorphism in the Bordetella pertussis virulence factors P.69/pertactin and pertussis toxin in The Netherlands: temporal trends and evidence for vaccine-driven evolution."; Infect. Immun. 66:670-675(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fry N.K., Neal S., Li Y.T., Hanauer S., Blank E., Harrison T.G.; "Sequence variation in the pertactin and pertussis toxin genes and amplified fragment length polymorphism analysis of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ORATIRRGDAPAGGGVPGGAV----PGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA
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Pertactin and Pertussis Toxin in Historical and Recent Clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                               Boursaux Eude C., Thiberge S., Carletti G., Guiso N.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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4AF56A29BAAFFED0 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.4%; Score 278.5; DB 2
86.9%; Pred. No. 4.1e-20;
tive 1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=98K320, AND DCH132;
MEDLINE=21391812; PubMed=11500425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolates in the United Kingdom.";
Infect. Immun. 69:5520-5528(2001).
                                                                                                           MEDLINE-98114370; PubMed-9453625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_v1
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
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EMBL; AF348484; AAK92092.1;
EMBL; AF348482; AAK92090.1;
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Best Local Similarity 86.9
Matches 53; Conservative
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915
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                       NCBI_TaxID=520;
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                                                                                                                                                                                                                                                                                                                 STRAIN-HAV;
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Q9AIX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98114370; PubMed-9453625;
Mooi F.R., Vanoirschot H., Heuvelman K., vanderHeide H., Gaastra W.,
Willems R.R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 QRATIRRGDAPAGGAVPGGAVPGGPCGFCPCGFCPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                                                     254 QRATIRRGDAPAGGAVPGGAVPGGRAVPGFGPGFGPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                             1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P.69B protein precursor (Pertactin outer membrane protein).
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.2%; Score 281; DB 2; Length 910; 92.9%; Pred. No. 2.3e-20; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                       Length 387;
                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Ofrschot H.F.L.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIBH; FF03412; PERTACTIN.
PRINTS; PRO1484; PRTACTINEAMLY.
PRINTS; PRO1484; PRTACTINEAMLY.
PRINTS; PRO1484; PRTACTOREAMLY.
                                            1 34 POTENTIAL.
35 >387 PERTACTIN.
387 AA; 38714 MW; 61195D45D347Aleb CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                       Score 281; DB 2;
Pred. No. 9.6e-21;
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InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
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EMBL; AJ006154; CAA06896.1; -.
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Pfam; PF03212; Pertactin; 1.
                                                                                                                                                     91.2%;
llarity 92.9%;
Conservative
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SEQUENCE
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Best Local
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Pfam;

Matches

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Gaps

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Indels

Length 915;

George R.C.;

Q9S6N1 Q9S6N1;

RESULT 9 **09**S6N1

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van Loo I.H., Mool F.R.;
"Changes in the Bordetella pertussis population in the first 20 years after the introduction of vaccination.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430832; CAD23609.1; ...
SEQUENCE 912 AA; 93680 MW; 7F417BA66B732EF7 CRC64;
                                                                                                                                                                                                                                                254 QRAITERGDAPAGGGVPGGAVPGGAVPGGAVPGGFGPGFGPGFGPULDGWYGVDVSGSSVELA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRATIREGDAPAGG-----VPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ORATIRREDAPA-----GGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Polymorphism of Borderella pertussis isolates circulating the last
ten years in France, a country using the same effective whole-cell
vaccine since more than thirty years.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ318056; CAC67458.1;
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                                                                                                                                                                           Score 274.5; DB 2; Length 912;
Pred. No. 1e-19;
1; Mismatches 2; Indels 5;
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     Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                           h 89.1%;
Similarity 86.9%;
53; Conservative 1
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NCBI_TaxID=520;
                                NCBI_TaxID-520;
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01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
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Best Local Simi
Matches 53;
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09ALQ1
ID 09ALQ1
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Pred. No. 7.4e-20;
1; Mismatches 2; Indels 10; Gaps
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                                                                                                                                                                                                         10;
                                                                                                                                                                             Length 851;
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Bordetella.
NCBL_TaxID=520;
                                                                                                                                                                                                       2; Indels
pertussis isolates from Missouri, USA.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR218(1901).;
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.
Interpro; IPR004899; pertactin.
Pfam. PF03212; pertactin. 1.
PRINTS; PR01482; PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heuvelman K., Peppler M.S., Lewandowski A., Mooi F.R.; "Bordetella pertussis prn gene for pertactin."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AJ318611; CAC42396.1; InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03212; Pertactin; 1. SEQUENCE 920 AA; 94317 MW; 62AA9461DCF53E54 CRC64;
                                                                                                                                                  86636 MW; B2D08B3519BDDBDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Last annotation update)
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Pred. No. 6.8e-20;
1; Mismatches 2;
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(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
                                                                                                                                                                             89.6%;
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al Similarity 80.3%;
53; Conservative
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                                                                                                                                                  851 AA;
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314 SVELAQ 319
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01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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Local S...
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PRN.
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SEQUENCE
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Best Local
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Q93L98
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Gaps

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GN PRN.

GN PROM.

GN Bordetella bronchiseptica (Alcaligenes bronchisepticus).

CC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

CC Bordetella.

CC Bordetella.

CC Bordetella.

CC Bordetella.

CO Bordetella.

CO Bordetella.

CO Bordetella.

CO Bordetella.

CO BORDETAXID-518;

RN (1]

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RN SEQUENCE FROM N.A.

RC STRAIN-MBORD591;

RN MEDLINE-21117018; PubMed-11179374;

RN Register K.B.;

RN Register R.B.;

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Search completed: May 7, 2003, 16:53:10 Job time: 29.6201 secs

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Sequence 23, Appli
Sequence 23, Appli
Sequence 76981, A
Sequence 76981, A
Sequence 21274, A
Sequence 3144, A
Sequence 3144, A
Sequence 11629,
Sequence 21, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2218, Appli
Sequence 49, Appli
Sequence 60, Appli
Sequence 2218, Appli
Sequence 2218, Appli
Sequence 2218, Appli
Sequence 2218, Appli
Sequence 22118, Appli
Sequence 22217, A
Sequence 22217, A
Sequence 22217, Appli
Sequence 36981, Appli
Sequence 36981, Appli
Sequence 22210, Appli
Sequence 36981, Appli
Sequence 36985, Appli
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GENERAL INFORMATION:
APPLICANT: BOUFSAUX-EUDE, CAROLINE
APPLICANT: BOUFSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
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2 US-09-855-754-4

2 US-09-855-754-19

1 US-09-731-537-50286

2 US-09-855-754-14

2 US-09-855-754-21

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1 US-09-791-537-784-3

1 US-09-791-537-784-3

1 US-09-791-537-784-2

1 US-09-380-693A-48

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2 US-09-380-693A-51

2 US-09-380-693A-51
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1larity 100.0%; Pred. No. 1e-12;
Conservative 0; Mismatches 0;
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US-60-191-637-36595
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US-09-855-754-17
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 52; Conserv
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SOFTWARE: PL
SEQ ID NO 17
LENGTH: 52
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                                                                                                                                              7, 2003, 16:47:16 ; Search time 131.727 Seconds (without alignments) 254.511 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
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13: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
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21: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/USONG_COMB.pep:*
                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-16
US-09-855-754-18
US-09-855-754-13
US-09-791-537-37413
US-09-791-537-85698
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPG-----PQPPQPPQPPQRPEAPAPQPPAGRELSAA 52
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Pred. No. 8.7e-12; .
0; Mismatches 0; Indels 7
1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQPPAGRELSAA 52
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Pred. No. 1.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella bronchiseptica US-09-855-754-16
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US-09-855-754-15
; Sequence 15, Application US/09855754
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91.1%;
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Best Local Similarity 88.1%;
Matches 52; Conservative (
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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SOFTWARE: Patentin Ver. 2.1
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Matches 51; Conservative
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LENGTH: 56
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Sequence 37413, Application US/09791537

Sequence 37413, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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TITLE OF INVENTION: POLYPEPTICAS CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTICAS CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: 05/09/85,754 CURRENT FILING DATE: 2001-09-10 PRIOR FILING DATE: 2001-09-10 PRIOR FILING DATE: 2001-09-25 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTING DATE: 2001-05-25 LENGTH: 52
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Pred. No. 6e-11;
0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: BLOOMLY. Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TILLO F INVENTION: THREE DIMENSIONAL STRUCTURI
TILLE OF INVENTION: THREE DIMENSIONAL STRUCTURI
TILLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SOFTWARE: Patentin version 3.0
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US-09-791-537-37413
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US-09-855-754-15
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US-09-791-537-85698
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE PATCHTIN VET. 2.1
                                                                                                                                                                                        Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISNS OF THE REPEATITIE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISNS OF THE REPEATITIE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                        Score 271; DB 21; Length 911; Pred. No. 7e-10;
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Pred. No. 7e-10;
                                                                                                                                                                                     0; Mismatches
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                                           ; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-791-537-85698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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96.2%;
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96.2%;
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Best Local Similarity 96.2
Matches 51; Conservative
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Matches 51; Conserv
SEQ ID NO 85698
LENGTH: 911
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LENGTH: 58
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DB 22;

Score 267;

89.68;

Query Match

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Sequence 50286, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biologia, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE; 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
SOFTWARE: PATENTING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTING DATE: 2001-02-22
SOFTWARE: PATENTIN VETSION 3.0
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APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILLING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
                                  Gaps
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                               Indels
  Pred. No. 1.2e-10;
0; Mismatches 1;
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Pred. No. 1.3e-09;
0; Mismatches 1;
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Pred. No. 1.3e-09;
0; Mismatches 1;
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US-09-791-537-50236
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US-09-855-754-14
; Sequence 14, Application US/09855754
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Sequence 6, Application US/09855754
GENERAL INFORMAÇION:
84.78
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Best Local Similarity 87.9%;
Matches 51; Conservative
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Best Local Similarity 87.9%;
Matches 51; Conservative
Best Local Similarity 87.9
Matches 51; Conservative
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Patentin Ver.
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US-09-791-537-50286
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LENGTH: 922
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US-09-855-754-6
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NUMBER OF SEQ ID NOS: 24
TITLE OF INVENTION:
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LENGTH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                          APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 65/206,969
PRIOR APPLICATION NUMBER: 66/206,969
PRIOR PILING DATE: 2000-05-25
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Pred. No. 1.3e-09;
0; Mismatches 0; Indels 5
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Pred. No. 3.3e-09;
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                        : BOURSAUX-EUDE, CAROLINE
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90.68;
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88.7%;
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SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver.
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Best Local Similarity
Matches 47; Conserv
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US-09-855-754-20
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LENGTH: 48
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LENGTH: 49
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISMPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2010-09-10
PRIOR PILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 52;
                                                                                                                                                                                                                                                                                                                                                                                              Score 236; DB 22;
Pred. No. 1.2e-08;
1; Mismatches 1;
IMMUNOGENIC COMPOSITIONS
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                       FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                PRIOR APPLICATION NUMBER: 2001-09-10;
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 21
LENGTH: 52
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US-09-855-754-22
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US-09-855-754-21
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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88.9%;
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18; Conservative
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APPLICANT: BOURSAUX-EUDE,
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Matches 48; Conserv
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Search completed: May 7, 2003, 17:21:56 Job time: 132.727 secs



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RESULT 2
US-09-855-754B-16
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                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGP.........PQRPEAPAPQPPAGRELSAA 52
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/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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92. 5 US-09-85-75-8.

93. 6 US-10-227-35-9.

94. 5 US-09-855-7548-2.

95. 5 US-09-855-7548-2.

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    protein search, using sw model

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ALIGNMENTS

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APPLICANT: GUISO-MACLOUE, CINCLES TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REGIONS OF THE REGIONS OF PREMACTIN IN BORDETELLA PERFUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: INMUNOSERIC COMPOSITIONS IN DIAGNOSTICS, AND IN FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: 05/09/855,754B PRIOR PALICATION NUMBER: 60/206,969 PRIOR PAPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 17
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILLING DATE: 2001-05-16
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100.0%; Score 298; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 52; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
PPPLICANT: BOURSOUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
Sequence 17, Aprlication US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bordetella bronchiseptica
US-09-855-7548-17
                                                                     APPLICANT: BOURSAUX-EUDE, CAROLINE
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51;
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-00500
CURRENT APPLICATION NUMBER: USX/09/855,754B
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PRETACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGEBLIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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Pred. No. 1.1
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Pred. No. 1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-15
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                                                                                               ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-16
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nilarity 91.1%;
Conservative
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ilarity 88.1%;
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
                  Patentin Ver. 2.1
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NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                           Query Match
Best Local Similarity
Matches 52; Conserv
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US-09-855-754B-15
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                    SOFTWARE: Pat
SEQ ID NO 16
LENGTH: 59
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LENGIH: 52
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                                                                  Gaps
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                            22
                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 911;
                                                                Indels
                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                  Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Score 271; DB 5; Le
Pred. No. 7.4e-11;
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4.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 271;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                               Sequence 4, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       GUISO-MACLOUF, NICOLE
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96.2%;
                       90.9%;
96.2%;
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COMPUTER READABLE FORM:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
                         Query Match 90.9
Best Local Similarity 96.2
Matches 51; Conservative
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SEQUENCE
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US-09-855-754B-14
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US-10-227-353-6
  SEQ ID NO 6
LENGIH: 922
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APPLICANT: BORSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREJONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELLA OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/455,754B
CURRENT PILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA PARAPERTUSSIS, AND SIN BONDETELLA PARAPERTUSSIS, AND BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-05-16
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Pred. No. 4.2e-10;
0; Mismatches 0
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Pred. No. 1.4e-10;
0; Mismatches 1;
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                  TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-227-353-4
                                      (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09855754B GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                        TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                           LENGTH: 911 amino acids TYPE: amino acid
                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                            90.9%;
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ilarity 87.9%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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nes 51; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local S
Matches 51
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Matches
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREX J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                    Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                            1; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                 Score 267; DB 5;
Pred. No. 7.6e-10;
0; Mismatches 1
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Pred. No. 7.6e-10;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/460,269C
BTUING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754B-6
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87.9%;
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87.98;
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                                                                             Query Match 89.67
Best Local Similarity 87.97
Matches 51; Conservative
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TELEFAX: (703) 24
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Best Local Similarity 87.99
Matches 51; Conservative
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2001-05-16

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CURRENT FILING DATE:
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LENGTH: 42
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPEABLE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/4855,754B
CURRENT FILING DATE: 2001-05-16
POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTURSIS, BORDETELLA PRARPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELA PARAPERTUSSIS, AND BORDETELA PARAPERTUSSIS, AND BORDETELA PARAPERTUSSIS IN DIÀGNOSTICS, AND IN
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPETCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 49;
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Pred. No. 3.5e-09;
0; Mismatches: 0; Indels
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                                                                                                     IMMUNOGENIC COMPOSITIONS
                                              TITLE OF INVENTION: BORDETELLA PARAPERTUSS TITLE OF INVENTION: BRONCHISEPTICA, THEIR TITLE OF INVENTION: IMMUNOGENIC COMPOSITIC CHEENENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-14
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Best Local Similarity 88.7%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.1%;
90.6%;
                                                                                                                                                                                                                                                                                : PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
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US-09-855-754B-21
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POLYMORPHISMS OF THE REPEATED
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYEPPIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGLISSPITICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.2e-08;
1; Mismatches 1;
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85.7%; Pred. No. 1.4e-08;
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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  7206,969
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88.9%;
PRIOR APPLICATION NUMBER: 60/:
PRIOR FILING DATE: 2000-05-25
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                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 52
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Best Local Similarity 88.9
Matches 48; Conservative
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                                                      NUMBER OF SEQ ID NOS: 25
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PatentIn Ver.
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
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US-09-855-754B-21
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                                                                                                                                    Gaps
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                                                                                                                                      10;
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Pred. No. 4e-06;
1; Mismatches 0; Indels
                                                                                      Score 207; DB 5; Length 42;
Pred. No. 6.7e-07;
1; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR PILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-09
PRIOR PLING DATE: 2000-10-09
PRIOR PLING DATE: 2000-10-09
PRIOR PLING DATE: 2000-10-33
PRIOR PLING DATE: 2000-11-27
PRIOR PURIOR DATE: 2000-11-27
PRIOR PULING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                Sequence 51012, Application US/10282122A GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordetella pertussis US-10-282-122A-51012
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78.8%;
                                                                                      Query Match 69.5%;
Best Local Similarity 78.8%;
Matches 41; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Best Local Similarity 78.8
Matches 41; Conservative
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US-10-282-122A-51012
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APPLICANT: BOURGAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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. US-09-791-537-37413

. US-09-791-537-85698

. US-09-855-754-14

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. US-09-855-754-20

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. US-09-856-754-3

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US-09-380-693A-53
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US-09-380-693A-50
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US-09-855-754-18
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1217
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      SEQ ID NO 18
LENGTH: 56
TYPE: PRT
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Matches 56
         Sequence 18, Appl
Sequence 19, Appl
Sequence 50286, A
Sequence 6, Appli
Sequence 16, Appl
                                                                                                                                                                                                          7, 2003, 16:47:16 ; Search time 141.86 Seconds (without alignments) 254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
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7: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
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US-09-855-754-19
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Maximum Match 100%
Listing first 45 summaries
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Sequence 1323, Ap Sequence 5, Appli Sequence 8, Appli

Sequence 38, Appl Sequence 53, Appl Sequence 22218, A Sequence 22218, p Sequence 50, Appl ö

Gaps

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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56

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REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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Best Local Similarity 91.7%;
Matches 55; Conservative (
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Best Local Similarity 94.8%;
Matches 55; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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APPLICANT: GUISO-MACLOUF
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APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: HERED DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VETSION 3.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GIISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                      APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTESSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 65/206,969
PRIOR FILING DATE: 2000-05-25
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94.8%; Pred. No. 6.3e-12;
11ve .0; Mismatches 1;
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Pred. No. 5.7e-13;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
                                                                                                                                     Sequence 19, Application US/09055754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 94.8%;
Matches 55; Conservative
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Best Local Similarity 94.8%
Matches 55; Conservative
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LENGTH: 922
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LENGTH: 58
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TITLE OF INVENTION: POLYPEPIDES CONTRINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR APPLICATION NUMBER: 60/206,969
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISBETICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSOFTWARE: PATENTIN VET. 2.1
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Pred. No. 2.1e-12;
0; Mismatches 0;
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Pred. No. 6.3e-12;
0; Mismatches 1;
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CURRENT FILING DATE: 2001-09-10
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US-09-855-754-16
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US-09-855-754-15
; Sequence 15, Application US/09855754
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: BRONCHISEPTLIA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHISEPTLOA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 06/206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 9.4e-11;
0; Mismatches 0;
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Pred. No. 1.2e-11;
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                           US-09-855-754-4; Squence 4, Application US/09855754; Squence 4, Application US/09855754; GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
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91.1%;
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Best Local Similarity 92.9%;
Matches 52; Conservative
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Best Local Similarity 91.19
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: GUISO-MACLOUF
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LENGTH: 52
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Sequence 85698, Application US/09791537

SEQUENCE 85698, Application US/09791537

SEQUENCE 85698, Application US/09791537

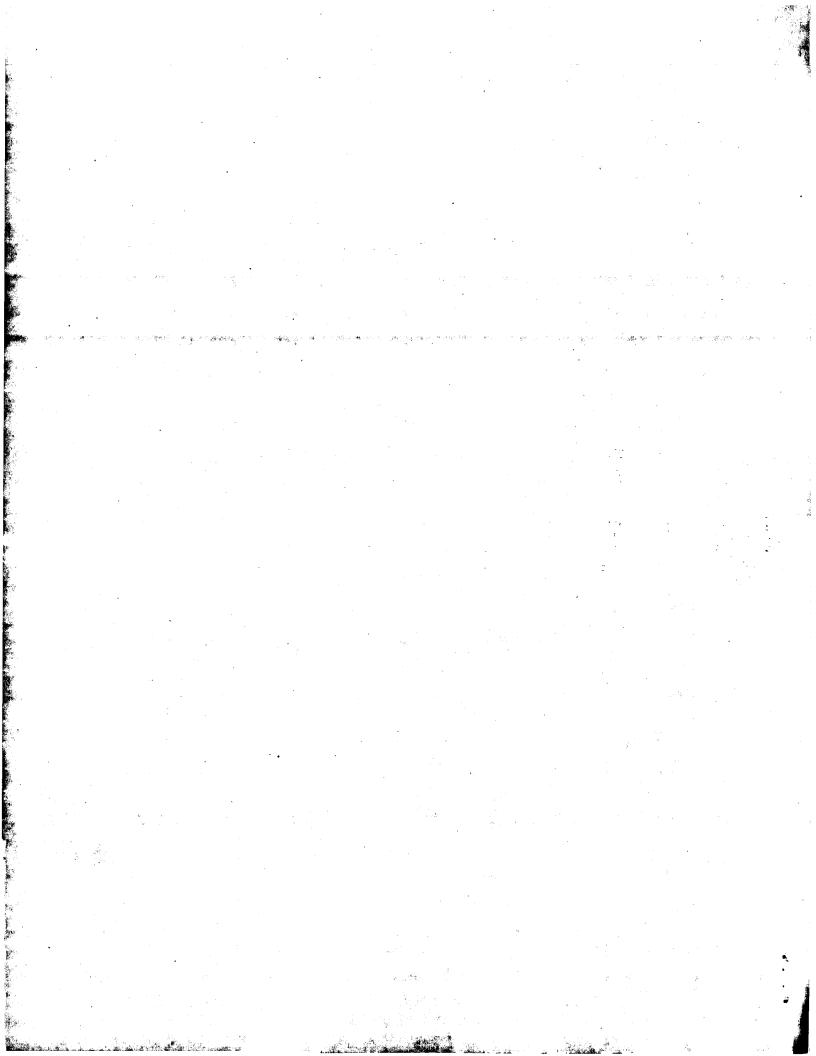
SEQUENCE INVENTION: The DEADLY DE
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Belonomix, Inc.
APPLICANT: Dence, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: 105/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 37413
LENGTH: 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 52;
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Pred. No. 7.8e-12;
0; Mismatches 0;
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Pred. No. 9.4e-11;
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92.9%; Pred. No. 9.4e-11;
tive 0; Mismatches 0;
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US-09-791-537-85698
    60/206,969
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ilarity 92.9%;
Conservative
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1 Similarity 92.9%;
52; Conservative
PRIOR APPLICATION NUMBER: 60/3 PRIOR FILING DATE: 2000-05-25
                                                                                  NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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Best Local Similarity 92.9
Matches 52; Conservative
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Best Local Similarity
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LENGTH: 911
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NUMBER OF SEQ ID NOS: 24
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SEQ ID NO 21
LENGTH: 52
TYPE: PRT
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LENGTH: 54
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Best Local S
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTION IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND ENGURELLE.
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 05/01-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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                                        APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIE OF INVENTION: REGIONS OF PERFACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
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Pred. No. 1.6e-10;
0; Mismatches 0;
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Pred. No. 4.2e-10;
0; Mismatches 0;
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US-09-855-754-14
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US-09-855-754-20
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APPLICANT: BOURSAUX EUDE, CAROLINE
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                      APPLICANT: BOURSAUX-EUDE, CAROLINE
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 82.18;
1 Similarity 87.5%;
49; Conservative
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SEQ ID NO 20
LENGTH: 48
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Best Local Similarity
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Best Local Similarity
GENERAL INFORMATION:
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LENGTH: 49
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TITLE OF INVENTION: PGACLOUE, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FITTLE OF INVENTION: MUNICERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERFACTINI IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Score 257; DB 22;
Pred. No. 5.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09855754 GENERAL INFORMATION:
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TITLE OF INVENTION: IMMUNOGENIC FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                         79.8%;
86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/3 PRIOR FILING DATE: 2000-05-25
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 49; Conserv
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Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein – protein search, using sw model

Мау Run on:

7, 2003, 16:48:21 ; Search time 33.0085 Seconds (without alignments) 289.347 Million cell updates/sec

Title: Perfect score:

US-09-855-754B-18 322 I GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA 56 Sequence:

Scoring table:

785622 seqs, 170552221 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

785622

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

1: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 18. Appl	0	۷,	ی ز	16,	15,	4, A	4	17,	Sequence 14, Appl	20,	21,	22,	23,	5101	5, A	7	7	417	Sequence 19541, A	Sequence 11684, A	Sequence 11684, A	Sequence 1982, Ap	51472,		2814,
q i	US-09-855-754B-18	-09-855	-855-7	2	-09-855-754	US-09-855-754B-15	US-09-855-754B-4	US-10-227-353-4	US-09-855-754B-17	US-09-855-754B-14	US-09-855-754B-20	US-09-855-754B-21	US-09-855-754B-22	US-09-855-754B-23	US-10-282-122A-51012	US-09-855-754B-5	US-10-227-353-2	US-09-855-754B-24	-10-218-140-4	US-60-452-680-19541	US-60-453-135-11684	US-60-453-050-11684	US-10-017-161-1982	US-10-282-122A-51472	PCT-US02-36123-2812	PCT-US02-36123-2814
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Score	322	303	303	303	294.5	285	285	285	282	264.5	258	257	256	210	210	210	210	189.5	155.5	155.5	155.5	155.5	151	144	143	143
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Sequence 12544, A Sequence 51470, A		Sequence 9652, Ap	Sequence 6756, Ap	Sequence 80, Appl	Sequence 80, Appl	Sequence 92543, A		Sequence 66157, A	Sequence 48029, A	Sequence 28564, A	Sequence 28564, A	Sequence 14385, A	Sequence 10081, A	Sequence 24873, A	Sequence 24873, A	Sequence 228, App	•
US-10-156-761-12544 US-10-282-122A-51470	US-10-224-999A-3465	US-09-949-016-9652	US-09-949-016-6756	US-60-423-586-80	US-60-427-194-80	US-09-724-676-92543	US-09-724-676A-92543	US-10-282-122A-66157	US-10-282-122A-48029	US-10-366-683-28564	US-10-419-128-28564	US-10-156-761-14385	US-10-156-761-10081	US-10-366-683-24873	US-10-419-128-24873	US-10-055-877-228	US-10-369-493-4092
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578 324	487	1444	2004	2004	2004	2040	2040	270	202	188	188	296	810	142	142	565	1822
44.4	43.9	13.5	43.5	43.5	43.5	43.5	13.5	43.0	42.5	42.2	12.2	11.6	11.3	40.7	40.7	40.5	40.5
143	141.5	140	140	140	14.0	140	140	138.5	137	136	136	134	133	131	131	130.5	130.5
27	53	30	31	32	33	34	32	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

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TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVERTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE 03495-0206-00000
CURRENT MAPLICATION NUMBER: US/09/855,754B
CURRENT MAPLICATION NUMBER: 60/206,969
PRIOR PELING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND IN BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILL REFERENCE: 03495-0206-00000
CURRENT FILLNG DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PELLING DATE: 2000-05-25
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100.0%; Score 322; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-855-754B-19
; Sequence 19, Aprlication US/09855754B
; GENERAL INFORMATION:
US-09-855-754B-18; Sequence 18, Application US/09855754B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                               CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
                                                                                            APPLICANT: BOURSAUX-EUDE,
APPLICANT: GUISO-MACLOUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 25
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Query Match
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Matches 5
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA SITLE OF INVENTION: BRONGHISEPETICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION UNMER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 САКАРРАРКРАРОРСРОРОРОРРОРРОРРОРРОРРОРРОРОВОРЕАРАРОРРАСКЕТСЯА 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE STATE OF THE S
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 922;
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                                                                                                                                                                                                                                                                                                                     Length 58;
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SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Millen, White, Zelano & Brani.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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Pred. No. 1e-11;
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APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                         Score 303;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella parapertussis
US-09-855-754B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAROLINE
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94.8%;
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94.8%;
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201
COMPUTER READABLE FORM:
    NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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ID NOS: 25
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hes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                               Similarity
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US-10-227-353-6
                                              SOFTWARE: Pa
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                                                                                                                                                                   TYPE: PRT
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Best Local
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Matches
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1 GAKAPPAPKPA----PQPGPQPGPQPPQPPQPPQPPQPPQRPQPPAGRELSAA 56
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1e-11;
0; Mismatches
PRIONG DATE: 26-Aug-2002
PRION APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTONEY/AGENT INFORMATION
REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINear ;
MOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-227-353-6
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ORGANISM: Bordetella bronchiseptica
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TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 922 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.18;
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91.7%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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Matches 55; Conservative
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US-09-855-754B-15
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APPLICANT: GUÍSO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYBEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYBEPIDES CONTAINING POLYMORPHELA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AND MANDAGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
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                                                  SOFWWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.6%; Score 282; DB 5;
91.1%; Pred. No. 3.4e-11;
Live 1; Mismatches 0
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Pred. No. 1.3e-10;
0; Mismatches 0
                                                                                                                                                        APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/855,754B
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-227-353-4
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                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       (703) 243
703) 243-6410
                                                                                                                    FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 911 amino acids TYPE: amino acid
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APPLICANT: GUISO-MACLOUF, NICOLE
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92.9%;
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Best Local Similarity 91.1%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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Best Local Similarity 92.99
Matches 52; Conservative
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 911;
                                                                                                                                                                                                                                                                                            Length 52;
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STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                       Score 285; DB 5;
Pred. No. 2.2e-11;
0; Mismatches 0;
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION WUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION WUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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Pred. No. 1.
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                     ORGANISM: Bordetella bronchiseptica US-09-855-7548-15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09855754B GENERAL INFORMATION:
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92.9%;
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illarity 92.9%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 52; Conser
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Best Local Similarity
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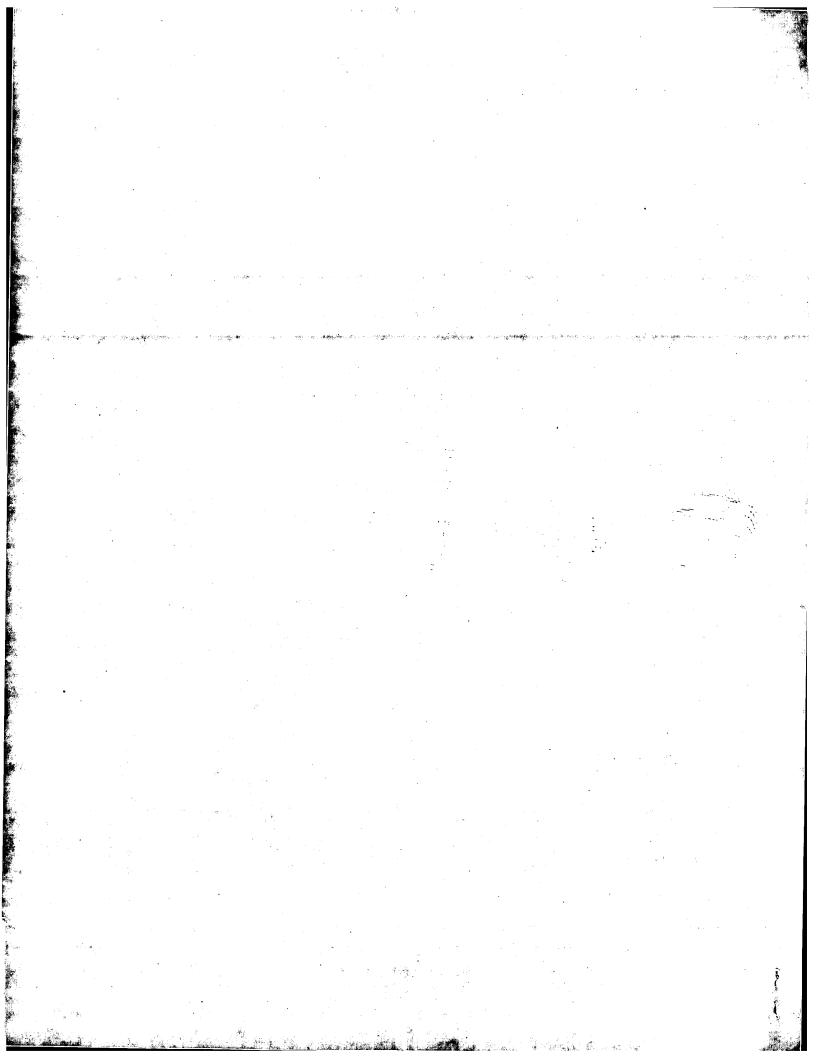
Gaps

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SEQ ID NO 23
LENGTH: 42
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                                                                                                                                                                        TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS, BORDETELLA PARABERTUSSIS, AND BORDETELLA PARABERTUSSIS, AND BORDETELLA, PREFE USE IN DIAGNOSTICS, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: RECIONS OF PREPARATIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQREAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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Pred. No. 3.9e-10;
0; Mismatches 0;
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Pred. No. 9.7e-10;
0; Mismatches 0;
                                                                                                IMMUNOGENIC COMPOSITIONS
                                          TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS TITLE OF INVENTION: BRONCHISEPTICA, THEIR US TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS FILER REFERENCE: 03495-0206-00000; CURRENT APPLICATION NUMBER: US/09/855,754B CORRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACTORE MITOTO
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85.7%;
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87.5%;
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SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.13
Best Local Similarity 85.73
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
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PRIOR FILING DATE: 2000-05
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
  INVENTION:
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ORGANISM:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTINI IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILLING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                      Score 257; DB 5;
Pred. No. 1.2e-09;
0; Mismatches 2
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
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     2001-05-16
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Best Local Similarity 86.0%;
Matches 49; Conservative
CURRENT FILING DATE: 2001-05
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTHARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 52
                                                           2000-05-25
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Matches 49; Conservative
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Pred. No. 4.7e-06;
0; Mismatches 1; Indels 14; Gaps
                                                                                                                  Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51012
LENGTH: 768
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                                                                                                                  14;
                                                                       Score 210; DB 5; Length 42;
Pred. No. 8e-07;
0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT SATE: 2003-02-20
                                                                                                                                                                                                                                                                           Sequence 51012, Application US/10282122A GENERAL INFORMATION:
; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/267,636
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APPLICATION NUMBER: 60/207,727
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                                                                       Query Match 65.2%;
Best Local Similarity 73.2%;
Matches 41; Conservative
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Best Local Similarity 73.2%;
Matches 41; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Trawick, John
Carr, Grant
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:49 Job time : 34.0085 secs



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Best Local S
Matches 58
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Sequence 50286, A
Sequence 6, Appli
Sequence 18, Appl
Sequence 16, Appl
Sequence 15, Appl
                                                                                                                                 ; Search time 146.927 Seconds
(without alignments)
254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/PCGCOMB.pep:*
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4: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/USO81_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/USO81_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/USO85_COMB.pep:*
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11: /cgn2_6/ptodata/1/paa/USO85_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/USO85_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
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22: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
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25: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USO92_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
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US-09-791-537-50286
US-09-855-754-6
US-09-855-754-18
US-09-855-754-15
US-09-855-754-15
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: GUISO-MACLOUE, CANCILLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA PERFUSSIS,
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR PELICATION NUMBER: 60/206,969
PRIOR PELICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 19
                                                  Sequence 4, Appli
Sequence 17, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 76968, A
Sequence 21274, A
Sequence 24, Appli
Sequence 21, Appli
Sequence 2285, A
Sequence 2216, Appli
Sequence 2285, A
Sequence 2285, A
Sequence 2211, Appli
Sequence 22211, A
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1 US-09-791-537-37413

1 US-09-791-537-85698

2 US-09-855-754-4

2 US-09-855-754-14

2 US-09-855-754-14

2 US-09-855-754-20

2 US-09-855-754-20

2 US-09-855-754-21

2 US-09-855-754-21

2 US-09-855-754-21

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2 US-09-855-754-21

2 US-09-855-754-21

1 US-09-791-537-76981

1 US-09-791-537-76981

1 US-09-791-537-1207

1 US-09-791-537-1207

2 US-09-855-754-24

1 US-09-791-537-11629

2 US-09-855-754-24

2 US-09-855-754-28

2 US-09-855-754-28

2 US-09-851-852

2 US-09-851-852

2 US-09-8631-40236

2 US-09-417-507-2218

8 US-09-417-507-2218

8 US-09-417-507-2215

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8 US-09-417-507-2215
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llarity 100.0%; Pred. No. 7.4e-15;
Conservative 0; Mismatches 0;
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US-09-855-754-19
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Gaps

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS, TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PARAPERTUSSIS, 
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FILE REFERENCE: 03495-0206-00000
                                                                           THEIR USE IN DIAGNOSTICS, AND
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Pred. No. 1.7e-12;
0; Mismatches 0;
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Pred. No. 8.5e-13;
0; Mismatches 1;
                                                                               BRONCHISEPTICA, THEIR USI IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BORDETELLA PRAPERTUSSI TITLE OF INVENTION: BRONCHISEPTICA, THEIR UF TITLE OF INVENTION: IMMUNGENIC COMPOSITION: FILE REFERENCE: 03455-0206-00000; CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILICA DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VER: 2.1
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), ORGANISM: Bordetella bronchiseptica US-09-855-754-18
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Best Local Similarity 95.0%;
Matches 57; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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US-09-855-754-16
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SEQ ID NO 16
LENGTH: 59
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Best Local S:
Matches 55;
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LENGTH: 56
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Sequence 50266, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Dancer, JOSeph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PRILING DATE: 201-02-22
NUMBER OF SEQ ID NOS: 153055
SOGTWARE: Patentin version 3.0
SEQ ID NO 50286
LENGTH: 922
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIESPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 2005-00000
CURRENT FILING DATE: 2001-09-10
PRICA PAPELICATION NUMBER: 60/206,969
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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Pred. No. 7.9e-14;
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US-09-791-537-50286
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100.0%; Pr
tive 0;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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Best Local Similarity 100.0
Matches 58; Conservative
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Best Local Similarity
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US-09-791-537-50286
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BEGINGS PERFACTIONS, AND BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA PERFUSINGS.
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
SUPPRIOR FILLING DATE: 2000-05-25
SUPPRIOR FILLING DATE: 2000-05-25
SUPPRIOR FILLING DATE: 2000-05-25
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APPLICANT: BOGGSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT PALLING, DATE: 2001-09-10
PRIOR FILING, DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VET. 2.1
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79.7%; Score 267; DB 22;
Best Local Similarity 87.9%; Pred. No. 1.7e-10;
Matches 51; Conservative 0; Mismatches 1;
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Pred. No. 1.6e-10;
0; Mismatches 0;
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US-09-855-754-17
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US-09-855-754-22
; Sequence 22, Application US/09855754
                                                                                                                                       Sequence 4, Application US/09855754 GENERAL INFORMATION:
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ilarity 89.7%;
Conservative
       APPLICANT: BOURSAUX-EUDE
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Best Local Similarity
Matches 52; Conserv
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TYPE: PRT
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILIX MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILIX MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
SOFTWARE: PATENT ON SEQ ID NOS: 153055
SOFTWARE: PATENT VESSION 3.0
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1.4e-11;
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Best Local Similarity 89.7%; Pred. No. 1.6e-10;
Matches 52; Conservative 0; Mismatches 0;
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Pred. No. 1.6e-10;
0; Mismatches 0;
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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US-09-791-537-85698
                                                                                                                                                             ORGANISM: Bordetella bronchiseptica
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89.7%;
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Local Similarity 89.7%;
les 52; Conservative
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Best Local Similarity
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LENGTH: 911
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IMMUNOGENIC COMPOSITIONS

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REFERENCE: 03495-0206-00000
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US-08-247-544-2
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LENGTH: 52
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                                     TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDEFELLA PERTACTIN IN BORDEFELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2001-09-20

PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPERTITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 2.7e-10;
0; Mismatches 0;
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Pred. No. 2.4e-10;
0; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/09/855,754
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: BOURSAUX-EUDE, CAROLINE
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 49; Conserv
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SEQ ID NO 22
LENGTH: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BROWCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQPPAGPACRELSAA
                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                            Length 48;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                       Score 257; DB 22;
Pred. No. 7.1e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%; Score 256; DB 22; ilarity 84.5%; Pred. No. 8.8e-10; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
CURRENT APPLICATION NUMBER: US/09/855,754
               CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-855-754-21; Sequence 21, Application US/09855754; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08247544
GENERAL INFORMATION:
APPLICANT: CHARLES, IAN G.
APPLICANT: FAIRWEATHER, NEIL F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VACCINES NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    76.7%;
llarity 82.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOURSAUX-EUDE,
                                                                                                                                                                                                                                                                                                                1 Similarity
48; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-08/247,544
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
                                                                                                                                                                                  CLASSIFICATION: 4.4

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,059
FILING DATE: 19-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,045
FILING DATE: 27-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,589
FILING DATE: 04-SEP-1990
PRIOR APPLICATION NUMBER: US 07/576,589
FILING DATE: 04-SEP-1999
PRIOR APPLICATION NUMBER: GB 991358.0
FILING DATE: 21-MAY-1990
ATTORNEY-AGENT INFORMATION:
NAME: CRAMFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-159
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 200797 NIXN UR
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: APPLICATION INFORMATION:
TYPE: ADDITION INFORMATION:
TYPE: AMINO acids
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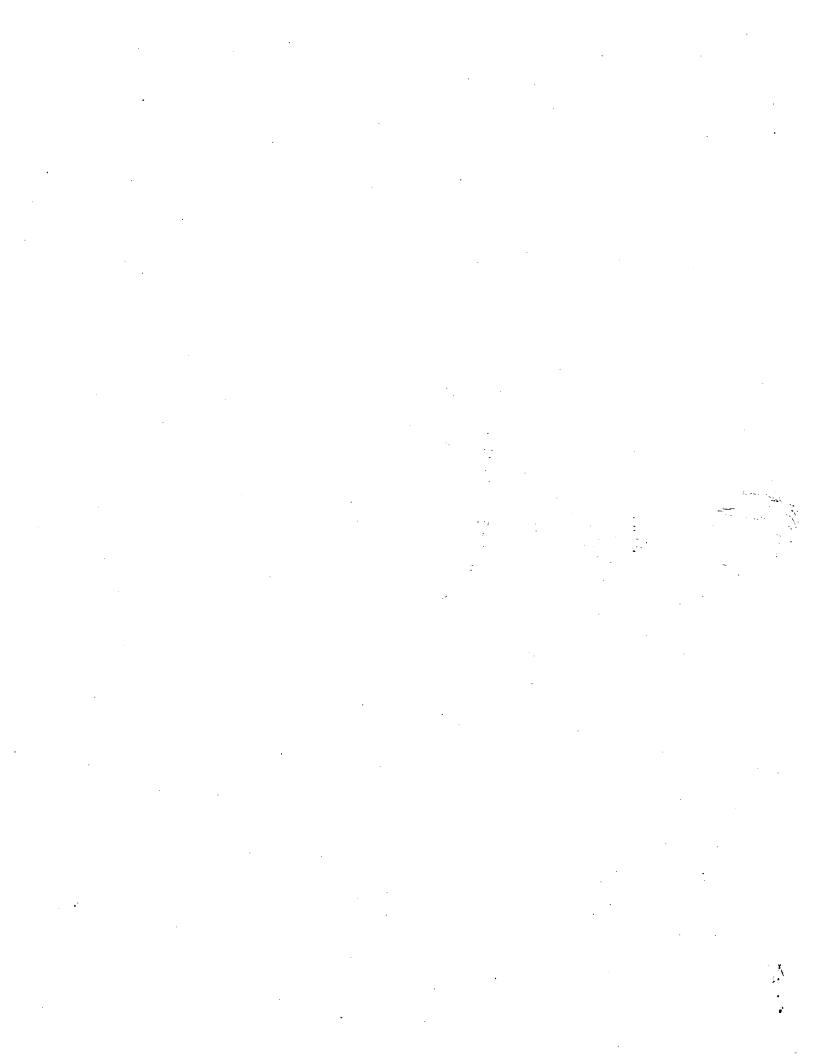
Query Match 70.4%; Score 236; DB 6; Length 39; Best Local Similarity 100.0%; Pred. No. 1.4e-08; Matches 39; Conservative 0; Mismatches 0; Indels

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Gaps

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Search completed: May 7, 2003, 17:21:57 Job time : 146.927 secs



Sequence 48029, A Sequence 24873, A Sequence 24873, A Sequence 66157, A Sequence 2812, Ap Sequence 7963, Ap Sequence 6756, Ap Sequence 80, Appl Sequence 92543, A Sequence 92543, A Sequence 12544, A Sequence 12544, A Sequence 12544, A Sequence 1364, A Sequence 1364, A Sequence 1364, A Sequence 6756, Ap Sequence 67656, Ap Appliance 67656, Appliance 67

Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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APPLICANT: BOURSHALE BOURS, AND APPLICANT: BOURSHALE BOURSHALE AND SELICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERFECUSSIS,
TITLE OF INVENTION: BORDETELLA PREPERFUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEC ID NOS: 25
SOFTWARE: PATENTING DATE: 2000-05-25
SOFTWARE: PATENTING DATE: 2000-05-25
LENGTH: 58
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                         US-10-866-683-24873
US-10-866-683-24873
US-10-419-128-24873
US-10-417-886-7963
PCT-USO2-36123-2812
US-09-949-016-6756
US-60-427-186-80
US-60-427-196-016-6756
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US-60-427-196-016-6756
US-09-724-676-92543
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US-10-369-493-4092
US-10-369-1228-64954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-369-493-3962
US-09-968-122D-7
US-10-282-122A-67656
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1larity 100.0%; Pred. No. 4.1e-14;
Conservative 0; Mismatches n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOURSAUX-EUDE, CAROLINE
200
1142
2240
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2004
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1824
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878
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Best Local Similarity
Matches 58; Conserv
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289.347 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPGP......QRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                    7, 2003, 16:48:21; Search time 34.1874 Seconds
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'cgn2_6/ptodata/2/paa_PCT_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS06_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

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'cgn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS00_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS00_NEW_COMB.pep:*
                                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754B-18
US-09-855-754B-15
US-09-855-754B-15
US-09-855-754B-17
US-09-855-754B-17
US-09-855-754B-12
US-09-855-754B-20
US-09-855-754B-21
US-09-855-754B-21
US-09-855-754B-21
US-09-855-754B-21
US-09-855-754B-21
US-09-855-754B-21
US-09-855-754B-5
US-10-227-353-2
US-10-227-353-2
US-09-855-754B-2
US-09-855-754B-5
US-10-218-140-4170
US-09-855-754B-24
US-10-218-140-4170
US-60-453-135-11684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       785622 segs, 170552221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
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Match Length
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Gaps

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Sequence Sequence Sequence

152.5

209 188.5 167.5 167.5 167.5 167.5 167.1

335 335 335 335 335 303 284 284 267 267 267 27 209 209

Score

Result

Length 58;

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REPEATED
            APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PESTONS OF PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND JITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND JITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSANY-EUDE, CAROLINE
APPLICANT: BOURSANY-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 3.5e-12;
0; Mismatches 1
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95.0%; Pred. No. 6.7e-12;
ive 0; Mismatches 0
                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09855754B
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.4%;
94.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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Matches 57; Conservative
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Matches 55; Conserv
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US-09-855-754B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
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100.0%; Score 335; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                   Score 335; DB 5;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                       ; ORGANISM: Bordetella parapertussis US-09-855-7548-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
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                                                                                                                                                                                   100.0%;
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                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703)
NUMBER OF SEQ ID NOS: 25
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                                       SEQ ID NO 6
LENGTH: 922
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US-10-227-353-6
                                                                                          TYPE: PRT
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APPLICANT: BOURSAUX-EUDE, CAROLINI APPLICANT: GUISO-MACLOUF, NICOLE
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US-09-855-754B-17
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US-09-855-754B-22
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TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVERTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERTION: BRONCHISSPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
GURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
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                                                                                                                                                                                                                                                                Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                              Score 284; DB 5;
Pred. No. 4.6e-11;
0; Mismatches 0;
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Pred. No. 2.6e-10;
0; Mismatches 0
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
                           PRIOR APPLICATION NUMBER: 60/206,969

PRIOR APPLICATION NUMBER: 60/206,969

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 52
                                                                                                                                                                                                  ) ORGANISM: Bordetella bronchiseptica US-09-855-7548-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10227353 GENERAL INFORMATION:
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89.7%;
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ilarity 89.7%;
Conservative
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SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                      52;
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                                                                                                                                                                                    TYPE: PRT
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APPLICANT: GGISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYBEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERPUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPGRELSAA 610
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                      OPERATING SYSTEM: PC-DOS/MS-DOS
SORTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 2.6e-10;
0; Mismatches 0
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Pred. No. 5e-10;
                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                             NAME: Lebovitz, Richard M.
RECISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOFOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
IBM PC compatible
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SUMMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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TELEFAX: (703) 243-6410
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LENGTH: 911 amino acids
TYFE: amino acid
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87.9%;
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Matches 52; Conservative
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Matches 51; Conserv
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    REPEATED
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                                           TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

FILE REPERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQRPQRPAPAPAPAPAGRELSAA 58
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE R. REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 САКАРРАРКРАРОРСРОРСРОРРОРРОРРОРРОРРОРРОРРОРРОРРАСКЕТ. SAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
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Pred. No. 6.7e-10;
0; Mismatches 5
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Pred. No. 7.8e-10;
0; Mismatches 0
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-855-754B-14
; Sequence 14, Application US/09855754B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUISO-MACLOUF, NICOLE
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84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                        79.1%;
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Best Local Similarity 84.55
Matches 49; Conservative
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Matches 49; Conserv
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                                                                                                                                                                                                                                                                                SEQ ID NO 22
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ORGANISM:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: 10495-0206-000000
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APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                            Length 48;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
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1 Similarity 84.5%; Pred. No. 2.3e-09;
49; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                         Score 257; DB 5;
Pred. No. 1.9e-09;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         76.7%;
82.8%;
CURRENT FILING DATE: 2001-05-
PRIOR APPLICATION NUMBER: 60/7
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-2
NUMBER OF SEQ ID NOS: 25
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 21
                                                                                NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                            48; Conservative
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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SEQ ID NO 23
LENGTH: 42
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                                                                                                                                                                                           Remaining Prior Application data removed – See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
                                                                                                                              16;
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Pred. No. 8e-06;
0; Mismatches 1; Indels 16;
                                                                                Score 209; DB 5; Length 42;
Pred. No. 1.4e-06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                              Sequence 51012, Application US/10282122A GENERAL INFORMATION:
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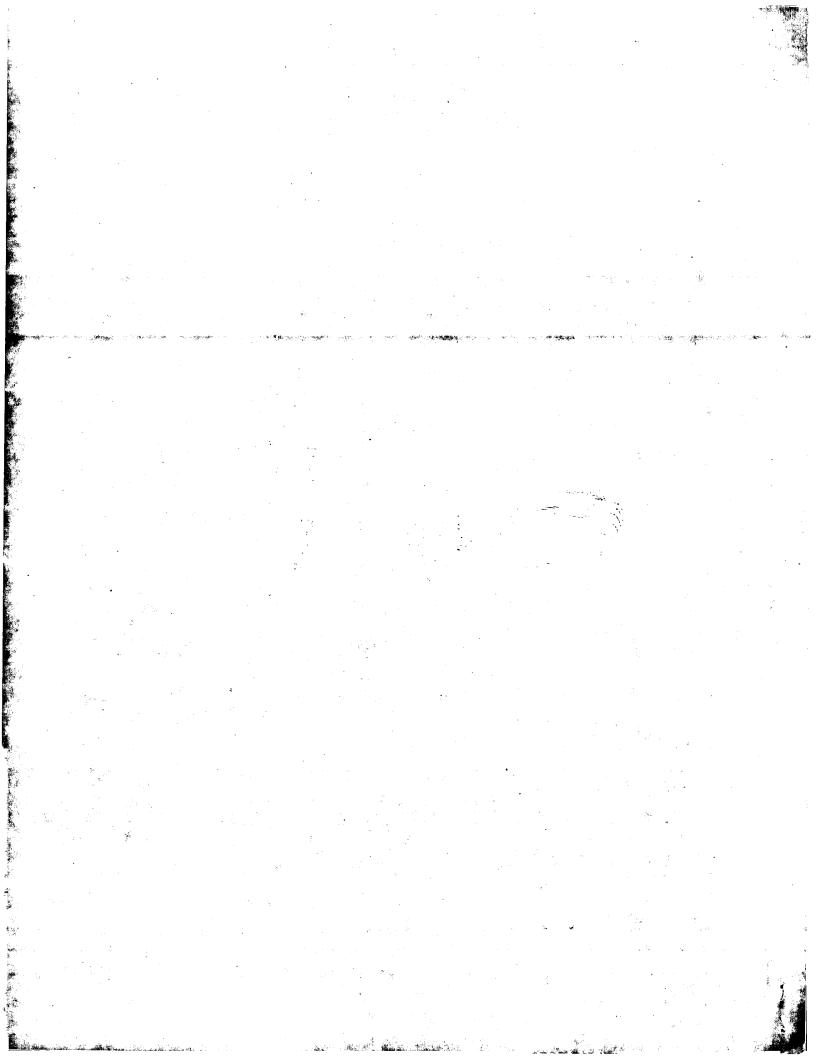
R APPLICATION NUMBER: 60/207,727

R FILING DATE: 2000-05-26

R APPLICATION NUMBER: 60/230,335

R FILING DATE: 2000-09-06
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APPLICATION UNMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-23
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APPLICATION NUMBER: 60/206,848
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-51012
                                                                                Query Match 62.4%;
Best Local Similarity 70.7%;
Matches 41; Conservative
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Best Local Similarity 70.7%;
Matches 41; Conservative
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Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                          Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:49 Job time : 34.1874 secs



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1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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Sequence 14, Appl
Sequence 15, Appl
Sequence 37413, A
Sequence 8698, A
Sequence 4, Appli
                                                                                                                                                                                    7, 2003, 16:47:16 ; Search time 121.595 Seconds (Without alignments) 254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPPQ......QRQPEAPAPQPPAGRELSAA
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(egn2_6/ptodata/1/paa/US06_COMB.pep:*
(egn2_6/ptodata/1/paa/US06_COMB.pep:*
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(egn2_6/ptodata/1/paa/US096_COMB.pep:*
(egn2_6/ptodata/1/pa
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6/ptodata/1/paa/US098_COMB.pep:*
6/ptodata/1/paa/US099_COMB.pep:*
6/ptodata/1/paa/US100_COMB.pep:*
6/ptodata/1/paa/US101_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-14
US-09-855-754-15
US-09-791-537-37413
US-09-791-537-85698
US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4569144 seqs, 644733110 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
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Match Length DB
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Perfect score:
Sequence:
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Maximum DB seq
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Sequence 18, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 21, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 21, Appl
Sequence 75841, A
Sequence 76961, A
Sequence 76961, A
Sequence 76961, A
Sequence 76961, A
Sequence 21, Appl
Sequence 112007, Sequence 11207, Sequence 11207, A
Sequence 24, Appl
Sequence 11207, Sequence 11629, Sequence 24, Appl
Sequence 21, Appl
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Sequence 21, Appl
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Sequence 21, Appl
Sequence 2285, Appl
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5-09-855-754-20
Sequence 20, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOUKSAUX-EUDE, CAROLINE
APPLICANT: BOUKSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS,
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
FILLE REFERENCE: 03495-0206-00000
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2 US-09-855-754-18

2 US-09-855-754-19

1 US-09-855-754-19

2 US-09-855-754-21

2 US-09-855-754-22

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

1 US-09-791-537-75841

1 US-09-791-537-75841

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1 US-09-791-537-754-24

1 US-09-791-537-711629

1 US-09-791-537-711629

1 US-09-791-537-711629

1 US-09-791-537-784-3

1 US-09-791-537-784-2

1 US-09-855-754-2

1 US-09-855-754-2

1 US-09-855-754-2

1 US-09-855-754-3

1 US-09-874-544-3

1 US-09-380-693A-49

2 US-08-247-544-3

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2 US-08-247-544-3

2 US-08-247-544-3

2 US-08-347-544-3

2 US-08-347-541-333

2 US-08-347-541-333

2 US-08-348-631-333

2 US-08-348-631-333

2 US-08-348-631-333

2 US-09-896-0032-11
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100.0%; Score 272; DB 22;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 48; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-10
PRIOR PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 48
TYPE: RT
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Query Match 95.6%;
Best Local Similarity 92.3%;
Matches 48; Conservative
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Matches 48; Conserv
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US-09-855-754-4
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERRACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03499-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN FILLE REFERENCE: 03495-0206-00000
FILLE REFERENCE: 03495-0206-00000
CUNRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
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1 GAKAPPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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Pred. No. 4.4e-11;
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Pred. No. 3.3e<sup>o</sup>
0; Mismatches
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                                                                                                                                    Sequence 14, Application US/09855754 GENERAL INFORMATION:
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92.3%;
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ilarity 98.0%;
Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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Matches 48; Conserv
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Best Local Similarity
Matches 48; Conserv
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; ORGANISM: BO
US-09-855-754-14
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Sequence 85699, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Dabe, Dese,
APPLICANT: Dabe, Dese,
APPLICANT: Dabe, Dese,
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE OF INVENTION: WETHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DAIE: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SOFTWARE: Patentin version 3.0
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREGIONS OF PERTACTIN IN BORDETELLA PERTUSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNICATION COMPOSITIONS
FILE PERFERENCE: 03495-0206-000000
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92.3%; Pred. No. 5.6e-10;
ive 0; Mismatches 0;
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Pred. No. 5.6e-10;
0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Bordetella bronchiseptica
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US-09-791-537-37413
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Best Local Similarity 82.8 Matches 48; Conservative
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US-09-791-537-50286
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED.

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS

FILE REFERENCE: 03495-0206-0000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT PILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 18

SEQ ID NO 18
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUGSIS, AND ENTRY INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGEBRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 6.5e-11;
0; Mismatches 0;
                                                                                                                    Score 260; DB 22;
Pred. No. 5.6e-10;
0; Mismatches 0;
                                       ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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US-09-855-754-18
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09855754 GENERAL INFORMATION:
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85.7%;
                                                                                                                      95.6%;
92.3%;
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Best Local Similarity 85.77
Matches 48; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
                                                                                                                                    Best Local Similarity 92.3
Matches 48; Conservative
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SEQ ID NO 4
LENGTH: 911
                                                                                                                      Query Match
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Length 58;

DB 22;

Score 257;

94.58;

Query Match

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APPLICANT: Bidnomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                       Gaps
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                                                                               APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF TITLE OF INVENTION: REGIONS OF PERFOCTIN IN BONDEFELLA TITLE OF INVENTION: BRONCHISEPTICA, THERR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS INVENTION: IMMUNOSENIC COMPOSITIONS CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10
                                                         GAKAPPAPKPAPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                     Indels
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Pred. No. 7.8e-11;
); Mismatches 0;
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Pred. No. 9.1e-10;
0; Mismatches 0;
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Pred. No. 9.1e-10;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50286
LENGTH: 922
                                                                                                                                                                                                     Sequence 50286, Application US/09791537 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-25
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US-09-791-537-50286
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US-09-855-754-21
; Sequence 21, Application US/09855754
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82.8%;
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Best Local Similarity 82.8%;
Matches 48; Conservative
82.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 24
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Best Local S
Matches 47
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Matches 4
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               APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT PILLING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION UNMBER: USO/09/855,754
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA PARABERTUSSIS, AND BORDETELLA PARABERTUSSIS, AND BORDETELLS, PARABERTUSSIS, AND BORDETELS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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85.2%; Pred. No. 3.1e-10;
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Pred. No. 2.5e-10;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-855-754-22; Sequence 22, Application US/09855754; GENERAL INFORMATION:
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BOURSAUX-EUDE, CAROLINE
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88.5%;
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Matches 46; Conserv
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Best Local Similarity
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BROBEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERRUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REPRENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
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                                                CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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ORGANISM: Bordetella bronchiseptica
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-855-754-16; Sequence 16, Application US/09855754; GENERAL INFORMATION:
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                                                                                                                                                              NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
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US-09-855-754-23
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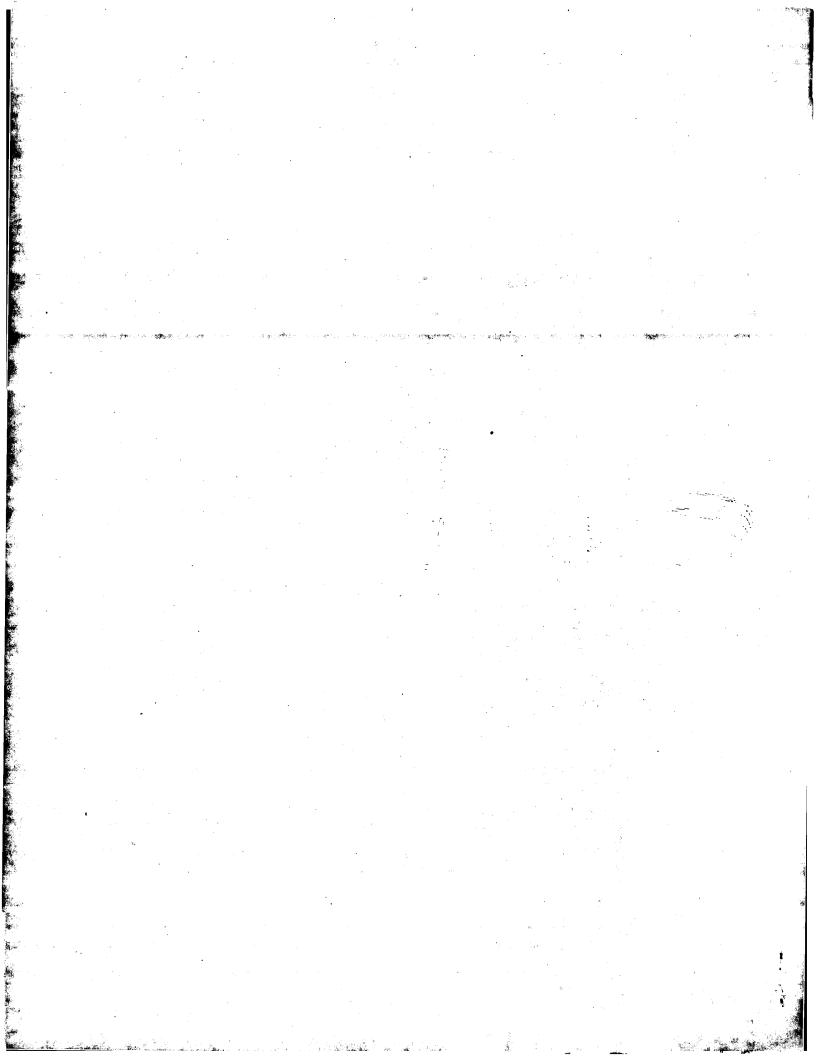
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENCYHH: 42
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
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Gaps 6; Query Match 82.0%; Score 223; DB 22; Length 42; Best Local Similarity 87.5%; Pred. No. 1.3e-08; Matches 42; Conservative 0; Mismatches 0; Indels

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Search completed: May 7, 2003, 17:21:58 Job time: 122.595 secs



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7, 2003, 16:48:21; Search time 28.293 Seconds (without alignments) 289.347 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPPQ......ORQPEAPAPQPPAGRELSAA 48
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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785622 Total number of hits satisfying chosen parameters: 785622 seqs, 170552221 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

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2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Appli Appli Appli Appli Appl Description Sequence Seguence Sequence Sequence Sequence 5-09-855-754B-17 5-09-855-754B-16 5-09-855-754B-23 5-10-282-122A-51012 5-09-855-754B-5 US-09-724-676A-84275 10-218-140-4170 SUMMARIES % Query Match Length D 257 257 257 249 248 240 240:5 202.5 135.5 135.5 135.5 135.5 129 Result

Sequence 84274, A Sequence 84274, A	Sequence 84278, A Sequence 84278, A Sequence 84280, A Sequence 84280, A	Sequence 84277, A Sequence 84277, A Sequence 84279, A			Sequence 09888, A Sequence 224, App Sequence 48029, A Sequence 9652, Ap
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US-09-724-676-84274 US-09-724-676A-84274	US-09-724-070-04278 US-09-724-676A-84278 US-09-724-676-84280 US-09-724-676A-84280	US-09-724-676-84277 US-09-724-676A-84277 US-09-724-676-84279	US-09-724-676A-84279 US-09-724-676-84276 US-09-724-676A-84276	US-09-949-016-10853 US-10-282-122A-51472 US-10-227-353-8	US-10-282-122A-09889 US-10-092-900A-224 US-10-282-122A-48029 US-09-949-016-9652
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ALIGNMENTS

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RESULT 1 US-09-855-754B-20 Sequence 20. Application US/09855754B Sequence 20. Application US/09855754B GENERAL INFORMATION: APPLICANT: BOOKSAUX EUDE, CAROLINE TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BROKHEREPTICE, THEIR USE IN DIAGNOSTICS, TITLE OF INVENTION: BROKHEREPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BROKHEREPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: 05/09/855,754B CURRENT FILING DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 25 SOSTWARE: PATCHIN VOF. 2.1 SEQ ID NO 20	; LENGTH: 48 ; TYPE: PRT ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-20 Query Match Query Match Best Local Similarity 100.0%; Score 272; DB 5; Length 48; Best Local Similarity 100.0%; Pred. No. 3.2e-11; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GAKAPPARKPAPQPGPPQPPQPPQRPQRPAPAPQPPAGRELSAA 48	RESULT 2 US-09-055-7548-14 Sequence 14, Application US/09055754B Sequence 14, Application US/09055754B GENERAL INFORMATION: APPLICANT: BORNSAUX. TITLE OF INVENTION: POLYPEDITIES CONTAINING POLYMORPHISMS OF THE REPEATED: TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN STILE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REPERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: 05/09/0855,754B CURRENT PILING DATE: 2001-05-16 PRIOR PELLING DATE: 2000-05-25
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US-09-855-754B-18
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN ATTLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-0000
CURRENT PELING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
RHOR APPLICATION NUMBER: 60/206,969
RHOR PRIOR APPLICATION NUMBER: 2001-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING VET: 2.1
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TITLE OF INVENTION: POLYMPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.5e-10;
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Pred. No. 2e-10;
                                                                                                                                                                                                                                0; Mismatches
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CURRENT FILING DAFE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-855-754B-15; Sequence 15, Application US/09855754B; GENERAL INFORMATION:
                                                                                                               ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF. NTOOLE
                                                                                                                                                                                ch 96.1%;
1 Similarity 98.0%;
48; Conservative
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nilarity 92.3%;
Conservative
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
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SOFTWARE: Patentin Ver.
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Best Local Similarity
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Best Local Similarity
Matches 48; Conserv
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US-09-855-754B-15
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US-09-855-754B-4
                                                SEQ ID NO 14
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                                                                                              TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BROWCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                  4
                                                                                                                       ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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  Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                             1 GAKAPPAPKPA----PQPGPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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92.3%; Pred. No. 1.2e-09;
ive 0; Mismatches 0;
Score 260; DB 5;
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-227-353-4
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GENERAL INFORMATION:
PPPLICANT: BOURSOUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 Sequence 4, Application US/10227353
Sequence 4, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
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95.6%;
92.3%;
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 92.33
Matches 48; Conservative
Query Match 95.6
Best Local Similarity 92.3
Matches 48; Conservative
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TELEPHONE:
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Matches 48; Conserv
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US-09-855-754B-21
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    SEQ ID NO 6
LENGTH: 922
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                                                                                                                                    Query Match
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APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTISSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENTIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPLCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRPPAPAPPAPAGRELSAA
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Pred. No. 2.8e-10;
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Pred. No. 3.3e-10;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
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PRIOR FILING DATE: 2000-05-25
                                                           PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
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                                         2001-05-16
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Best Local Similarity 85.7%;
Matches 48; Conservative
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82.8%;
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SEQ ID NO 19
LENGTH: 58
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hes 48; Conservative
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                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEO ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-855-754B-19
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US-09-855-754B-6
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Matches
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Gaps
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                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                         ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                   Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 257; DB 6;
Pred. No. 1.8e-09;
0; Mismatches 0;
                                                                                   Score 257; DB 5;
Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/460, 269C FILING DATE: 02-Jun-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/09855754B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703) 243-6333
; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-7548-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            Sequence 6, Appilcation US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 922 amino acids
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                                                                                 94.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                          48; Conservative
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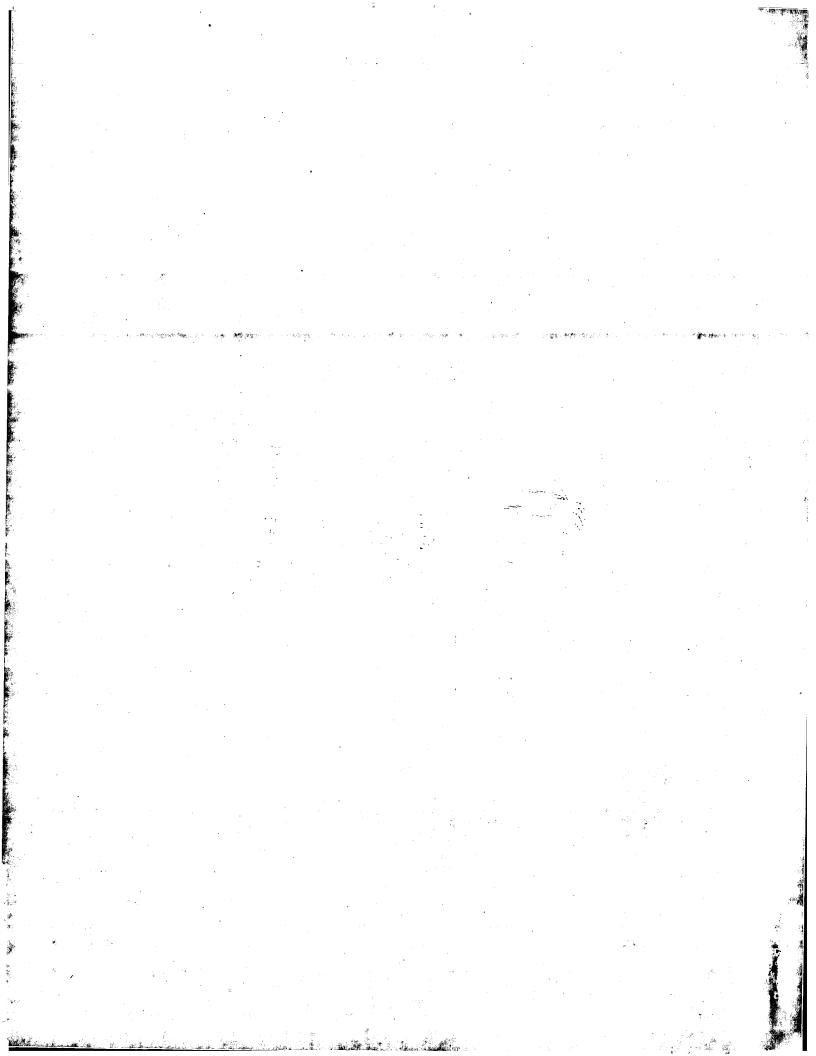
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US-09-855-754B-17
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US-09-855-754B-16
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US-09-855-754B-16
                                                                                                                 SEQ ID NO 17
LENGTH: 52
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LENGTH: 59
                                                                                                                                                                   TYPE: PRT
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POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDETELIA PERTUSSIS, BORDETELIA PARAPERTUSSIS, AND BORDETELIA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN IMMINOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-05-16
FILE REPERENCE: 2001-05-16
FILE REPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GUISO-WACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIESPICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 249; DB 5;
Pred. No. 9.9e-10;
0; Mismatches 2
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Pred. No. 1.2e-09;
0; Mismatches 2
                                        TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR US. TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                               91.5%;
88.5%;
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 85.2
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 46; Conserv
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US-09-855-754B-17
                                                                                                                                                                                                                                                           SEQ ID NO 21
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LENGTH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND STITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
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                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPRPAPQPGPQP----PQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                        Length 52;
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Pred. No. 3.7e-09;
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Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.4%; Scor. 78.3%; Pred. No. 3... 78.3%; O; Mismatches
                                                                                                                                                                                                                                                                                              0; Mismatches
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                      ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                89.78;
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.7
Matches 47; Conservative
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SOFTWARE: Patentin Ver. 2.
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
Matches 47; Conserv
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                            Query Match . 82.0%; Score 223; DB 5; Length 42; Best Local Similarity 87.5%; Pred. No. 3.9e-08; Matches 42; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPPQPPQPPQRPQREAPAPQPPAGRELSAA 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // Robert
forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind, Judith
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Carr, Grant
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:50 Job time: 29.293 secs



Sequence 18, Appl Sequence 50, Appl Sequence 50, Appl Sequence 14, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 23, Appl Sequence 76981, A Sequence 76981, A Sequence 11629, Sequence 11629, Sequence 24, Appl Sequence 2, Appl Sequence 11629, Sequence 11629, Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 78, Appl Sequence 6, Appl Sequence 11629, Sequence 6, Appl Sequence 6, Appl Sequence 2285, Appl Sequence 4, Appl Sequence 2285, Appl Sequence 1188, Appl Sequence 1318, Apl Se

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Sequence 21, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOUNSAUX-EUDE, CAROLINE
APPLICANT: BOUNSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE PEFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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2 US-09-855-754-18

2 US-09-855-754-19

2 US-09-855-754-10

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2 US-09-855-754-11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
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PRIOR FILING DATE: 2000-05-25
  NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3
SEQ ID NO 21
LENGTH: 52
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Sequence 22
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                     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-22
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US-09-791-537-37413
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gaps

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Length 52;

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SOFTWARE: PatentIn Ver.
    GENERAL INFORMATION:
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US-09-791-537-85698
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 192/99/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BORNSAUX EUDE, CAROLINE
APPLICANT: BORNSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 1.3e-10;
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Pred. No. 1.8e-12;
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US-09-791-537-37413
; Sequence 37413, Application US/09791537
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US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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                                                                                                                               Sequence 22, Application US/09855754 GENERAL INFORMATION:
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92.5%;
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52; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 54
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                                                                                                                                                                            APPLICANT: BOURSAUX-EUDE,
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Matches 49; Conserv
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US-09-855-754-22
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APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TILLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARES PAREIT PAREIT OF SEQ ID NOS: 153055

LENGTH: 911
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 1.6e-09;
0; Mismatches 2;
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Pred. No. 1.6e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261,210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 85698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 85688, Application US/09791537; GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-791-537-85698
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Best Local Similarity 92.5%;
Matches 49; Conservative (
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92.5%;
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Matches 49; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
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Best Local Similarity 84.5
Matches 49; Conservative
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 49; Conserv
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LENGTH: 922
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 120/99/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                Gaps
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGTELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGTHISPTICA, THEIR USE IN DIAGNOSTICS, AND INTELE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKVPPAPKPAPQPGPQP-----PQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                         Length 911;
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                                                                                                                      Score 259; DB 22;
Pred. No. 1.6e-09;
0; Mismatches 2;
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Pred. No. 1.9e-10;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEO ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 18
LENGTH: 56
                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754-19
                                                                                                                                                                                                                                                                                                                      US-09-855-754-18; Sequence 18, Application US/09855754; GENERAL INFORMATION:
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                                                                                                                    86.9%;
nilarity 92.5%;
Conservative 0
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86.0%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENOTH: 58
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                                                                                                                                                                49.
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SEQ ID NO 4
LENGTH: 911
                                                                                                                        Query Match
Best Local
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: MITHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTHARE: PATENTIN VERSION 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 120,709/855,754
CURRENT FILLING DATE: 2001-09-10
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 256; DB 21;
Pred. No. 2.5e-09;
0; Mismatches 3;
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Pred. No. 2.5e-09;
0; Mismatches 3;
84.5%; Pred. No. 2.3e-10; ive 0; Mismatches 3
                                                                                                                                                                                                 US-09-791-537-50285
; Sequence 50286, Application US/09791537
; GENERAL INFORMATION:
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US-09-791-537-50286
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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ilarity 84.5%;
Conservative
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ilarity 84.5%;
Conservative
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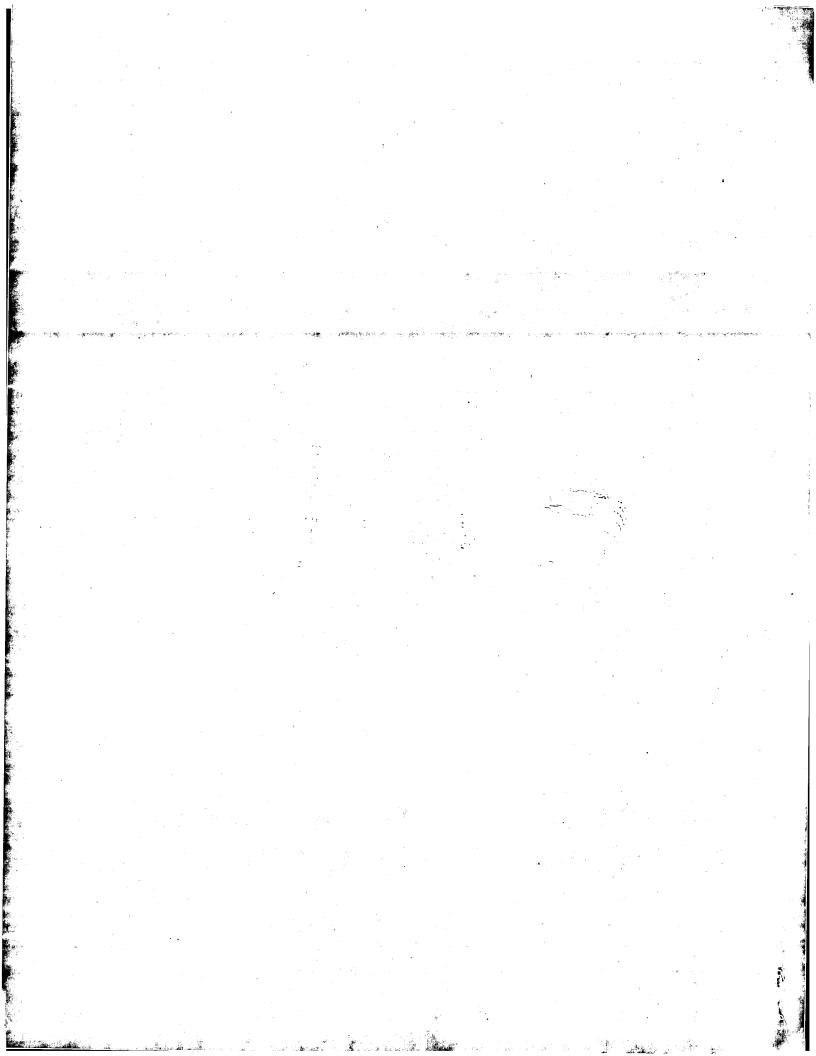
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LENGIH: 49
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LENGTH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDEFELLA PARAPERTUSSIS, AND BONDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOSTWARE: PATENTIN VET: 2.1
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PAPLICATION NUMBER: 06/206,969
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA PARABERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 59;
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Pred. No. 1.9e-09;
1; Mismatches 3;
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Pred. No. 5.8e-10;
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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88.58;
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l Similarity 81.4%;
48; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
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Best Local Similarity
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; ORGANISM: BO:
US-09-855-754-16
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LENGTH: 59
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEO ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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CURRENT FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 3e-09;
0; Mismatches 2;
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Pred. No. 4.7e-09;
1; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                             ORGANISM: Bordetella bronchiseptica
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US-09-855-754-17
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 86.8%;
Matches 46; Conservative (
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Best Local Similarity 88.9
Matches 48; Conservative
                                                                                                              NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
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US-09-855-754-23
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                                                                                                                                                                       ; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENCHH: 42
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
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Search completed: May 7, 2003, 17:22:08 Job time : 141.727 secs



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Sequence 22, April cation US/09855754B
GENERAL INFORMATION:
APPLICANT: BOUKSANA: EDGE, CARCLINE
APPLICANT: BOUKSANA: EDGE, CARCLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS,
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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PRIOR FILING DATE: 2000-05-25
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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APPLICANT: BOURSACX-EUDE, CAROLINE
APPLICANT: BOURSACX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEC ID NOS: 25
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 21
LENGTH: 52
                                                                                                         10081, A
3465, Ap
51472, A
7963, Ap
51470, A
2812, Ap
12363, A
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24873, A
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US-09-724-676-92543

US-10-156-92543

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US-10-282-122A-1472

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US-10-282-122A-48029

US-10-366-683-24873

US-10-282-122A-44931

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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
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US-10-227-353-4
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHIESPRICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 195/09/985,754B
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GUISO-MACLOUF, NICOLEA TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDEFELLA PERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNICABLICA, THEIR USE IN DIAGNOSTICS, AND IN FILLE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754B
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Pred. No. 1.7e-10;
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Pred. No. 2.7e-12;
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ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-22
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ilarity 92.5%;
Conservative
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96.3%;
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SOFTWARE: Patentin Ver. 2.1
                      PatentIn Ver. 2.1
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NUMBER OF SEQ ID NOS: 25
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                        Query Match
Best Local Similarity
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  NUMBERS PALS
SOFTWARE: PALS
SEQ ID NO 22
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                     APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                             22
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  Length 911;
                                                                                             1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
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ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                Indels
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Score 259; DB 5;
Pred. No. 1e-09;
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FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                  0; Mismatches
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APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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92.5%; Pred. No. 1
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                       Sequence 4, Application US/10227353 GENERAL INFORMATION:
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  86.9%;
illarity 92.5%;
Conservative
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Matches 49; Conserv
       Query Match
Best Local Similarity
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                             Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branic
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                           Score 256; DB 5;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 256; DB 6;
Pred. No. 1.6e-09;
0; Mismatches 3
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                                                                                                                                                                                         0; Mismatches
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APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
RFFFRENCE/DOCKET NUMBER: Popov-2
                                                                                                                                             Score 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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                                                                        ORGANISM: Borcetella parapertussis
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10227353 GENERAL INFORMATION:
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                                                                                                                                           85.9%;
84.5%;
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84.5%;
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                                                                                                                                                                Best Local Similarity 84.5
Matches 49; Conservative
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Best Local Similarity 84.59
Matches 49; Conservative
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                                                                                                                                             Query Match
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NIMBER: 2007/99/485,754B
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PINTILE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 02004-0516
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                                                                                                                                                                                                                                                                                                Length 56;
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Pred. No. 2.4e-10;
0; Mismatches 2
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Pred. No. 2.8e-10;
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-18
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PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754B-19
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Local Similarity 84.5%;
les 49; Conservative
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1 Similarity 86.0%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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Matches
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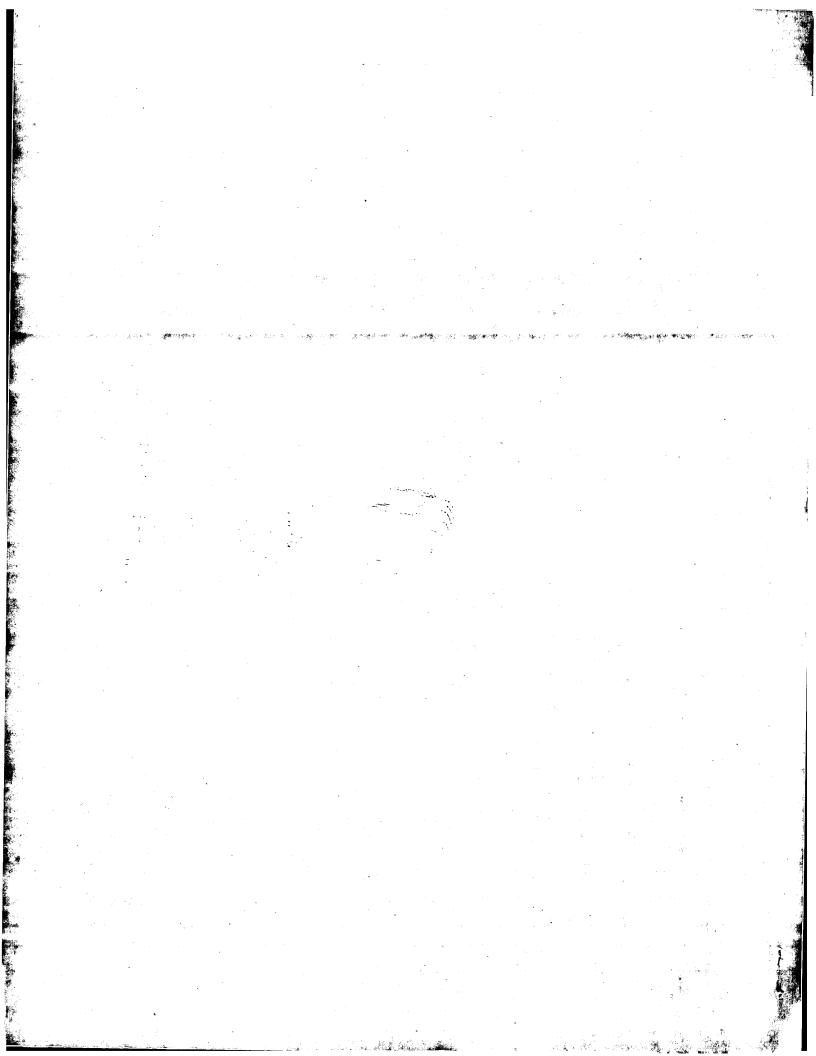
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CURRENT FILING DATE:
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LENGTH: 52
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LENGTH: 42
                                                                                                                                                                                  TYPE: PRT
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INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERPACTIN IN BONDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHIELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHIESPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
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Pred. No. 7e-10;
0; Mismatches 2; Indels
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1; Mismatches 3
                 TITLE OF INVENTION: REGIONS OF PERTACTIN IN ITILE OF INVENTION: BORDETELLA PRAPERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USS, TILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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PRIOR PLLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-20
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88.5%;
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Best Local Similarity 81.4%;
Matches 48; Conservative 1
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Best Local Similarity
Matches: 46; Conserv
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US-09-855-754B-16
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                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PELLING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BRONDETELLA PRARAPERTUSSIS, AND BORDSTELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 49;
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                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                80.0%; Score 238.5; DB 5
86.8%; Pred. No. 3.4e-09;
iive 0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                            60/206,969
                                                                                                                                                                                                              ORGANISM: Bordetella bronchiseptica US-09-855-7548-14
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2001-05-16
                      PRIOR APPLICATION NUMBER: 60/3 PRIOR FILING DATE: 2000-05-25
                                                                         NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                Query Match 80.0 Best Local Similarity 86.8 Matches 46; Conservative
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Best Local Similarity
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us-09-855-754b-21.rapn

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LE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                      Gaps
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SOFTWARE: PatentIn version 3.1
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Pred. No. 4.5e-07;
0; Mismatches 1; Indels
                                                                             Length 42;
                                                                                                                  1; Indels
                                                                           Score 217; DB 5;
Pred. No. 7.4e-08;
0; Mismatches 1
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CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                       Application US/10282122A
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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NG DATE: 2000-10-23
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NG DATE: 2000-11-27
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: 2000-05-26
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PRIOR FILING DATE: 2001-02-16
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                         Query Match 72.8%;
Best Local Similarity 78.8%;
Matches 41; Conservative
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Best Local Similarity 78.8%;
Matches 41; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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: Zamudio, Carlos
: Malone, Cheryl
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1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                      GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-21
US-09-855-754-19
US-09-791-537-50286
US-09-855-754-6
US-09-855-754-15
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Match Length
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Sequence 22, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BUCKSAUX-EUDE, CAROLINE
APPLICANT: BUCKSAUX-EUDE, CAROLINE
APPLICANT: GUISSO-MACLOUF, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: DRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: DRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: DRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 2040-05-25
CURRENT FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 22
LENGTH: 54
TYPE: PAT
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CURRENT FILING DATE:
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US-09-855-754-15
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
                                                                                                                                                             APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2002-09-10
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1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA
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Pred. No. 8.7e-11;
0; Mismatches 5;
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Pred. No. 2.7e-12;
0; Mismatches 0;
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; Sequence 50286, Application US/09791537
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PRIOR FILING DATE: 2000-05-25
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                                                                                                 Sequence 21, Application US/09855754 GENERAL INFORMATION:
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Local Similarity 96.3%;
nes 52; Conservative
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SOFTWARE: Patentin Ver. 2.1
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nes 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver.
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LENGTH: 58
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APPLICANT: Dancer, Derek

APPLICANT: Dancer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

TITLE OF INVENTION: MTHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SEQ ID NO 50286

LENGTH: 922

TYPE
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TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVERTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVERTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVERTION: IMMUNGEN: COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PELING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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FILE REPREBLY: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 9.3e-10;
0; Mismatches 5;
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Pred. No. 9.3e-10;
0; Mismatches 5;
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US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
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1 Similarity 84.5%;
49; Conservative
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ilarity 84.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PELLING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDEFELLA
TITLE OF INVENTION: BONDEFELLA PARAPERTUSSIS, AND BONDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2201-09-10
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Pred. No. 2.7e-09;
0; Mismatches 2;
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Pred. No. 3.4e-10;
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US-09-855-754-18
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US-09-855-754-16
; Sequence 16, Application US/09855754
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                                                                                                                                   Sequence 4, Application US/09855754 GENERAL INFORMATION:
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87.58;
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Best Local Similarity 89.1%;
Matches 49; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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US-09-855-754-18
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Balonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 261/210
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GENERAL INFORMATION:
APPLICANT: BLOOMIX, Inc.
APPLICANT: Debe, Derek
APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 85598
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                                                                                                                                                                                                                                                                       2; Indels
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Pred. No. 2.7e-09;
0; Mismatches 2;
                                                                                                                                                                                                                        Score 258; DB 22;
Pred. No. 2.3e-10;
0; Mismatches 2;
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Pred. No. 2.7e-09;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella bronchiseptica US-09-791-537-37413
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  60/206,969
                                                                                                                                                        ORGANISM: Bordetella bronchiseptica
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89.1%;
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1 Similarity 89.1%;
49; Conservative
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ilarity 89.1%;
Conservative
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
                                       NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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Best Local
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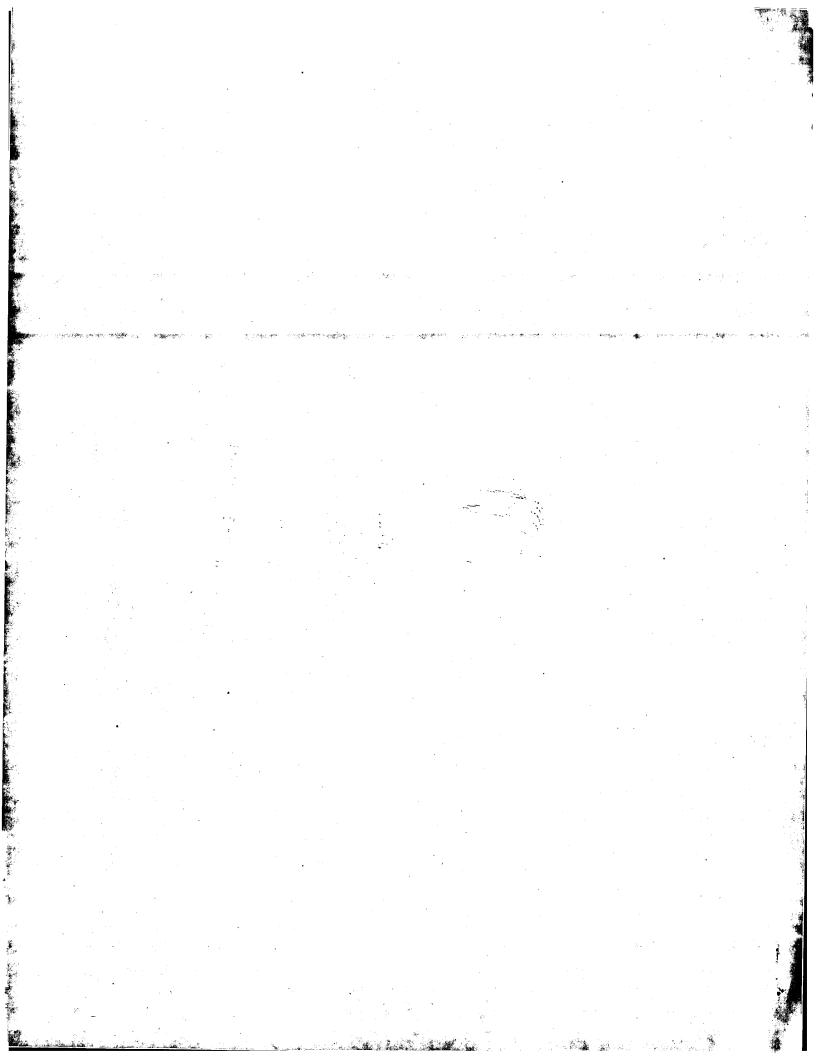
IMMUNOGENIC COMPOSITIONS

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LE REFERENCE: 03495-0206-00
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TITLE OF INVENTION:
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US-09-855-754-23
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US-09-855-754-17
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Matches 4
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                                       APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHELA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BORDETELIA PARABERTUSSIS, AND BORDETELIA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 1e-09;
0; Mismatches 2; Indels
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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US-09-855-754-14
Sequence 14, Application US/09855754
GENERAL INFORMATION:
                        CAROLINE
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81.7%;
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1 Similarity 85.2%;
46; Conservative
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Best Local Similarity 81.77
Matches 49; Conservative
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Best Local Similarity
Matches 46; Conserv
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APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERIOSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERIOSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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FILE REFERENCE: 03495-0206-00000
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Pred. No. 7.9e-09;
1; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 49
                                                                                                                                                                                                                                                     .; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 85.7%;
Matches 48; Conservative
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05
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Search completed: May 7, 2003, 17:22:08 Job time : 136.794 secs



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APPLICANT: BORSAUX-EUDE, CAROLINE
APPLICANT: BORSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-25
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LENGTH: 54
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Sequence 4
Sequence 1
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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S-09-855-754B-23
S-10-282-122A-51012
S-09-855-754B-5
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    785622 seqs, 170552221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                US-09-855-754B-22
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                          Scoring table:
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155.5
155.5
155.5
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249.5
248
237.5
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                                                                                                                                                                                                                                                     Searched:
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                                                                                       Run on:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABETRISSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,7548
CURRENT FILING DATE: 2001-05-16
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ALIGNMENTS
                                                                                                                                     Sequence 22, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILIND DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Aprlication US/09855754B GENERAL INFORMATION:
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US-09-855-754B-22
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US-10-227-353-6
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                              Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BRONDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONDEFILA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
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1.1e-10;
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Pred. No. 4.2e-12;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                                                                                   ORGANISM: Bordetella bronchiseptica
US-09-855-7548-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bordetella bronchiseptica
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US-09-855-754B-6
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96.3%;
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PRIOR FILING DAME: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEr. 2.1
                                                                                                                                                            Query Match
Best Local Similarity 96.39
Matches 52; Conservative
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SOFTWARE: Patentin Ver.
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver.
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GENERAL INFORMATION
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US-09-855-754B-19
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US-09-855-754B-6
                                      SEQ ID NO 21
LENGTH: 52
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                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BONGHISHLA PARAPERTUSST
TITLE OF INVENTION: BORDETELLA PARAPERTUSST
TITLE OF INVENTION: BORDETELLA PARAPERTUSST
TITLE OF INVENTION: BORDETELLA PARAPERTUSST
TITLE OF INVENTION: BRONCHISER...
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                                                                                       1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                              4.
                                                                                                                                                                                                                                        Sequence 6, Application US/10227353
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 922;
  Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.5%; Score 265; DB 6;
84.5%; Pred. No. 6.3e-10;
live 0; Mismatches 5
Score 265; DB 5;
Pred. No. 6.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/460,269C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 243-6410
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SEQUENCE CHARACTERISTICS
85.5%;
1larity 84.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Best Local Similarity
    Query Match
Best Local Similarity
Matches 49; Conserv
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SEQUENCE
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITILE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITILE OF INVENTION: BEGIONS OF PERTAPORTION IN BONDETELLA PERTUGSIS, AND BONDETELLA PERTUGSIS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INFITE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFFWARE: PATENTIN VET. 2.1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                              Length 52;
                                                                                                                                                                                                                                                                        83.2%; Score 258; DB 5; L
nilarity 89.1%; Pred. No. 2.9e-10;
Conservative 0; Mismatches 2;
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llarity 89.1%; Pred. No. 1.7e-09;
Conservative 0; Mismatches 2
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
                                     CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-4
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MEDIUM TYPE: Floppy disk
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
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hes 49; Conserv
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LENGTH: 911
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US-10-227-353-4
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Matches
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND JITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0306-00000
CURRENT PARICATION NUMBER: 02/09/855,754B
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 258; DB 6;
Pred. No. 1.7e-09;
0; Mismatches 2
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Pred. No. 4.1e-10;
0; Mismatches 5
                                                              APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEBOVITZ, RICHARD M.
REGISTRATION NUMBER: 37,067
REFERENCE/POCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQ ID NO: 4: US-10-227-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-855-754B-18; Sequence 18, Application US/09855754B; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-18
                                                                                                                                                                                                                                                                                                              (703) 243-6333
                                                                                                                                                                                                                                                                                                                                     243-6410
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LENGTH: 911 amino acids
TYPE: amino acid
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89.1%;
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Best Local Similarity 87.5%;
Matches 49; Conservative (
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INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 89.18
Matches | 49; Conservative
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SOFTWARE: Patentin Ver.
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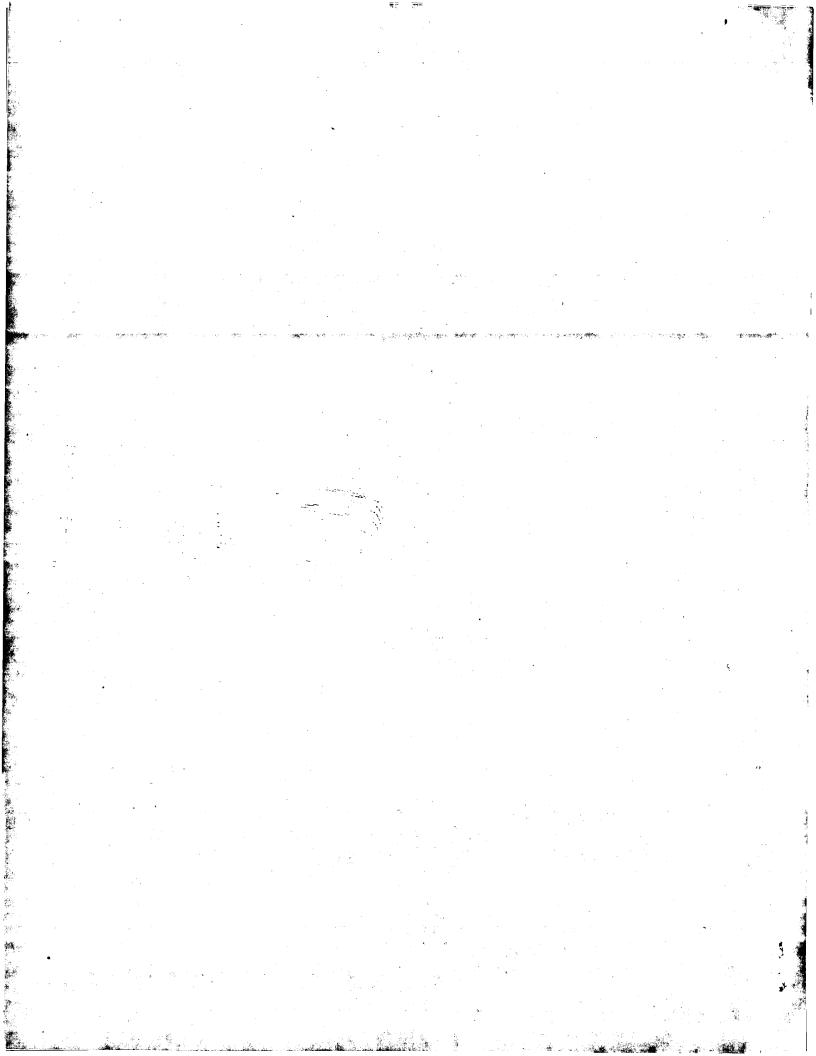
2001-05-16

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CURRENT FILING DATE:
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                                                                                                                                                                                           TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA,
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION UNMERS: 028/09/855,754B
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENTIC, COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENTIC, COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
     POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKVPPAPKPAPQPGPQP-----PQP-PQPPQPPQPQPQPQPQPPQPPAGRELSAA 54
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS RILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-16-16
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 59;
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Pred. No. 1.1e-09;
1; Mismatches 3;
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Pred. No. 1.2e-09;
0; Mismatches 2;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,969
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81.7%;
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Best Local Similarity 85.2%;
Matches 46; Conservative
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2:1
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Best Local Similarity 81.7
Matches 49; Conservative
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TRNGTH: 59
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APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BONDETELLA PARAPERRUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND FILLE OF INVENTION: IMMUNGEBRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/006-056
PRIOR APPLICATION NUMBER: 60/206,969
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APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: PORTEPETIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPRESENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/655,754B
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                                                                                                                                                                                                                                                                                           Length 49;
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85.7%; Pred. No. 8.5e-09;
ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                           Query Match 76.6%; Score 237.5; DB 5; Best Local Similarity 83.6%; Pred. No. 5.7e-09; Matches 46; Conservative 0; Mismatches 2;
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PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09855754B GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
                                                         NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 49
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Best Local Similarity
Matches 48; Conserv
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                                                                                                               Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                               12;
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Pred. No. 7.3e-07;
0: Mismatches 1: Indels 12;
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                                                                                                                                              1 GAKVPPAPKPAPQPGPPQPPQPPQPPQPPQPQPQPGPEAPAPPAGRELSAA 54
                                                                         Length 42;
                                                                                                             1; Indels
                                                                       Score 216; DB 5;
Pred. No. 1.2e-07;
0; Mismatches 1
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                           Sequence 51012, Application US/10282122A
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/191,078
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APPLICATION NUMBER: 60/206,848
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PPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
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Best Local Similarity 75.9%;
Matches 41; Conservative
                                                                     Query Match 69.7%;
Best Local Similarity 75.9%;
Matches 41; Conservative
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Zyskind, Judith
Wall, Daniel
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Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
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Trawick, John
Carr, Grant
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Search completed: May 7, 2003, 17:27:51 Job time : 31.8296 secs



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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-4
US-10-227-353-4
US-09-855-7548-20
US-09-855-7548-20
US-09-855-7548-20
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27	30 31	3 3 3 4 3 3 4	35 36 37	38 40 40	4444

ALIGNMENTS

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TITLE OF INVENTION: POLYEPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI N BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPETICAL PARAPETER PARAPETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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1jarity 100.0%; Pred. No. 1.7e-14;
Conservative 0; Mismatches 0;
; Sequence 16, Application US/09855754B; GENERAL INFORMATION:
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                                                                                                                 CAROLINE
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SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 16
LENGTH: 59
TYPE: PRT
                                                                                                                 APPLICANT: BOURSAUX-EUDE,
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Best Local Similarity
Matches 59; Conserv
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TYPE: PRT

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APPLICANT: GUISO-MACIOEF NICOLE TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PREPACTION IN BORDETELLA PERFUSSIS, TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNICANI COMPOSITIONS INVENTION: IMMUNICANI COMPOSITIONS INVENTION: IMMUNICANI COMPOSITIONS TITLE OF INVENTION: IMMUNICANI COMPOSITIONS CURRENCE: 03495-0206-00000 CURRENT PILING DATE: 2010-65-16 PRIOR PRIOR PELING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA DEPRTACTION: RORDETELLA DEPARTACTION: RORDETELLA DEPART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 298.5; DB 6;
Pred. No. 3.7e-11;
0; Mismatches 0;
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Pred. No. 1.2e
0; Mismatches
                                                                    APPLICATION NUMBER: US/08/460, 269C
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-227-353-6
                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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US-09-855-754B-18
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                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                        FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.3%;
95.0%;
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQUENCE CHARACTERISTICS
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ilarity 91.7%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
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Matches 57; Conserv
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Matches 55; Conserv
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LENGTH: 56
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TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2001-05-16
PRIOR PRILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING VET. 2.1
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 922;
                                                                                                                                                                                                                                                                                    Length 58;
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STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                        .1e-12;
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APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 298.5;
Pred. No. 3.7
                                                                                                                                                                                                                                                                                 Score 298.5;
Pred. No. 7.1
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                                                                                                                                                                 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella parapertussis
US-09-855-754B-6
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95.0%;
                                                                                                                                                                                                                                                                                 87.3%;
ilarity 95.0%;
Conservative
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CORRESPONDENCE ADDRESS
                                           Patentin Ver. 2.1
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          NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
Matches 57; Conserv
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Best Local Similarity
Matches 57; Conserv
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US-10-227-353-6
                                                                           SEQ ID NO 19
LENGTH: 58
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Length 922;

DB 6;

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Length 56;

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COUNTRY: USA
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR TELING DATE: 2001-05-16
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GUISO-MACLOUF, MICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: HAMONOGRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
                                                                                                                                                                                                                                                                                                                                                         Length 52;
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hes 0;
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Pred. No. 4.6e-11;
0; Mismatches 0;
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Pred. No. 4.9e
0; Mismatches
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,7
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                             ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,969
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ilarity 85.0%;
Conservative
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Best Local Similarity 88.1%;
Matches 52; Conservative
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                    Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CIȚ: ARLINGTON
                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.2%; Score 267.5; DB 6;
85.0%; Pred. No. 2.7e-09;
11ve 0; Mismatches 0;
                                                                                    DB 5;
                                                                                  Score 267.5; DB 5
Pred. No. 2.7e-09;

 Mismatches

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REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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GENERAL INFORMATION:
PPPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 243-6333
TELEFAR, (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 911 amino acids
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                                                                                    78.2%;
85.0%;
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Best Local Similarity 85.08
Matches 51; Conservative
                                                                                  Query Match
Best Local Similarity 85.08
Matches 51; Conservative
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CURRENT FILING DATE:
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LENGTH: 42
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                                                                                                                      SEQ ID NO 21
LENGTH: 52
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FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03455-026-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 САКАРРАРКРАРОРСРОРСРОРСРОРСРОРРОРРОР-РОРРОКРЕАРАРОРРАСКЕЦSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
IMMUNOGENIC COMPOSITIONS
                         REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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Pred. No. 8.2e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 249.5; DB 5
Pred. No. 6.1e-09;
1; Mismatches 3
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYPEPTIDES CONTAINING POLYPEPTIDES CONTAINING POLYPEPTIDES CONTAINING POLYPEPTIDE OF INVENTION: BRONGHIGEPTICA, THEIR US; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS; FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORCANISM: Bordetella bronchiseptica
US-09-855-754B-22
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Best Local Similarity 81.7%;
Matches 49; Conservative 1
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Best Local Similarity 80.0%;
Matches 48; Conservative
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PRIOR FILING DATE: 2000-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 3
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; ORGANISM: Bord
US-09-855-754B-14
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                                                                                                                                                                                                                                                                                                                             LENGTH: 54
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                                                                                                                                                                                                                                                                                                      SEQ ID NO 22
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PEGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDETSPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSCHIC COMPOSITIONS FILLS REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR FILLING DATE: 2001-05-25
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Pred. No. 2e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      Score 242.5; DB 5;
Pred. No. 1.6e-08;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-20
                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09855754B GENERAL INFORMATION:
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2001-05-16
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Best Local Similarity 78.3%;
Matches 47; Conservative
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Best Local Similarity 81.4%;
Matches 48; Conservative
                          PRIOR APPLICATION NUMBER: 60/3 PRIOR FILING DATE: 2000-05-25
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                                                 PRIOR FILING DATE: 2000-05-:
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 203.5; DB 6; Length 768;
Pred. No. 1.8e-05;
1; Mismatches 0; Indels 17; Gaps
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                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                               Score 203.5; DB 5; Length 42;
Pred. No. 3.2e-06;
1; Mismatches 0; Indels 17;
                                                                                                                                                                                                                                                                                                                 Sequence 51012, Application US/10282122A GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/230,347
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                               Query Match 59.5%;
Best Local Similarity 69.5%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /amamoto, Robert
forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
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Best Local Similarity 69.5 Matches 41; Conservative
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arr, Grant
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Search completed: May 7, 2003, 17:27:47 Job time: 34.7768 secs

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Sequence 16, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOUKSAUX-EUDE, CAROLINE
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159.F
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183
178.5
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-09-380-693A-49 US-09-380-693A-48 US-09-380-693A-38 US-09-380-693A-51 US-09-380-693A-51 US-09-380-693A-51 US-09-380-693A-51 US-09-380-693A-50 US-09-380-693A-50 US-09-380-693A-50 US-09-380-693A-50 US-09-380-693A-50 US-09-380-693A-50 US-09-417-507-22215 US-09-417-507-22215 US-09-417-507-22036-6 US-09-417-507-25036

Sequence 15, Appl Sequence 85698 A Sequence 4, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 21274 A Sequence 31, Appl Sequence 2217, A Sequence 31, Appl Sequence 2211, A Sequence 31, Appl Sequence 2211, A Sequence 2213, Appl Sequence 233, Appl Seq

US-09-855-754-15 US-09-791-537-37413 US-09-791-537-85698 US-09-855-754-22 US-09-855-754-21 US-09-855-754-21 US-09-855-754-21 US-09-855-754-20 US-09-855-754-20 US-09-855-754-20 US-09-855-754-20 US-09-855-754-20 US-09-91-537-76981 US-09-791-537-76981 US-09-791-537-34443 US-09-791-537-112007 US-09-791-537-112007 US-09-791-537-11629 US-09-791-537-11629

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GENERAL INFORMATION:
CHORACLINE
APPLICANT: BOUGSAUX-EDDE, CAROLINE
APPLICANT: BOUGSAUX-EDDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOEBRIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOEBRIC COMPOSITIONS
TITLE OF INVENTION IMMUSER: US/09/855,754
CURRENT APPLICATION NUMBER: 00/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN Ver. 2.1
SEQ ID NO 16
LENGTH: 59
TYPE: PRT

CORRANTEM: Bordetella bronchiseptica
US-09-855-754-16

COMETY MATCH

MATCHES 59; CONSELVATIVE 0; MISMATCHES 0; Indels 0; Gaps 0;
MATCHES 59; CONSELVATIVE 0; MISMATCHES 0; Indels 0; Gaps 0;
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1 GAKAPPAEKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59

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Sequence 16, Appl Sequence 19, Appl Sequence 50286, A Sequence 6, Appli Sequence 18, Appli Sequence 17, Appl

US-09-855-754-16 US-09-855-754-19 US-09-791-537-50286

US-09-855-754-6 US-09-855-754-18 US-09-855-754-17

52 922 922 56 56

342 298.5 298.5 298.5 294.5

Description

SUMMARIES

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Query Match Length

Result

3;

Gaps

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PRECIOUS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNOGENETICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
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    САКАРРАРКРАРОРСРОРСРОРСРОРОРОРОРРОРРОРОРО РЕАРАРОРРАСКЕ СВАА 59

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  REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA BORDCHIELA BORDCHIELA THEIR USE IN DIAGNOSTICS, AND IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 298.5; DB 22;
Pred. No. 3.8e-11;
0; Mismatches 0;
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BORDETELLA PARAPERTUSS; TITLE OF INVENTION: BRONCHISEPTICA, THEIR (1) TITLE OF INVENTION: IMMUNOGENIC COMPOSITION; FILE REFERENCE: 03495-0206-00000; CURRENT FILING DATE: 2001-09-10; PRIOR APPLICATION NUMBER: 60/206,969; PRIOR FILING DATE: 2000-05-25
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US-09-855-754-18
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91.7%;
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95.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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Best Local Similarity
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US-09-855-754-17
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNIOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 02009-09-10
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 3.7e-12;
); Mismatches 0;
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Pred. No. 3.8e-11;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50286
LENGTH: 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-791-537-50286; Sequence 50286, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica
                                                                                                                                                 Sequence 19, Application US/09855754 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
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illarity 95.0%;
Conservative
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PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 95.09
watches 57; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Best Local Similarity
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US-09-855-754-19
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APPLICANT: Bioiomix, Inc.
APPLICANT: Bioiomix, Inc.
APPLICANT: Bioiomix, Inc.
APPLICANT: Daider, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SSOTUARE: Patentin version 3.0
LENGTH: 911
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA, PARAPERTUSSIS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR US IN DIAGNOSTICS, AND IN FILE REFERBNCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 05/01-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                     9; Gaps
                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAFKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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Pred. No. 3.6e-09;
0; Mismatches 0; Indels 9;
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Pred. No. 3.6e-09;
0; Mismatches 0;
         85.0%; Pred. No. 3.6e tive 0; Mismatches
                                                                                                                                                                                                                                       Sequence 85698, Application US/09791537 GENERAL INFORMATION:
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US-09-791-537-85698
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US-09-855-754-4
; Sequence 4, Application US/09855754
; GENERAL INFORMATION:
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Best Local Similarity 85.0%;
Matches 51; Conservative
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Best Local Similarity 85.0%;
Matches 51; Conservative
                                 51; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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         Best Local Similarity
Matches 51; Conserv
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US-09-791-537-85698
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GENERAL INFORMATION:
APPLICANT: Bloomin. Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: BLOOMIN. THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VETSION 3.0
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GENERAL INFORMATION:
APPLICANT: BOURSALONE:
CAROLINE
APPLICANT: BOURSALONE:
CAROLINE
APPLICANT: GUISO-MACLOUF, CAROLINE
APPLICANT: GUISO-MACLOUF, CAROLINE
APPLICANT: GUISO-MACLOUF, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FALLING DATE: 2001-09-10
PRIOR PLILAGION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 2.6e-11;
0; Mismatches 0; Indels
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Pred. No. 3.1e-10;
0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
                                                                                                                                                               ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
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1 Similarity 85.0%;
51; Conservative
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1 Similarity 88.1%;
52; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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; ORGANISM: Borde
US-09-791-537-37413
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LENGTH: 911
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TITLE OF INVENTION:
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                                                 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUS CONDOCURRENT APPLICATION NUMBER: 92/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABETRUSSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: USA(09/955,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN DENDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 4.5e-
1; Mismatches
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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81.7%;
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SEQ ID NO 22
LENGTH: 54
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 48; Conserv
GENERAL INFORMATION
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US-09-855-754-22
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREGIONS OF PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: AND MANUGGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                  70.9%; Score 242.5; DB 2
81.4%; Pred. No. 1.2e-08;
tive 1; Mismatches 3
IMMUNOGENIC COMPOSITIONS
                FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
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PPLICATION NUMBER: 60/206,969
ILING DATE: 2000-05-25
                                                                                                  PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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US-09-855-754-20
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EDUB, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUISO-MACLOUF, NICOLE
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 52
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Matches 47; Conservative
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NUMBER OF SEQ ID NOS: 24
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SOFTWARE: Patentin Ver
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Matches 48; Conserv
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US-09-855-754-23
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LENGTH: 48
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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5-09-855-7548-22
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Sequence 51470, A Sequence 9652, Ap					Sequence 248/3, A Sequence 84275, A Sequence 84275, A Sequence 84274, A
US-10-282-122A-51470 US-09-949-016-9652 US-09-949-016-6756	US-60-423-586-80 US-60-427-194-80 US-09-724-676-92543	US-09-724-676A-92543 US-10-366-683-28564 US-10-419-128-28564	US-10-282-122A-48029 PCT-US02-36123-2812 US-10-282-122A-66157	PCT-US02-36123-2814 US-10-417-886-7963 US-10-36-683-24873	US-10-419-128-248/3 US-09-724-676-84275 US-09-724-676A-84275 US-09-724-676-84274
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ALIGNMENTS

on US/09855754B UDE, CAROLINE LIOUE, NICOLE NICOLE NICOLE REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS, BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INMUNCENIC COMPOSITIONS IMMUNCENIC COMPOSITIONS 2001-05-16 2001-05-16 BER: 60/206,969 11. 2.1	DB 5; Length 52; 1e-12; 0; Indels 0; Gaps 0; APAPQPPAGRELSAA 52 1 HAPQPPAGRELSAA 52	n US/09855754B UDE, CAROLINE LOUE, NICOLE OLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED EXCITORS OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA BORNCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN IMMUNGENIC COMPOSITIONS -0206-00000 UNDER: US/09/855,754B 2001-05-16 BER: 60/206,969
RESULT 1 US-99-855-754B-15 Sequence 15. Application US/09855754B SEQUENCE INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDETELA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORNCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS TITLE REPEATED CURRENT APPLICATION NUMBER: 02/09/855,754B PRIOR FILING DATE: 2001-05-16 PRIOR FILING DATE: 2001-05-16 PRIOR FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 25 SOFTWARE: PATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN FILING DATE: 2001-05-25 SEQ ID NO 15 LENGTH: 52 THEN FILING DATE: 2001-05-25 SOFTWARE: DATE: DATE: 2001-05-25 SOFTWARE: DATE: 2001-05-25 SOFTWARE: DATE: 2001-05-25 SOFTWARE: DATE: 2001-05-25 SOFTWARE: BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 LENGTH: 52 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER PRIOR BATCHILIN VET. 2.1 SEQ ID NO 15 THEN EPPER	Query Match 100.0%; Score 297; DB 5; Length 5; Best Local Similarity 100.0%; Pred. No. 2.1e-12; Matches 52; Conservative 0; Mismatches 0; Indels Oy 1 GAKAPPAPKRAPQPGPQPPQPPQPPQPPQRPPQRPPGRAPAPQPPAGRELSAA	RESULT 2 US-09-855-754B-4 Sequence 4. Application US/0985554B Sequence 4. Application US/0985554B GENERAL INFORMATION: APPLICANT: BOUKSAUX EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT FILING DATE: 2001-05-056,969 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25

Sequence

Sequence Sequence

US-10-017-161-1982 US-10-224-999A-3465 US-10-282-122A-51472 US-10-156-761-12544

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; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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US-09-855-754B-6
Sequence 6, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSANX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-18
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Best Local Similarity 89.7%;
Matches 52; Conservative (
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92.9%;
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                                                                                                                                                                                                                                                                               SEQ ID NO 18
LENGTH: 56
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                    Length 911;
                                                                                                                                                              Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Score 297; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 52; Conservative 0; Mismatches 0;
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FILING DATE: 02-Jun-1995
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APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
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US-09-855-754B-18
Sequence 18, Application US/09855754B
; GENERAL INFORMATION:
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                                                                                  ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-227-353-4
; Sequence 4, Application US/10227353
; GENERAL INFORMATION:
    APPLICANT: CLARE, JEFFREY J.
    ROMANOS, MICHAEL
    ROMANOS, WICHAEL
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 4
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Best Local Similarity
Matches 52; Conserve
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPECTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIESPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: INMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PRIOR PAPE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.1
             THE REPEATED
TITLE OF INVENTION: POLICY AND SECURTAINING POLYMORPHISMS OF THE REI TITLE OF INVENTION: POLICY OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA AND BORDETELLA TITLE OF INVENTION: BORNETIELLA PARABERUSISIS, AND BORDETELLA TITLE OF INVENTION: BORNETIELLA PRAFER TOSE IN DIAGNOSTICS, AND ITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: MUMBER: US/09/855,754B
CURRENT FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PALEALIN VOIS: 21
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Pred. No. 1.4e-11;
0; Mismatches 0;
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Pred. No. 1.2e-11;
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91.2%;
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85.0%;
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Best Local Similarity 96.23
Matches | 51; Conservative
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Best Local Similarity 85.09
Matches 51; Conservative
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SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
                                                                                                   APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUE
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US-09-855-754B-14
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                  Length 922;
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STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 284; DB 6;
Pred. No. 7.9e-11;
0; Mismatches 0;
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Pred. No. 7.9e-11;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEDOVILE, RICHARD M.
REGISTRATION NUMBER: 37,067
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-227-353-6
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                                                                                                                                                                                        ; ORGANISM: Bordetella parapertussis
US-09-855-754B-6
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-227-353-6; Sequence 6, Application US/10227353; GENERAL INFORMATION:
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llarity 89.7%;
Conservative
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Best Local Similarity 89.7%;
Matches 52; Conservative
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CORRESPONDENCE ADDRESS:
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mes 52; Conserv
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Matches
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                                                                          APPLICANT: GUÍSO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
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Pred. No. 8.6e-11;
0; Mismatches 0
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Pred. No. 1.5e-10;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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US-09-855-754B-16
; Sequence 16, Application US/09855754B
; GENERAL INFORMATION:
Sequence 17, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Bordetella bronchiseptica
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PRIOR FILING DATE: 2000-05-25
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CURRENT FILING DATE:
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; ORGANISM: Bord
US-09-855-754B-22
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,

TITLE OF INVENTION: BORDETELLA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMONGENIC COMPOSITIONS

TITLE OF INVENTION: IMMONGENIC COMPOSITIONS

FILE REPERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754B

PRIOR APPLICATION NUMBER: 00/206,969

PRIOR FILING DATE: 2001-05-16

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 25

SEQ ID NOS: 25

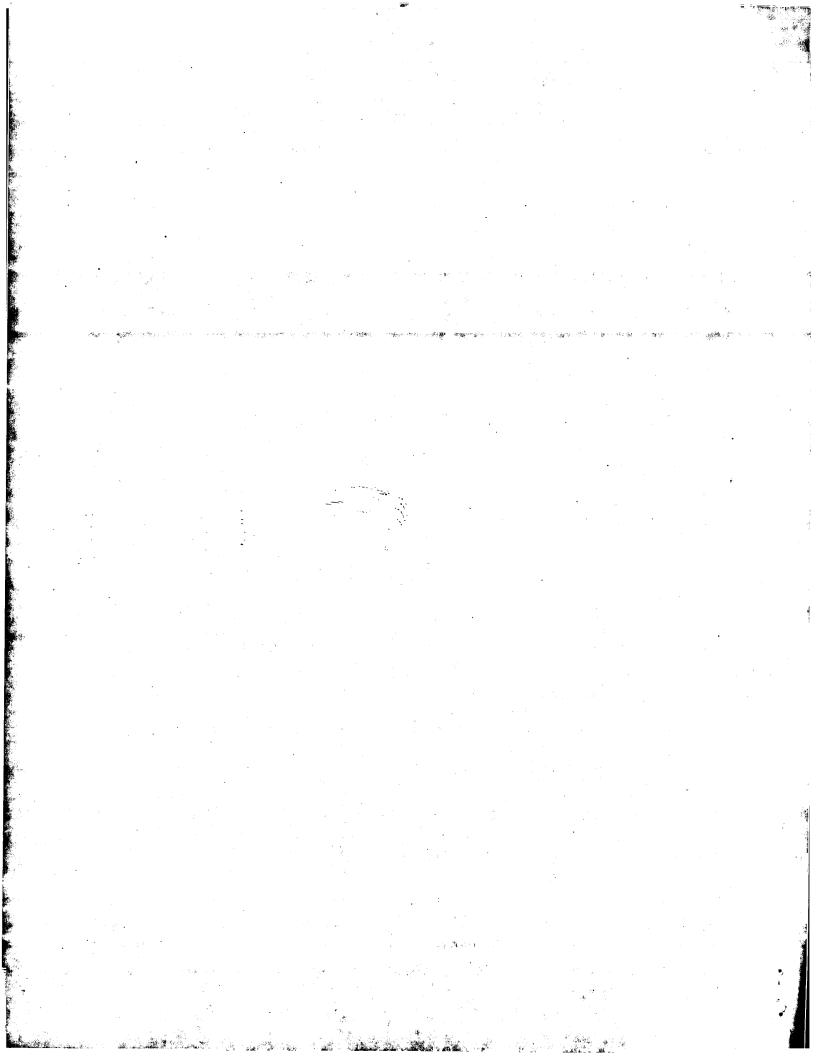
LENGRA:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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US-09-855-754B-21
: Sequence 21. Application US/09855754B
: Sequence 21. Application US/09855754B
: Sequence 21. Application:
: APPLICANT: BOURSAUX-EUDE, CAROLINE
: APPLICANT: BOURSAUX-EUDE, NICOLE
: TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
: TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERUSSIS,
: TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
: TITLE OF INVENTION: IMMUOGENIC COMPOSITIONS
: FILE REFERENCE: 03495-0206-00000
: CURRENT APPLICATION NUMBER: US/09/855,754B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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Pred. No. 1.6e-10;
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US-09-855-754B-20
Sequence 20, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURGAUX-EDDD, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bordetella bronchiseptica
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PRIOR FILING DATE: 2000-05-25
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94.2%;
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92.3%;
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 92.39
Matches 48; Conservative
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Matches 49; Conserv
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PRITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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                                                                                                                                                                                                                                                                                                                  Score 259; DB 5;
Pred. No. 4.9e-10;
0; Mismatches 2
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CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 22
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PRIOR FILING DATE: 2000-05-25
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2001-05-16
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Best Local Similarity 92.5%;
Matches 49; Conservative
                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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                                                                            NUMBER OF SEQ ID NOS: 25
SOFWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENCTH: 52
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SOFTWARE: Patentin Ver. 3
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us-09-855-754b-15.rapn

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                                                                             Query Match 71.4%; Score 212; DB 5; Length 42; Best Local Similarity 78.8%; Pred. No. 3.7e-07; Matches 41; Conservative 0; Mismatches 1; Indels 10;
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78.8%; Pred. No. 2.2e-06;
.ive 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                          Application US/10282122A
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APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/206,848
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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US-10-282-122A-51012
                                                                                                                                                                                                                                                                                                                                               : Wang, Liangsu
: Zamudio, Carlos
: Malone, Cheryl
: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 55012
LENGTH: 768
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 78.8
Matches 41; Conservative
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Search completed: May 7, 2003, 17:27:47 Job time: 31.6508 secs



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APPLICANT: BOURSACX-EUDE, CAROLINE
APPLICANT: BOURSACX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FAPILICATION NUMBER: 60/206,969
PRIOR PALING DATE: 2000-05-25
NUMBER OF SEC 1D NOS: 24
SOFTWARE: PATENTIN ONS: 24
SOFTWARE: PATENTIN ONS: 24
SEQ 1D NO 15
LENGTH: 52
TYPE: PRT
1 US-09-791-537-50286
2 US-09-855-754-6
2 US-09-855-754-10
2 US-09-855-754-11
2 US-09-855-754-14
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US-00-417-507-22218

US-60-389-997-2285

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US-60-312-418-2285

US-60-312-40235

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PCT-USO1-08631-40235

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100.0%; Score 297; DB 22;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 52; Conservative 0; Mismatches 0;
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US-09-855-754-15
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Sequence 37413, A
Sequence 85698, A
Sequence 4, Appli
Sequence 18, Appli
Sequence 19, Appl
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254.511 Million cell updates/sec
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/ggn2_6/ptodata/1/paa/D866_COMB.pep:*
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/ggn2_6/ptodata/1/paa/US086_COMB.pep:*
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/ggn2_6/ptodata/1/paa/US082_COMB.pep:*
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/ggn2_6/ptodata/1/paa/US082_COMB.pep:*
/ggn2_6/ptodata/1/paa/US092_COMB.pep:*
                     GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-791-537-37413
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Listing first 45 summaries
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Perfect score:
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Maximum DB
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Sequence 1323, Ap Sequence 22217, A Sequence 42632, A Sequence 22215, A

Sequence 23, Appl 1
Sequence 2, Appl 1
Sequence 76981, A
Sequence 76981, A
Sequence 21274, A
Sequence 3144, A
Sequence 3148, A
Sequence 11200,
Sequence 2, Appl 1
Sequence 2218, Ap
Sequence 2218, Ap
Sequence 22285, Ap
Sequence 40235, A
Sequence 40235, A

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PRETUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Best Local Similarity 100.0%; Pred. No. 6.5e-12;
Matches 52; Conservative 0; Mismatches 0;
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Pred. No. 3.6e-12;
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               CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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; ORCANISM: Bordetella bronchiseptica
US-09-855-754-18
                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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FILE REFERENCE: 03495-0206-00000
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Best Local Similarity 92.9%;
Matches 52; Conservative
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PRIOR APPLICATION NUMBER: 60/3
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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US-09-855-754-18
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APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Derek
APPLICANT: Debe, Derek
APPLICANT: Deney
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTI VETSION 3.0
                                                                                                                                                                                                                            APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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100.0%; Pred. No. 6.5e-12;
Live 0; Mismatches 0;
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100.0%; Pred. No. 6.5e-12;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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US-09-791-537-85698
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Matches 52; Conservative
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Best Local Similarity
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US-09-791-537-85698
                                                                                                        RESULT 2
US-09-791-537-37413
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LENGTH: 911
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Sequence 16, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOUKSAUX-EUDE, CAROLINE
APPLICANT: BOUKSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: RECIOUS OF PERTACTIN IN BORDETELLA PERTUCSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE 03495-0206-00000
CURRENT APPLICATION NUMBER: USO(0)0855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                         APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREGIONS OF PERPACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 271; DB 22;
Pred. No. 2.9e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING | DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ 1D NOS: 24
SOFTWARE: PATCHTIN VET: 2.1
SEQ 1D NO 17
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ TO NOS: 24
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 16
LENGTH: 59
TURNER: FAILER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bordetella bronchiseptica
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                                                                                                                                         Sequence 17, Application US/09855754 GENERAL INFORMATION:
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                                                                                                                                                                                      CAROLINE
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96.2%;
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Best Local Similarity 96.2
Matches | 51; Conservative
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Best Local Similarity
Matches 51; Conserv
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Sequence 50286, Application US/09791537

Sequence 50286, Application US/09791537

Sequence 50286, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Blonomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TITLE OF INVENTION: HTREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE

TITLE OF INVENTION: WETHODS OF USE THEREOF

TITLE OF INVENTION: WUMBER: US/09/791,537

CURRENT APPLICATION UNDER: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 50286

LENGTH: 922
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000;
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                      Gaps
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                                                                                                                                         Length 58;
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Pred. No. 4.9e-11;
0; Mismatches 0;
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Pred. No. 4.9e-11;
0; Mismatches 0;
                                                                                                                                  Score 284; DB 22;
Pred. No. 4.3e-12;
0; .Mismatches 0;
                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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89.78;
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ilarity 89.7%;
Conservative
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Best Local Similarity 89.7
Matches 52; Conservative
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Matches 52; Conservative
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LENGTH: 922
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SEQ ID NO 19
LENGTH: 58
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Best Local S
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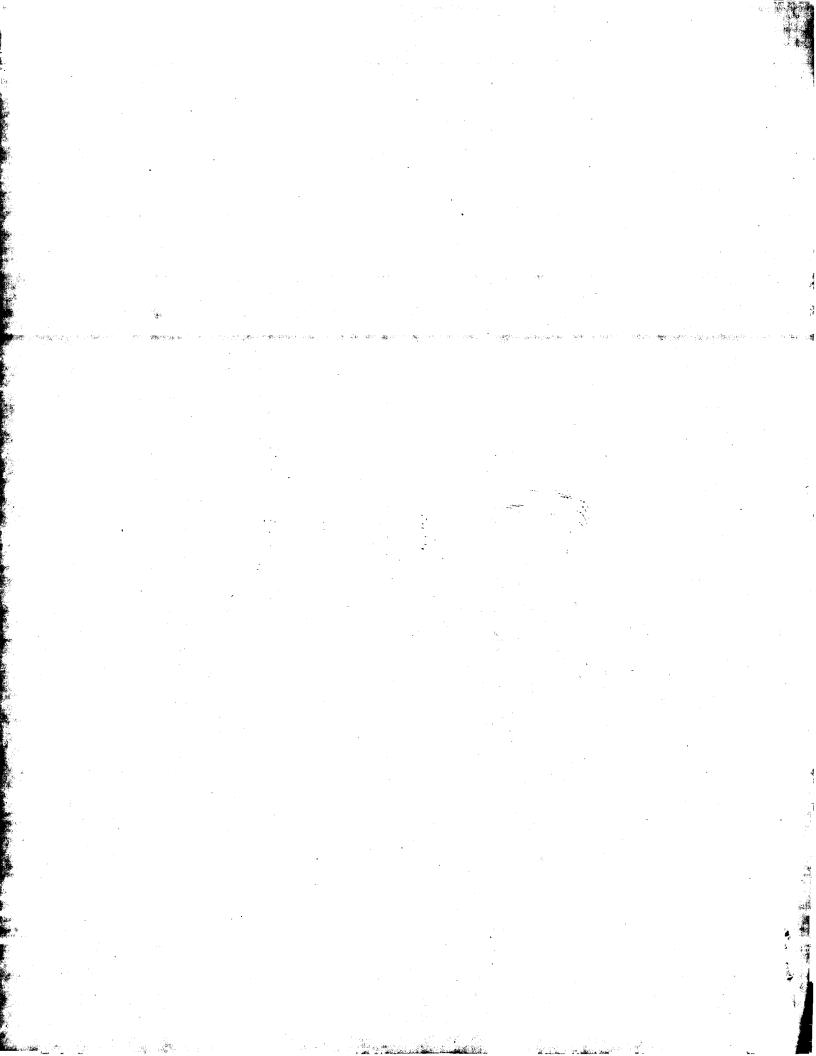
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TITLE OF INVENTION:
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US-09-855-754-23
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LENGTH: 52
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                                        APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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                                                                                        TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.5e-10;
0; Mismatches 0; Indels
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J.5e-11;
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Pred. No. 5.5e-
0; Mismatches
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                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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92.3%;
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1 Similarity 94.2%;
49; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                    BOURSAUX-EUDE,
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Best Local Similarity
Matches 48; Conserv
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Best Local Similarity
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LENGTH: 48
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TITLE OF INVENTION: POLYPERTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPERTIDES CONTAINING PORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: MANDHOGENET COMPOSITIONS IN DIAGNOSTICS, AND IN FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.2%; Score 259; DB 22; Length 52;
llarity 92.5%; Pred. No. 1.8e-10;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 54;
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1 Similarity 89.1%; Pred. No. 2.2e-10;
49; Conservative 0; Mismatches 2;
IMMUNOGENIC COMPOSITIONS
               FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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CURRENT FILING DATE: 2001-00-10
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
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US-09-855-754-22
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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SOFTWARE: Patentin Ver
SEQ ID NO 22
LENGTH: 54
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Matches 49; Conserv
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754B-15
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Sequence 19541,
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Sequence 2812,
Sequence 2814,
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 49
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Sequence 4
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'Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
'Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
'Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
'Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
'Cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
'Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754B-4

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US-09-855-754B-19

US-09-855-754B-6

US-09-855-754B-6

US-09-855-754B-17

US-09-855-754B-17

US-09-855-754B-17

US-09-855-754B-17

US-09-855-754B-22

US-09-855-754B-22

US-09-855-754B-22

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US-09-855-754B-5

US-10-218-140-4170

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JS-10-224-999A-3465
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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GENERAL INFORMATION:
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TOTAL OF INVENTION:
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Sequence 84278, A
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Sequence 84280, A
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Sequence 84277, A
Sequence 84277, A
Sequence 84277, A
Sequence 84276, A
Sequence 84276, A
Sequence 84276, A
Sequence 10853, A
Sequence 12544, A
Sequence 9552, Ap
Sequence 9552, Ap
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GENERAL INFORMATION:
APPLICANT: BOURSANY-EUDE, CAROLINE
APPLICANT: BOURSANY-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONGHISEPPTICA, THEIR USE IN DIAGNOSTICS,
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICANTON NOBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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US-09-724-676-84274
US-09-724-676A-84278
US-09-724-676A-84280
US-09-724-676-84280
US-09-724-676-84280
US-09-724-676-84277
US-09-724-676A-84277
US-09-724-676A-84277
US-09-724-676A-84277
US-09-724-676A-84276
US-09-724-676A-84276
US-09-724-676A-84276
US-09-724-676A-84276
US-09-724-676A-84276
US-09-949-016-10853
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Query Match

à a Sequence 4,

TYPE: PRT

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; TOPOLOGY: LINear; MOLECTLE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-227-353-4
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-18
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                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                       LENGTH: 911 amino acids
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.1%;
Best Local Similarity 87.5%;
Matches 49; Conservative
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94.28;
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 94.2
Matches 49; Conservative
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US-09-855-754B-19
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LENGTH: 56
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                         Gaps
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 911;
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                                                                                                                                                                              Length 52;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branic STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                              DB 5;
                                                                                                                                                                                                  5e-11;
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                                                                                                                                                              95.9%; Scc. No. , . . 94.2%; Pred. No. , . . 0; Mismatches
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Pred. No. 4.5
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CURRENT FILING DATE: 2001-05-16
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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US-09-855-754B-15
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illarity 94.2%;
Conservative
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COMPUTER READABLE FORM:
                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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  NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
Matches 49; Conserv
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Matches 49; Conserv
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US-10-227-353-4
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHIESPPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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Pred. No. 4.5e-10;
0; Mismatches 0
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Pred. No. 1.1e-10;
0; Mismatches 0
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                       NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
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TYPE: protein
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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Best Local Similarity 84.5
Matches 49; Conservative
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Best Local Similarity 98.0°
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-855-754B-20
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPERTITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION UNMER: US/09/055,754B
CURRENT PILING DATE: 2001-05-16
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 922;
                                                                                                                                                                                                                                                             Length 58;
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STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                  Indels
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hes 0;
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Pred. No. 1.2e-
0; Mismatches
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Pred. No. 7.1
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                             ORGANISM: Bordetella bronchiseptica
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US-10-227-353-6
Sequence 6, Application US/10227353
GENERAL INFORMATION:
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Best Local Similarity 84.5%;
Matches 49; Conservative
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84.5%;
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                                                                                              NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
TYPE: PRT
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VA
COUNTRY: USA
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Best Local Similarity
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APPLICANT: BORSAUX-BUDE, CAROLINE
APPLICANT: BORSAUX-BUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILLING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILLING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 263.5; DB 6;
Pred. No. 7.1e-10;
0; Mismatches 0;
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Pred. No. 1.5e-10;
0; Mismatches 0;
                                                                                                                                                                                                       NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09855754B GENERAL INFORMATION:
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US-09-855-754B-17
Sequence 17, Aprilication US/09855754B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   (703) 243-6333
703) 243-6410
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ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 922 amino acids TYPE: amino acid
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84.5%;
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98.0%;
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754B-22
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US-09-855-754B-23
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LENGTH: 42
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POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                  TITLE OF INVENTION: BORDETELA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: INMUNOSEDRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
PRIOR PELICATION NUMBER: 60/206,969
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR PELICATION DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 7.9e-10;
0; Mismatches 0
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Pred. No. 1.4e-09;
0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                              ORGANISM: Bordetella bronchiseptica
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90.6%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Conservative
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US-09-855-754B-16
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LENGIH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PREPACTION IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: USA/09/855,754B
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/4855,754B
CURRENT FILING DATE: 2001-05-16
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Pred. No. 4.6e-09;
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Pred. No. 5.5e-09;
0; Mismatches 2
                                                                                                                                                                                                                                                                                 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
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ORGANISM: Bordetella bronchiseptica
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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86.8%;
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PRIOR APPLICATION NUMBER: 60/7. PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 86.83
Matches 46; Conservative
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                                         NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 21
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SOFTWARE: Patentin Ver. 3
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SOFTWARE: Patentin Ver
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Best Local Similarity
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 51012
LENGTH: 768
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Pred. No. 9.9e-07;
0; Mismatches 1; Indels 7
                                                                                   Score 213.5; DB 5; Length 42;
Pred. No. 1.6e-07;
0; Mismatches 1; Indels
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                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPPQPPQPPQRPQREAPAPQPPAGRELSAA 49
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FILE REFERENCE: ELLTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                            Sequence 51012, Application US/10282122A GENERAL INFORMATION:
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R APPLICATION NUMBER: 60/257,931

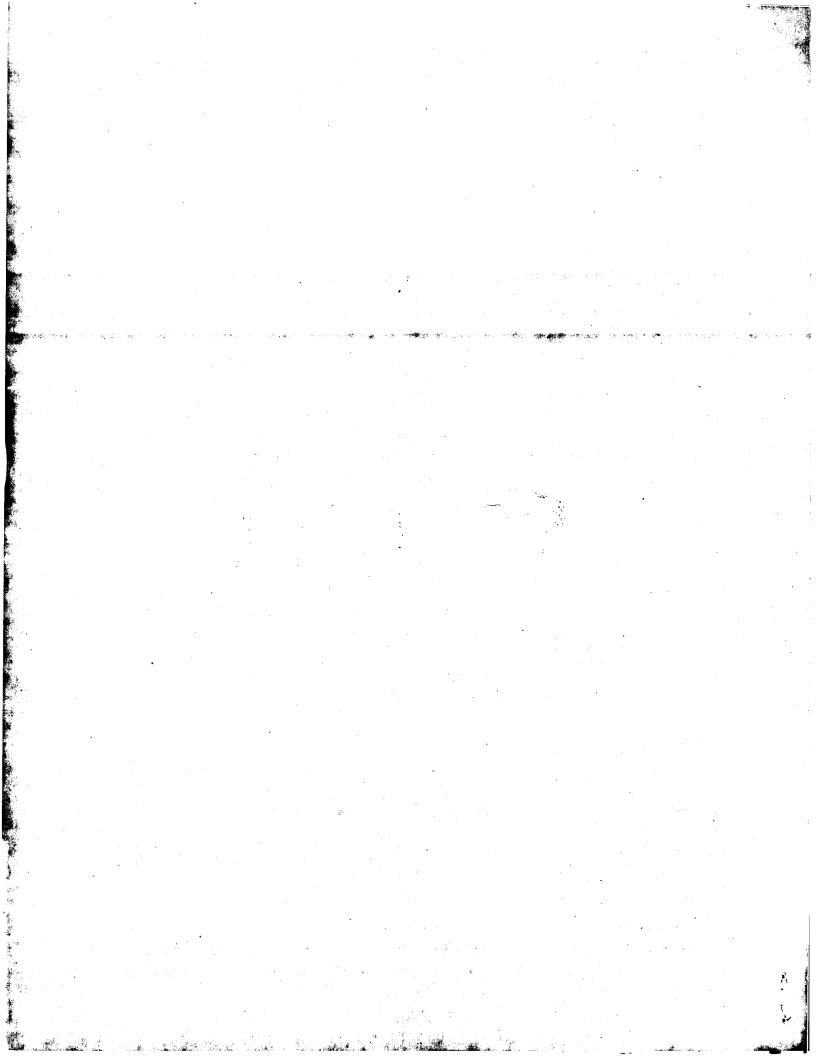
R FILING DATE: 2000-12-22

R PPLICATION NUMBER: 60/267,636

R FILING DATE: 2001-02-09

R APPLICATION NUMBER: 60/269,308
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R APPLICATION NUMBER: 60/206,848
R PILING DATE: 2000-05-23
R APPLICATION NUMBER: 60/207,727
R FILING DATE: 2000-05-26
R APPLICATION NUMBER: 60/230,335
R FILING DATE: 2000-09-06
R FILING DATE: 2000-03-06
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Best Local Similarity 83.7%;
Matches 41; Conservative
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Best Local Similarity 83.7%;
Matches 41; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:46 Job time: 29.8825 secs



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                               SEQ ID NO 9
LENGTH: 56
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754B-12
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US-09-855-754B-13
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PCT-US02-18256-43
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Perfect score:
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27 82 26.6 617 1 PCT-US03-01096-334 Sequence 334, App 28 26.6 759 5 US-09-724-676-72624 Sequence 72624, A 30 82 26.6 759 5 US-09-724-676-72624 Sequence 72624, A 31 82 26.6 2234 5 US-09-724-676-72631 Sequence 72631, A 32 26.6 2234 5 US-09-724-676-72631 Sequence 72631, A 32 26.6 2234 5 US-09-724-676-72631 Sequence 72631, A 34 82 26.6 2234 5 US-09-724-676-72631 Sequence 72631, A 34 82 26.6 2270 5 US-09-724-676-72631 Sequence 72639, A 35 82 26.6 2270 5 US-09-724-676-72639 Sequence 72639, A 36 26.6 2270 5 US-09-724-676-72629 Sequence 72629, A 36 26.6 2270 5 US-09-724-676-72629 Sequence 72629, A 36 26.6 2270 5 US-09-724-676-72629 Sequence 73629, A 37 82 26.6 2270 5 US-09-724-676-72629 Sequence 73629, A 38 82 26.6 2270 5 US-09-724-676-72629 Sequence 73629, A 39 82 26.6 2910 7 US-60-453-13303 Sequence 73629, A 40 82 26.6 2913 5 US-09-724-676-72627 Sequence 72627, A 42 82 26.6 2913 5 US-09-724-676-72627 Sequence 72637, A 42 81 26.3 291 6 US-09-724-676-72627 Sequence 72637, A 42 81 26.3 291 7 US-09-724-676-72627 Sequence 72637, A 42 81 26.3 291 7 US-09-724-676-72627 Sequence 72637, A 5 26.1 417 7 US-60-453-050-8494 Sequence 8494, Ap 7 US-60-453-050-8494
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ALIGNMENTS

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SEQ ID NO 51012
LENGTH: 768
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US-09-855-754B-11
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BONDETELIA PARAPERTUSSIS, AND BONDETELIA.
TITLE OF INVENTION: INMUNICEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: INMUNICEBRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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Pred. No. 1.9e-20;
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CURRENT APPLICATION NUMBER: US/10/282,122A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-10
                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.2%;
Best Local Similarity 92.9%;
Matches 52; Conservative
                                                                                                                                   94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Forsyth, R.
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                     53; Conservative
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Carr, Grant
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver.
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                                                                                                                                    Query Match
Best Local Similarity
Matches 53; Conserv
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US-09-855-754B-10
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SEQ ID NO 10
              SOFTWARE: POSE SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
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90.4%; Score 278.5; DB 5; Length 61;
Best Local Similarity 86.9%; Pred. No. 3e-19;
Matches 53; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 281; DB 6; Length 768;
Pred. No. 1.9e-18;
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R FILING DATE: 2000-05-26
R APPLICATION NUMBER: 60/230,335
R FILING DATE: 2000-09-06
A PPLICATION NUMBER: 60/230,347
R FILING DATE: 2000-09-09
R APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION UNMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                               FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-09 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Bordetella pertussis US-10-282-122A-51012
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illarity 92.9%;
Conservative
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Best Local Similarity
Matches 52; Conserv
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA PARABUNGGENIC COMPOSITIONS
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                   Gaps
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                                                   Length 910;
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                                             Score 271; DB 6;
Pred. No. 1.9e-17;
1; Mismatches 4
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Pred. No. 4.4e-17;
1; Mismatches 1
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Pred. No. 1.2e-
2; Mismatches
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                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica
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                                             Query Match
Best Local Similarity 91.1%;
Matches 51; Conservative
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I Similarity 80.4%;
45; Conservative
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illarity 87.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver.
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Best Local Similarity
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Best Local Similarity
Matches 45; Conserv
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US-09-855-754B-7
US-10-227-353-2
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TYPE: PRT
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FILE REFERENCE: -03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 274; DB 5;
Pred. No. 9.9e-18;
1; Mismatches 4
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FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                    Application US/09855754B
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                                                                                           GUISO-MACLOUF, NICOLE
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ORGANISM: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CLARE, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.0%;
91.1%;
                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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COMPUTER READABLE FORM:
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Best Local Similarity 91.17
Matches 51; Conservative
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                                             GENERAL INFORMATION
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
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SOFTWARE: Patentin Ver.
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Matches 42; Conserv
                                                                                                                                                               Local Similarity
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US-09-855-754B-4
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LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 46
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Matches
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTINI IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 228.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703) 243-6333
03) 243-6410
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                  Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis
                                                                                                                                                               CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-227-353-6; Sequence 6, Application US/10227353; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.2%;
Best Local Similarity 80.4%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60% PRIOR FILLNG DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                             RESULT 10
US-09-855-754B-6
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LENGIH: 922
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RESULT 11

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Sequence 4, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOUSSUX.*
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDSTELLA PERTUSSIS,
TITLE OF INVENTION: BORDSTELLA PARAPERTUSSIS, AND BORDSTELLA PETTICS OF INVENTION: BROWNINSEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,

TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA

TITLE OF INVENTION: BRONCHISEPTICA, THETR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: BRONCHISEPTICA, THETR USE IN DIAGNOSTICS, AND IN

FILE REFERENCE: 03409-00000

CURRENT APPLICATION NUMBER: US/09/855,754B

CURRENT PILING DATE: 2001-05-16

PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                               1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                            1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
          Length 922;
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          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%; Score 212; DB 5; 1 ilarity 75.0%; Pred. No. 3.8e-13; Conservative 2; Mismatches 2;
74.2%; Score 228.5; DB 6 ilarity 80.4%; Pred. No. 1.8e-13; Conservative 2; Mismatches 4
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APPLICANT: DON A. Roth
APPLICANT: Randolph V. Lewis
APPLICANT: The University of Wyoming
TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
FILE REFERENCE: UNYO 02-004
CURRENT APPLICATION NUMBER: PCT/US02/18256
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 60/296,184
                                                   Gaps
                                                                                                                      254 QRATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ 299
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                                                      10;
                                                                                             1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                      Sequence 4, Application US/10227353
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHARL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.8%; Score 212; DB 6; Length 911; Best Local Similarity 75.0%; Pred. No. 6.3e-12; Matches 42; Conservative 2; Mismatches 2; Indels
       Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
  Score 212; DB 5;
Pred. No. 6.3e-12;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 911 amino acids TYPE: amino acid
  ch 68.8%;
1 Similarity 75.0%;
42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Query Match
Best Local Similarity
Matches 42; Conserva
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US-10-227-353-4
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sequence 50.286, A sequence 6, Appl. Sequence 17, Appl. Sequence 17, Appl. Sequence 22, Appl. Sequence 23, Appl. Sequence 2, Appl. Sequence 7584, A sequence 7698, A sequence 7698, A sequence 111629, Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 11, Appl. Sequence 23, Appl. Sequence 21, Appl. Sequence 22, Appl. Appl. Sequence 22, Appl. A
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERPEATED
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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2 US-09-855-754-19

1 US-09-791-537-50286

2 US-09-855-754-6

2 US-09-855-754-10

2 US-09-855-754-10

2 US-09-855-754-11

2 US-09-855-754-22

2 US-09-855-754-22

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1 US-09-791-537-75841

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5 US-09-380-693A-50

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1larity 100.0%; Pred. No. 6.4e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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GENERAL INFORMATION:
APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
      Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-754-14
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LENGTH: 49
TYPE: PRT
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      Sequence 14, Appl
Sequence 15, Appl
Sequence 37413, A
Sequence 85698, A
Sequence 4, Appli
Sequence 18, Appli
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-15
US-09-791-537-37413
US-09-791-537-85698
US-09-855-754-4
US-09-855-754-18
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Maximum Match 100%
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONDETELLA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION INVENTION: 104095-0206-00000
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Pred. No. 4.9e-10;
0; Mismatches 0
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Pred. No. 4.9e-10;
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 85598
LENGTH: 911
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-791-537-85698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09855754; GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 95.9%;
11 Similarity 94.2%;
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PRIOR FILING DATE: 2000-03
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Matches 49; Conserv
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US-09-855-754-4
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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TILE CONTROL TRRED DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHOD OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION WUBBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VEFSION 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT RILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 65/206,969
PRIOR FILING DATE: 2000-05-25
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1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica US-09-791-537-37413
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                                                                                                                                         Sequence 15, Application US/09855754 GENERAL INFORMATION:
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llarity 94.2%;
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I Similarity 94.2%;
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SEQ ID NO 15
LENGTH: 52
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
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Best Local Similarity
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US-09-791-537-85698
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                                                                                                                   US-09-855-754-15
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US-09-855-754-15
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APPLICANT: GUISO-MACLOUE, CAROLLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVERYION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERYION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERYION: BORDETELLA PRRAPERTUSSIS, AND BORDETELLA
TITLE OF INVERYION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVERYION: IMMORGENIC COMPOSITIONS
TITLE OF INVERTION: IMMORGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PLILING DATE: 2000-05-25
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GENERAL INFORMATION:
APPLICANT: BOUFSAUX-EUDE, CAROLINE
APPLICANT: BOUFSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERPRETURISIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0050-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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Pred. No. 7.9e-10;
0; Mismatches 0;
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-20
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US-09-855-754-6
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US-09-855-754-17
; Sequence 17, Application US/09855754
                                                                                                                                    Sequence 6, Application US/09855754 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 84.5%;
Matches 49; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 922
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                       Length 56;
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Pred. No. 7.9e-10;
0; Mismatches 0; ]
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Pred. No. 7e-11;
0; Mismatches 0;
                                                                                                                                       DB 22;
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Pred. No. 5.8e-
0; Mismatches
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                                         ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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US-09-855-754-19
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84.5%;
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1 Similarity 84.5%;
49; Conservative
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ilarity 87.5%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Best Local Similarity
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Matches 49; Conserv
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US-09-791-537-50286
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LENGTH: 922
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SEQ ID NO 18
LENGTH: 56
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US-09-855-754-23
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUGSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR ELLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARABERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 9.2e-10;
0; Mismatches 0; Indels
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Pred. No. 4.8e-10;
0; Mismatches 0
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US-09-855-754-17
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90.6%;
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SEQ ID NO 16
LENGTH: 59
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Best Local Similarity
Matches 48; Conserv
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Best Local Similarity
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US-09-855-754-16
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LENGTH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA.
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-00000
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                                                                                                                                                                                                                                                                                                                                                                             Score 238.5; DB 22;
Pred. No. 3.1e-09;
0; Mismatches 2;
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITION
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 21
LENGTH: 52
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bordetella bronchiseptica US-09-855-754-22
                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-855-754-22; Sequence 22, Application US/09855754; GENERAL INFORMATION:
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ilarity 86.8%;
Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOURSAUX-EUDE,
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Search completed: May 7, 2003, 17:21:53 Job time : 125.128 secs



11, Appl 111629, 5, Appli 31601, A

31601, A 98868, A 76981, A 13, Appl 75841, A 76968, A

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GENERAL INFORMATION:
APPLICANT: BOUGSAUX-EDDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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Sequence
Sequence
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                US-09-791-537-78243

US-09-791-537-21274

US-09-855-754-11

US-09-971-537-111629

US-09-791-537-111629

US-09-791-537-111629

US-09-791-537-98668

US-09-791-537-76961

US-09-791-537-76961

US-09-791-537-76968

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US-09-791-537-76968

US-09-791-537-76968

US-09-791-537-4603

US-09-791-537-4603

US-09-791-537-4540

US-09-855-754-6

US-09-91-537-4560

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US-09-791-537-4560
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Llarity 100.0%; Pred. No. 2.1e-24;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANIŚM: Bordetella bronchiseptica
US-09-855-754-9
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SOFTWARE: Patentin Ver. 2.1
Similarity
                                     SEQ ID NO 9
LENGIH: 56
TYPE: PRI
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224.5
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Best Local Si
Matches 56;
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Sequence 4640, Ap
Sequence 12, Appl
Sequence 12, Appl
Sequence 112007,
Sequence 78242, A
                                                                                                                           7, 2003, 16:47:16 ; Search time 141.86 Seconds (without alignments) 254.511 Million cell updates/sec
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Compugen Ltd.
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US-09-791-537-4640
US-09-791-537-4644
US-09-855-754-12
US-09-791-537-112007
US-09-791-537-78242
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ptodata/1/paa/US094_COMB.
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/cgn2_6/ptodata/1/paa/US102_COMB.
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                GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Title:

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QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ

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308 308 308 291 291

Score

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78242, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danker, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY STILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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Pred. No. 1.2e-22;
1; Mismatches 2;
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Pred. No. 6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112007, Application US/09791537, GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
             CURRENT APPLICATION NUMBER: US/09/855,7 CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
LENGTH: 56
                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-12
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NOS: 153055
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SEQ ID NO 78242
LENGTH: 907
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SEQ ID NO 112007
LENGTH: 910
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94.6%;
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94.68;
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Best Local Similarity 94.6%
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US-09-791-537-78242
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Best Local Similarity
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US-09-791-537-112007
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US-09-791-537-78242
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                    APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PELICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 4640
LENGTH: 160
TYPE:
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APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: HERBED DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 4644
LENGTH: 161
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GENERAL INFORMATION:
APPLICANT: BOUNGRAUX = EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Length 161;
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100.0%; Score 308; DB 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-24;
Matches 56; Conservative 0; Mismatches 0;
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1 Similarity 100.0%; Pred. No. 6.3e-24;
56; Conservative 0; Mismatches п.
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US-09-791-537-4644
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US-09-791-537-4644
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US-09-855-754-12
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                    APPLICANT: DEBOX LOSCEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATEIT VERSION 3.0
SOFTWARE: PATEIT VERSION 3.0
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APPLICANT: BOGGSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE FERENCE: 03405-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT RILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 QRATIRRGDAPAGGAVPGGAVPGGRAVPGFGPGFGPVLDGWYGVDVSGSSVELAQ 309
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Pred. No. 2.5e-20;
1; Mismatches 3;
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Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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APPLICANT: Blonomix, Inc.
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                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella pertussis
US-09-791-537-21274
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US-09-791-537-33443
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SEQ ID NO 33443
LENGTH: 910
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92.9%;
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Best Local Similarity 92.9%;
Matches 52; Conservative
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Best Local Similarity 92.99
Matches 52; Conservative
         APPLICANT: Bionomix, Inc
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                                                                                                                                                                                                                                                                    APPLICANT: GUISO-MACCOUE, MICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: INMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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Pred. No. 1.3e-21;
1; Mismatches 3;
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Pred. No. 1e-20;
1; Mismatches
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 387
  Mismatches
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; GENERAL INFORMATION:
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                                                                                                                                                                                                     Sequence 10, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
  1;
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US-09-791-537-78243
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Length 910;

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Sequence 31601, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Pred. No. 1.6e-19;
1; Mismatches 4; Indels
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Pred. No. 2.7e-19;
1; Mismatches 4;
                                       Score 274; DB 22;
Pred. No. 1.3e-19;
1; Mismatches 4;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 98868
LENGTH: 910
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; ORGANISM: Bordetella pertussis
US-09-791-537-98868
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LENGTH: 539
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Best Local Similarity 91.1%;
Matches 51; Conservative
                                         89.0%;
91.1%;
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Best Local Similarity 91.1%;
Matches 51; Conservative
                                       Query Match 89.0
Best Local Similarity 91.1
Matches 51; Conservative
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US-09-791-537-31601
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US-09-855-754-5
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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Deseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA PARAPERTUSSIS, AND BONDETICLA PARAPERTUSSIS, AND BONDETICLA PARAPERTUSSIS, AND BONDETICLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 20026-00000
CURRENT PILLING DATE: 2001-09-10
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Pred. No. 2.6e-21;
1; Mismatches 2;
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Pred. No. 4.6e-
1; Mismatches
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-25
                       ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-11
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                                                                                                          Query Match 90.4%;
Best Local Similarity 86.9%;
Matches 53; Conservative
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Best Local Similarity 86.9%;
Matches 53; Conservative
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LENGTH: 915
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Sequence 6, Application US/09855754B
GENERAL INFORMATION:
APPLICANT BOUFSONX-EUDE, CAROLINE
APPLICANT: BOUFSONX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: EMONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754B-6
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Sequence
Sequence
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1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-10
US-09-855-7548-13
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US-09-855-7548-4
US-10-227-533-4
US-10-227-533-4
US-09-855-7548-9
US-09-855-7548-12
US-09-855-7548-12
US-09-855-7548-12
US-09-855-7548-12
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US-10-310-154-508
PCT-US02-18256-52
PCT-US02-18256-46
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Sequence 7, Application US/09855754B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUGRAUX-EUDE, CAROLINE
APPLICANT: BOUGRAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REPERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 7
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                           Sequence 27635, A Sequence 31381, A Sequence 31381, A Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 2507, Ap Sequence 1200, A Sequence 12130, A Sequence 12130, A Sequence 12536, A Sequence 19536, A Sequence 19536, A Sequence 47675, A Sequence 19536, A Sequence 19536, A Sequence 19536, A Sequence 47675
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US-10-366-683-27635
US-10-419-128-27635
US-10-366-683-31381
US-10-319-128-31381
US-10-311-096-28
US-10-341-097-28
US-10-341-097-28
US-10-146-782-28
US-10-146-782-28
US-10-166-761-1169
US-10-276-774-2507
US-10-26-683-30130
US-10-36-683-30130
US-10-156-761-1210
US-10-166-761-1210
US-10-166-761-10088
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Similarity 100.0%; Pred. No. 2.1e-20;
51; Conservative 0; Mismatches 0;
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US-09-855-7548-7
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Sequence 51012, Application US/10282122A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754B-5
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Best Local Similarity 83.9%;
Matches 47; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                               91.4%;
85.7%;
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Best Local Similarity 85.7
Matches 48; Conservative
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US-10-282-122A-51012
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US-09-855-754B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
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                                                                                                                                                      Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                        1 ORATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAO
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Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                        Score 272; DB 5;
Pred. No. 3.7e-19;
; Mismatches 0;
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FILING DATE: 02-Jun-1995
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/227,353 , FILING DATE: 26-AUG-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067 ,
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
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TELEPHONE: (703) 243-6333
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                                                                              ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-7548-6
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US-10-227-353-6
; Sequence 6, Application US/10227353
; GENERAL INFORMATION:
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                                                                                                                                                            100.0%;
100.0%;
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ADDRESSEE: Millen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                              Query Match 100.0
Best Local Similarity 100.0
Matches 51; Conservative
                     SOFTWARE: Patentin Ver. 2.1
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NUMBER OF SEQ ID NOS: 25
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US-09-855-754B-5
                                          SEQ ID NO 6
                                                                 LENGTH
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPPLICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYCHOLAGE CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERVUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERVUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE: IN DIAGNOSTICS, AND ITLLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTIN NOS: 22
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Pred. No. 8.2e-17;
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Pred. No. 2.6e-17;
3; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 00/206,969
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SECTION NO.10
LENGTH: 56
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Zyskind, Judith
Wall, Daniel
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Gaps

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Indels

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Mismatches
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                                                                                                                                                                                                                                                       Sequence 8, Application US/09855754B GENERAL INFORMATION:
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90.2%;
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90.2%;
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 90.2
Matches 46; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 90.29
Matches 46; Conservative
  Conservative
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                                                                                                                                                                                                                            US-09-855-754B-8
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms File Reference: Elitera.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 QRATIRRGDAPAGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRATIRRGDAPAGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 768;
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Pred. No. 3.5e-16;
3; Mismatches 1
                                                                                                                                                                                                          CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-02-16
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.8%;
83.9%;
                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.99
Matches 47; Conservative
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LENGTH: 51
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ORGANISM:
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Length 51;

Score 241; DB 5; Pred. No. 2.6e-17

88.6%; 88.2%;

Query Match Best Local Similarity

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APPLICANT: GUISO-MACKOUF, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR PILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 8
LENGHALE 46
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TILLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TILLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TILLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA.
TILLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TILLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION UNMER: US/09/855,754B
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  51
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1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                              1 ORATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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Pred. No. 1.7e-16;
0; Mismatches 0;
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Pred. No. 3.3e-15;
0; Mismatches 0;
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REPEATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 QRATIRRGDALAGGAVPGGAVPGGAVPGGFGPGPGPGPUDGWIGVDVSGSSVELAQ 309
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.1%; Score 231.5; DB 6; 82.1%; Pred. No. 4.1e-15; ive 3; Mismatches 2;
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80.4%; Pred. No. 5.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 03495-0206-0000 CURRENT APPLICATIONS CURRENT APPLICATION NUMBER: US/09/855,754B PRICH PILLIC DATE: 2001-05-16
                                                                                           APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-10n-1995
ATTORNEY/AGBUT INFORMATION:
NAME: Lebovitz, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                      APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                         REGISTRATION NUMBER: 37,067

FERERENCE/POCKET NUMBER: POPOV-2

TELEPOMMUNICATION INFORMATION:

TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 910 amino acids TYPE: amino acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                        TELEFAX: (703) 243
INFORMATION FOR SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
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Matches 45; Conserv
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Matches 46; Conserv
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                                                                                                                     ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                       ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
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Pred. No. 3.3e-15;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10227353 GENERAL INFORMATION:
                                           Sequence 4, Application US/10227353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                         APPLICANT: CLARE, JEFFREY
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90.2%;
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                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 90.2°
Matches 46; Conservative
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-05-16
PRICE APPLICATION NUMBER: 2001-05-16
PRICE APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Don A. Roth
APPLICANT: Mandolph V. Lewis
APPLICANT: The andolph V. Lewis
TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
FILE REFERENCE: UWYO 02-004
CURRENT APPLICATION NUMBER: PCT/US02/18256
CURRENT FILING DATE: 2002-06-06
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QRATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
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Pred. No. 5.2e-16;
3; Mismatches 3.
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Pred. No. 1e-15;
3; Mismatches
                                                                          US/09/855,754B
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                                                                                               CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09855754B GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-11
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PRIOR APPLICATION NUMBER: 60/296,184
                                               FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/05
CURRENT FILING DATE: 2001-05-16
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73.8%;
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Best Local Similarity 80.4%;
Matches 45; Conservative
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 73.8
Matches 45; Conservative
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                                                                                                                                                                                                        SEQ ID NO 12
LENGTH: 56
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LENGTH: 61
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PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 54

SOFTWARE FastSEQ for Windows Version 3.0

SEQ ID NO 45

LENGTH: 171

TUBE: PRT

ORGANISM: Artificial Sequence
FEATURE: PRT

CONGANISM: Artificial Sequence

FEATURE: PRT

ORGANISM: Artificial Sequence

Sequence

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ON 8 GDAPAGGAVPGGAVPGGAVPGGFQ 32

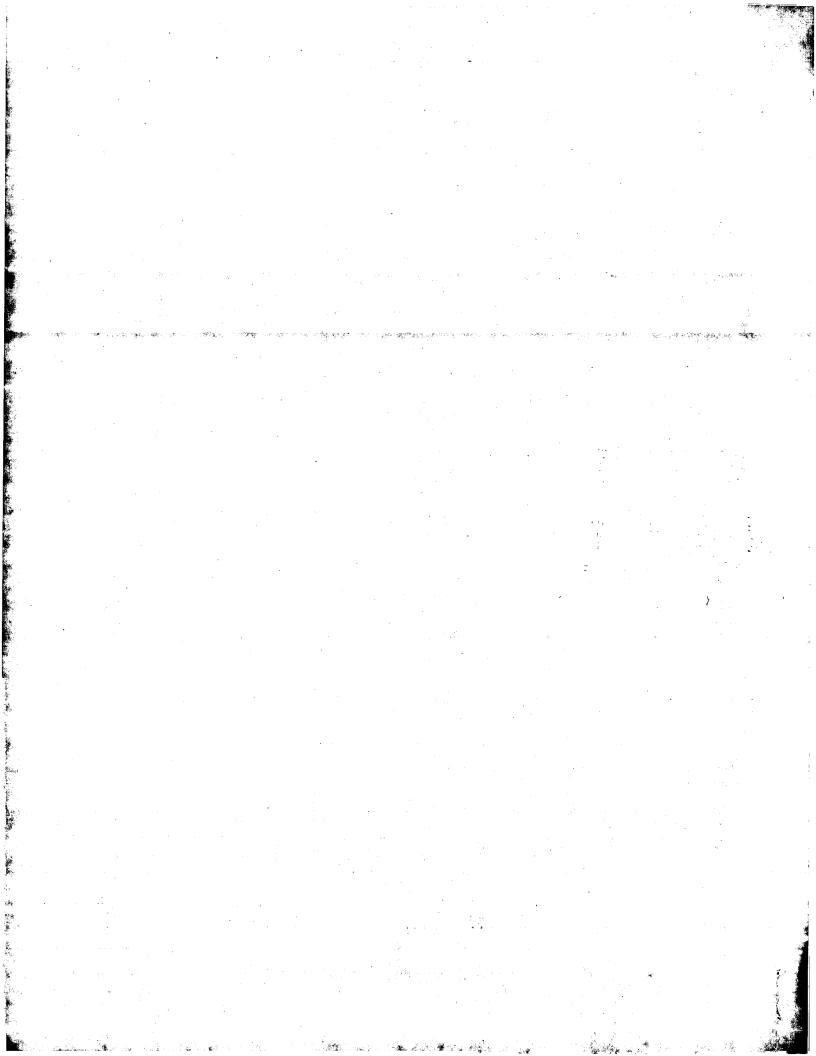
ON 8 GGAPAGGAVPGGAVPGGAVPGGFQ 32

ON 8 GGAPAGGAVPGGAVPGGAVPGGTQ 112

Db 88 GGSGPGGYGPGGACPGGTQ 112

Search completed: May 7, 2003, 17:27:44

JOD time: 32.0613 secs
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11, Appl 111629,

Sequence 1 Sequence 7 Sequence 1 Sequence 1 Sequence 2 Sequence 2

Sequence 2 Sequence 4 Sequence 2 Sequence 1 Sequence 5 Sequence 5 Sequence 1

ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: BOURSAUX-EUDE, NICOLE

TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,

TITLE OF INVENTION: BORNCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS

FILE REFERENCE; 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2000-09-10

PRIOR FILING DATE: 2000-06-25

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 7

LENGTH: 51

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US-09-915-37-754-10
US-09-791-537-21274
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Llarity 100.0%; Pred. No. 1.6e-22;
Conservative 0; Mismatches 0;
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US-09-855-754-7
      Similarity
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Sequence 4609, Ap
Sequence 4603, Ap
Sequence 4519, Ap
Sequence 50286, A
Sequence 6, Appli
                                                                                                                                                                                                         ; Search time 129.194 Seconds
  (without alignments)
  254.511 Million cell updates/sec
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1 QRATIRRGDAPAGGAVPGGA......PLLDGWYGVDVSDSTVDLAQ
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                             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-791-537-4609
US-09-791-537-4603
US-09-791-537-4519
US-09-791-537-50286
US-09-855-754-6
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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APPLICANT: Balonomia, Inc.
APPLICANT: Debe, Debe
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 125/99/85,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 4.1e-21;
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hilarity 100.0%; Pred. No. 5.6e-22;
Conservative 0; Mismatches 0;
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; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                      ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bordetella parapertussis US-09-791-537-50286
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; Sequence 6, Application US/09855754
; GENERAL INFORMATION:
APPLICANT: BOURSAUX EUDE, CAROLINE
; APPLICANT: GUISO-MACLOUF, NICOLE
2001-02-22
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100.0%;
                             NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 4519
LENGTH: 160
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Best Local Similarity
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Best Local Similarity
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LENGIH: 922
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Matches 51
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APPLICANT: BLONOMIX, INC.
APPLICANT: BLONOMIX, INC.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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APPLICANT: Bobb, Derek
APPLICANT: Dobb, Derek
APPLICANT: Dabb, Derek
APPLICANT: Dabb, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 251/210
CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                                                                                        APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Dabe, Derek
APPLICANT: Dabe, Derek
APPLICANT: Dabe, DEREK
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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      1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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100.0%; Score 272; DB 21;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 51; Conservative 0; Mismatches 0;
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Pred. No. 5.6e-22;
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Best Local Similarity
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US-09-791-537-4603
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LENGTH: 159
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LENGTH: 158
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Score 241.5;
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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APPLICANT: Bionomix, Inc.
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US-09-791-537-21274
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella pertussis
US-09-791-537-78243
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Best Local Similarity 83.9%;
Matches 47; Conservative
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Best Local Similarity 83.99
Matches 47; Conservative
                                                                                             APPLICANT: Bioriomix, Inc.
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US-09-791-537-21274
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN ATTLE OF INVENTION: IMMUNGENTIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CONRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 160/206,969
PRIOR PLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PRILING DATE: 2001-09-10
PRIOR PLILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 2.3
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                                                                   21
                                          1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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    0; Indels
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85.7%; Pred. No. 1.6e-18;
11ve 3; Mismatches 0; 1
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1.6e-18;
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Pred. No. 4.2e-19;
3; Mismatches 1
  Mismatches
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                                                                                                                                                                                                Sequence 5, Application US/09855754 GENERAL INFORMATION:
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83.9%;
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Matches 48; Conservative
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Matches 47; Conservative
Conservative
                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE,
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51;
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Matches
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APPLICANT: Debe, Derek, APPLICANT: Debe, Derek, Derek, Derek, Derek, Derek, Derek, Derek, Joseph
TITLE OF INVENTION: HREED DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: PATENTIN Version 3.0
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFRERNCE: 261/210
CURRENT MAPPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 78243
LENGTH: 387
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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83.9%; Pred. No. 9.7e-18;
ive 3; Mismatches 1
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LENGTH: 910

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Sequence 78.42, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, inc.
APPLICANT: Debc, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILIATION DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOGTWARE: Patentin version 3.0
SEQ ID NO 78242
LENGTH: 907
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                                                               Sequence 76968, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7, 2003, 17:21:51
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                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-791-537-76968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 88.6%;
1 Similarity 88.2%;
45; Conservative
                                                                                                                       APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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GENERAL INFORMATION:
Sequence 75841, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANTON: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin Version 3.0
SEQ ID NO 75841
LENGTH: 905
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APPLICANT: BOUNGSAUX-EUDE, CAROLINE
APPLICANT: BOUNGSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLXMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGTHELLA PREPUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION UNBBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PPLICATION UNBBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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                                                                 Score 241.5; DB 21; Length 910;
Pred. No. 9.7e-18;
3; Mismatches 1; Indels 5;
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4.3e-19;
ches 3;
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US-09-791-537-75841
; ORGANISM: Bordetella pertussis US-09-791-537-33443
                                                                    Query Match 88.8%;
Best Local Similarity 83.9%;
Matches 47; Conservative
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Matches 45; Conserv
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US-09-791-537-75841
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Gaps

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DB 21; Length 907;

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ TEMPORE: Patentin version 3.0
SEQ ID NO 76968
LENGTH: 905
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254 QRATIRRGDAPAGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 304
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Pred. No. 1.1e-17;
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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 7, 2003, 16:31:49 ; Search time 5.24361 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-855-754B-22 310 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 54

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ption		bordetella	_	herpes simp		owenia fusi	homo sapien	epstein-bar	brassica na	arabidopsis	chlamydomon	_		plasmodium	plasmodium	nicotiana t	mus musculu	rattus norv	trypanosoma	_	mus musculu	autographa	trypanosoma	trypanosoma	_	_	homo sapien	neisseria g	mus musculu	mus musculu	sus scrofa	homo sapien	autographa
	Description	P24328	003035	P14283	P10220	P21997	P21260	092794	P12978	P40603	P40602	09fpq6	083949	P48038	P06915	P23093	003211	070324	P51111	P09791	063943	064467	P41467	P08469	006084	P22670	P04723	P42858	006432	005859	005860	P08001	09p2y4	P41479
SUMMARIES	QI	PERT_BORPA	PERT_BORBR	PERT_BORPE	TEGU_HSV11	SSGP_VOLCA	YPRO_OWEFU	MOZ_HUMAN	EBN2_EBV	APG_BRANA			a.		CSP_PLABE	CSP_PLABA	EXLP_TOBAC	MOTB_MOUSE	HD_RAT					PAR1_TRYBB	PARC_TRYBB	RFX1_HUMAN	GDA3_WHEAT	HD_HUMAN	TONB_NEIGO	FM14_MOUSE	FMN1_MOUSE	ACRO_PIG		Y091_NPVAC
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	Query Match Length	922	911	910	3164	485	141	2004	487	449	534	555	875	431	339	347	426	565	3110	129	514	440	808	143	145	979	282	3144	283	1206	1468	415	722	224
æ	Query Match	85.5	83.2	69.7	20.8	49.4	48.7	48.1	47.7	47.6	46.1	45.3	45.2	45.0	44.4	44.4	44.2	44.0	43.7	43.4	43.1	42.9	42.9	42.7	42.7	42.7	42.6	42.3	42.1	42.1		•	41.8	41.3
	Score	265	258	216	157.5	153	151	149	148	147.5	143	140.5	140	139.5	137.5	137.5	137	136.5	135.5	134.5	133.5	133	133	132.5	132.5	132.5	132	131	130.5	130.5	130.5	129.5	129.5	128
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791 1139	1790 261 443	421 3119	293 815 1362	232 296
41.1	60.5 60.5	60.3 E.E.C	300	9.0
127.5	125.5 125.5 125.5	125	124.5 124.5 124.5	123.5
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                     ï
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Gen. Microbiol. 138:1697-1705(1992).
-!- FUNCTION: AGGLUGITHOGEN THART.BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                      -:- SUBCELLULAR LOCATION: Outer membrane.
-:- DISBASE: MAY CONTRIBUTE TO THE DISBASE STATE OF WHOOPING COUGH.
-:- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                 4 (APPROXIMATE).
9 X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                                                                                                                                                         1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
          LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-92407514; PubMed-1527510;
L1 J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
bronchiseptica.";
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacterla; Proteobacterla; beta subdivision; Alcaligenaceae;
                                                                                                              DB 1; Length 922;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                               Pertactin precursor (Outer membrane protein P.68) (P.94)
                                                                                                         85.5%; Score 2bɔ; Lo.;
84.5%; Pred. No. 6.4e-10;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                        911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 35-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A47675; A47675.
Interpro: IPR0040899; Pertact_sup.
Interpro: IPR003992; pertactin.
Interpro: IPR003991; pertactin_vir.
                                                                                                                                                                                                                                        PRT;
                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRIACTNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54815; CAA38584.1; -. EMBL; A19180; CAA01453.1; -.
                                                                                        95178
                                                                                                                        1 Similarity 84.5'
49; Conservative
                                                                                                                                                                                                                                        STANDARD;
                                                     280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER
                                                                                        922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane;
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CN7531;
                                                                                                                                                                                                                                     PERT_BORBR
Q03035;
                                                                                                                                                                                                                                                                                                                                           Bordetella.
                                                                                        SEQUENCE
                                                                                                              Query Match
                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                     DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGNAL
                                                      REPEAT
                                             REPEAT
                                                                   REPEAT
                                                                             DOMAIN
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                                                                                                                                                                                                                             PERT_BORBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                     Matches
                                                                                                                                                                                                                 RESULT 2
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96196517; PubMed-8609998; Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.; "Structure of Bordetella pertussis virulence factor P.69 pertactin."; Nature 381:90-92(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

1- SUBGUIT: MONOMER.

1- SUBCELLULAR LOCATION: Outer membrane.

1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.

1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                       SITE (POTENTIAL).
REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE=92407514; PubMed=1527510;
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPPAPPAPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                              Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRI OR OMPOSA
                                                                                                                                                                                                                                                                            Score 258; DB 1; Length 91
Pred. No. 1.7e-09;
0; Mismatches 2; Indels
                                                                                                                                                                280 3 (APPROXIMATE).
501 7 X 3 AA REPEATS OF P-Q-P.
93995 MW; 3078DF6ECZD987A1 CRC64;
                             LINES).
CELL ATTACHMENT
3 X 5 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO 264 AND 332.
MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89264462; PubMed-2542937;
                                                                                                                                                                                                                                                                              83.2%;
                                                                                                                                                                                                                                                                                                            89.1%;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                       703
275
270
275
280
                                                                                                                                                                                             601
                                                                                                                                                                                                                       911 AA;
                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CN2992
                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERT_BORPE
P14283;
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                               Local
                                                                              DOMAIN
                                                                                                                                                                      REPEAT
                                                                                                                                                                                             DOMAIN
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                                                                                                                                      REPEAT
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us-09-855-754b-22.rsp

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50.8%;
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            Ouery Match
Best Local Similarity 72.3
Matches 34; Conservative
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                             Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A33647; A33647
                                                                                                                                                                                                       Volvox carteri
                                                                                                                                    SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPRO_OWEFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88274327; PubMed-2839594; McGeoch D.J., Dallymple M.A., Davison A.J., Dolan A., Frame M.C., McGeoch D., Perry L.J., Scott J.E., Taylor P.; The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                   X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                   CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                  Score 216; DB 1; Length 910;
Pred. No. 5.3e-07;
0; Mismatches 1; Indels 12;
                                                                                                                                                                                                                          (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-O-P. A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus
                                                                                                              PERTACTIN (P.69).
                                                                                                                                                                                                                 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein Ul36).
                                                                           membrane; Signal; Virulence; Repeat.
                                                                                                                          POTENTIAL
       InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03586; Herpes_UL36; 1.
                                        Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                 93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                        69.78;
                                                                                                                                                                                                                                                                                 1 Similarity 75.9%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
PIR; A32560; A32560
                                                                                                                                                                                                  276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                  TEGU_HSV11
P10220;
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SEQUENCE
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DOMAIN
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REPEAT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
-!- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIRROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CHELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carter1: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- PTM: A.CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical proline-rich protein (Fragment).
Owenia fusiformis.
Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                              3,
       DB 1; Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
49.4%; Score 153; DB 1; Length 485;
Best Local Similarity 57.1%; Pred. No. 0.002;
Matches 24; Conservative 1; Mismatches 17; Indels
                                                                                                                                                                                   Indels
                                                                                                                                          PAPKPAPQPGPQP-PQP-PQP-PQP-PQPQPQPQPEAPAPQPPAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 295 POLY-PRO.
435 AA; 50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 РРАРКРАРОРОРОРРОРРОРРОРОРОРОРОРОРОР 46
Score 157.5; DB 1;
Pred. No. 0.0041;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Sulfation; Hydroxylation.
DOMAIN 228 340 PRO-RICH.
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MEDLINE=90094551; PubMed=2689458;
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EBN2_EBV
P12978;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                 Query Match
                                                                                DOMAIN
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                            AEQUENCE FROM N.A.

MEDLINE=90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bakalara invertebrate genomes of sequences characterized by the repetition of the triplet CCPurline.";
Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; A34043; A34043.
Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              ;
0
                                                                                                                                                                                      Score 151; DB 1; Length 141;
Pred. No. 0.0011;
0; Mismatches 20; Indels
                                                                                                                                                                    15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                   5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОР 49
                                                                                                                                                                                                                                               H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                           PRT; 2004 AA
                                                                                                                                       POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96376968; Pubmed-8782817;
                                                                                                                                                                                                                                                                                                                                Created)
Sabellida; Oweniidae; Owenia.
NCBI_TaxID=6347;
                                                                                                                                                                                         48.78;
                                                                                                                                                                                                    55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U47742; AAC50662.1;
Genew; HGNC:13013; ZNF220.
                                                                                                                                                                                                              25; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                      141 AA;
                                                                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601408;
                                                                                                                                                                                                                                                                                                                                15-JUL-1998
                                                                                                                                                                                                                                                                                                           MOZ_HUMAN
Q92794;
                                                                                                                                      DOMAIN
DNA_BIND
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                      RESULT 7
MOZ_HUMAN
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Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
-1- PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petti L., Sample C., Kieff E.; "Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins."; Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BREAKPOINT FOR TRANSLOCATION TO FORM MOZ-CBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91202599; PubMed-1850028;
Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
                                                 translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1651 PPPPPPQPQPPPPPQPQPPPPPQQPQQPQQPQQPQPPPP 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 РАРКРАРОРСРОРРОРРОРРОРРОРР 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 1;
Pred. No. 0.0094;
1; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
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POLY-GLU.
POLY-LYS.
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MEDLINE=84270667; PubMed=6087149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90266473; PubMed=2161150;
PROSITE; PS01359; ZF_PHD_1; 1. PROSITE; PS50016; ZF_PHD_2; 2. Proto-oncogene; Chromosomal tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004 AA; 225054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.18;
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1150
1242
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                                                                        Nuclear protein.
ZN_FING 206
ZN_FING 259
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DB 1; Length 449;

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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-i- DEVELOPMENTAL. STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
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6 X 2 AA TANDEM REPEATS OF R-G.
DEF40D7F8ED61DIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 47.7%; Score 148; DB 1; Length 487; Similarity 53.2%; Pred. No. 0.0039; 25; Conservative 1; Mismatches 21; Indels
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PROSITE; PS01098; LIPASE_GDSL_SER; 1.
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TRANSFAC; T01618; -.
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345 3
487 AA;
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428
449 AA;
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P40603;
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Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O. Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehle E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chun G.W., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Dunn P., Etgi P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y., Glill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lez C.A., Li J.H., Li Y.-P., Militscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.K., Shin P., Southwick A.M.,
                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter specific proline rich protein APG precursor.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudloctyledons; core eudicots; Rosidae;
                                                     Gaps
                                                                                                              КУРРАРКРАРОРОРОРОРОРО------ЕАРАР 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES. CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Columbia;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Submitteed (SEP-2001) to the BMBL/Genbank/DDBJ databases.
-1-Tissub SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL
TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-1-DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE BYELOPMENT, HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pal G, Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
                                                   19;
                                                 Indels
        Score 147.5; DB 1;
Pred. No. 0.0039;
1; Mismatches 12;
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MEDLINE-21016719; PubMed-11130712;
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          47.68;
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                                                 Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
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NCBL_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                      ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Glycosylated polyproline II rods-with-kinks as a structural motif in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Eukaryota, Virldiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                  JULIANE STANDARD; PRT; 555 AA.

OFPO6; 003927; Fel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyprollne-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J., Goodenough U.W.;
                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                Score 143; DB 1; Length 534;
Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                     3 KVPPAPKPAPQPGPQP-----PQPPQPPQPQPQPQPQPGPAPQPP
                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                  S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: Associates with GP2 and GP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant hydroxyproline-rich glycoproteins.";
Blochemistry 40:2978-2987(2001).
                                                                                            EMBL, X60377; CAA42925.1; -
EMBL, AC022472; AAF79900.1; ALT_SEQ.
EMBL, X4058847; AAL24235.1; -
PIR, S21961; S21961.
InterPro; IPR001087; Lipase_GDSL,
Pfam; PF00657; Lipase_GDSL, 1.
PROSITE; PS01098; LIPASE_GDSL,SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21159092; Pubmed=11258910;
                                                                                                                                                                                                                          141 E -
325 E -
58007 MW; I
                                                                                                                                                                                                                                                                 46.18;
52.98;
  model prediction.
                                                                                                                                                                                                                                                                                   27; Conservative
                                                                                                                                                                                                                                             534 AA;
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                          141
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ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                             SEQUENCE
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the Euror
                                                                                                                                                                            SIGNAL
                                                                                                                                                                   Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECULNE-95343549; PubMed-7618274;
MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                             VEGETATIVE CELL WALL PROTEIN GP1.
                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y065_NPVOP STANDARD; PRT; 875 AA.
983949; 065364; 010323;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71).
07971a pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of the Orgyla pseudotsugata multinucleocapsid polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97271300; Pubmed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
            as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ahrens C.H., Rohrmann G.F.;
"The DNA polymerase and helicase genes of a baculovirus of pseudosugata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication.";
Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VPPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPGAPA---PQPPA 47
                                                                                                                                                                                                                                                                                                                                          VEGETATIVE CELL WALL
non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO.
                                                                                                                                                                                                                InterPro; IPR003882; Pistil_extensin.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                              SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eudosugata.";
Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54219 MW;
                                                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                    18;
Repeat; Si
29
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455
493
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455 4
493 4
555 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-164623;
                                                                                                                                                                                                                                                                                      Glycoprotein;
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CSP_PLABE
P06915;
                                                                                           DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                DISULFID
DISULFID
DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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         CHAIN
CHAIN
PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGE STANDARD DESCRIPTION OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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STRAIN-New Zealand white; TISSUE-Testis;
STRAIN-New Zealand white; TISSUE-Testis;
STRAIN-New Zealand white; TISSUE-Testis;
SCHARGSON R.T., O'Rand MGS;
"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";
Blochim. Blophys. Acta 1219:215-218(1994).
IT STATESTISE STREAMATIAN SPERMATOZOA.
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENCYS: 201.4.2.).
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PR0712; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
SIGNAL
1 431 ACROSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBL_TaxID=9986,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PPAPKP-----APQPGPQPPQPPQPPQPPQPQPQPQPQPQPQPQPAPAPQPP 46
                                                                                                                                                                                                                                                                                                                           Score 140; DB 1; Length 875;
Pred. No. 0.018;
1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                     F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                            POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                         DOMAIN 86 91 P
SEQUENCE 875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                                                       45.2%;
                                                                                     EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U05204; AAA61630.1; -.
                                                                                                                                             EMBL; D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                                                       Local Similarity ___
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, 01-FEB-1996 (Rel. 33,
                                                                                                                                                                                                      Hypothetical protein.
DOMAIN 86 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS.
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P48038;
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACRO_RABIT
                                                                                                                                                                                                                                                                                                                                                                                   Matches
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-1- MISCELLARIPOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

-1- SIMILARIEY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;
Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;
Circumsporozoite protein of Plasmodium berghei: gene cloning and
identification of the immunodominant epitopes.;
Mol. Cell. Biol. 6:3965-3972(1986).
-!- FUNCTION: THE CIRCUMSPORZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPORZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPKPAPQPGPQPPQ-----PPQPPQPQPQPQPQPQPEAPAPQPPA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

45.0%; Score 139.5; DB 1; Length
Best Local Similarity 51.0%; Pred. No. 0.011;
Matches 25; Conservative 1; Mismatches 16; Indels
                                                                                                               INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             1C015A4E0BC0C668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                   SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dircumsporozoite protein precursor (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A25083; O220MB.
Interpro; IPR003067; Crcmsprzoite.
Interpro; IPR000884; TSP1.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       46422 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                             86
140
238
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 18:376-376(1990).
-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                           186 ANDPPPPNPNDPAPPQGNNNPQPQPRPQPQPQPQPQPQPQPQPQPQPQPQPG 239
                                                                                                                                2 AKVPPAPK---PAPQPG---PQPPQPPQPPQPPQPQPQPQPGPE-APAPQPPAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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  238 16 X 2 AA TANDEM REPEATS OF P-Q. 37138 MW; E8068A6D11D9551B CRC64;
                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 X 8 AA REPEATS.
17 X 2 AA REPEATS OF P-Q.
0EC240EE35681AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIRCUMSPOROZOITE PROTEIN.
                                            Score 137.5; DB 1;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137.5; DB 1;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                        347 AA
                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Circumsporozoite protein precursor (CS).
Plasmodium berghei (strain Anka).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                          PRT;
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IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO1303; CRCMSPRZOITE.
                                                          44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
55.68;
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                                                      Query Match
Best Local Similarity 55.69
Matches 30; Conservative
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Best Local Similarity 55.69
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  206 2
339 AA;
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P23093;
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                    CSP_PLABA
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194 ANDPPPPNPNDPAPPQGINNNPQPQPRPQPQPQPQPQPQPQPQPQPQPQPQPQPG 247

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Search completed: May 7, 2003, 16:48:15 Job time : 6.24361 secs 09alq4 bordetella 09khh bordetella 09khh bordetella 09khh bordetella 09khy bordetella 09ahy bordetella 09ahy bordetella 09ahy bordetella 09am bordetella 09s6n0 bordetella 09s6n0 bordetella 06925 bordetella 06925 bordetella 06925 bordetella 06927 bordetella 06927 bordetella 09139 bordetella 09139 bordetella 09139 bordetella 09139 bordetella 09139 bordetella 06927 bordetella 06927 bordetella 06927 bordetella 06927 pordetella 06927 pordetella 06927 bordetella 06927 pordetella 06921 poeumocysti 09941 pneumocysti 09641 pneumocysti 09641 pneumocysti 09641 pneumocysti 09641 pneumocysti 09611 bomo sapien 09115

Sequence:

Run on:

Searched:

Database

Result š

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MEDLINE-20159389; PubMed=10899896;

Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Boursaux-Ende C., Guiso N.;

Infect: Immun. 68:4815-4817(2000).

EMBL: AJ250095; CAB76449.1;

Interpro; IPR004899; Pertact_sup.

Interpro; IPR004899; Pertact_sup.

Interpro; IPR002965; P_rich_extensn.

PRINTS; PR01217; PRICHEXTENSN.
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Best Local Similarity 100.0%; Pred. No. 2.9e-19;
Matches 54; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Barderia; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA; 11073 MW; AOA339BFF0EAB8C6 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P\68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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06908
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09AHP0
09AIX8
09S6M9
09S6M9
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Q9ULL5
Q8T1Y6
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SEQUENCE
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Q9K5G1
  ACCOCCOS OCT REPRESENT THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                         1 GAKVPPAPKPAPQPGPPQ......QPQPEAPAPQPPAGRELSAA
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                    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
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09K7X9
                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_mammal:*
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sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rvirus:*
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                                                                                               1 GAKVPPAPKPAPQPGPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                               1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 231;
                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MBORD51;
MEDLINE-21117018; PubMed-11179374;
Register K.B.;
Register K.B.;
Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007267; AAG38443.1; -.
InterPro; IPR003992; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).

EMBL; AV007277; AAG38453.1; InterPro; IPR003992; pertaction. InterPro; IPR003999; Pertact. Sup. InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 274; DB 2; Length 13.
Pred. No. 5.2e-16;
Pred. Totches 0; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23930 MW; 5FB281B95E74678C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Query Match 90.2%; Score 279.5; DB 2; Best Local Similarity 94.4%; Pred. No. 2.3e-16; Matches 51; Conservative 0; Mismatches 0;
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92.6%; Pred. No. o...
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MEDLINE-21117018; PubMed-11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 92.6
es 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1
NON_TER 231 2
SEQUENCE 231 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                        Bordetella.
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Polymorphism of Repeated Regions of Pertactin in Bordetella pertuasis, Bordetella parapertussis, and Bordetella bronchiseptica."; prifect. Immun. 68:4815.4817(2000).

EMBL; AJ250092; CAB76446.1; ...

InterPro; IPR004899; Pertact_sup.

InterPro; IPR002965; P_ICL_extensn.

Pfam; PF03212; Pertactin: 1.

PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 287; DB 2; Length 107;
Pred. No. 2.3e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella Novel Genetic and Phenotypic Heterogeneity in Bordetella Infonchiseptica Pertactin.";
EMBL; AY007273; AAG38449.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin._vir.
InterPro; IPR004899; Pertact.aup.
InterPro; IPR002965; P.rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA; 11076 MW; C32F321161C9E400 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09ALP7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                 01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AA
                                               107 AA.
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MEDLINE-21117018; PubMed-11179374;
                                                 PRT;
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NON_TER 304 304

NON_TER 304 A34

SEQUENCE 304 AA; 31759 MW;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.68;
                                                                                                                                             Pertactin (P.68) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Conservative
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                                                 PRELIMINARY;
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304 AA;
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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13 GAKAPPAEKPAPQPGPOPGPQPPQPPQPPQP---PQRQPEAPAPQPPAGRELSAA 72
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                    "Novel Generic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
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SEQUENÇE 167 AA; 11036 MW; 1AC13209D0238107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P 68) (Fragment).
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 83.5%; Score 259; DB 2; L
Best Local Similarity 88.9%; Pred. No. 1.3e-14;
Matches 48; Conservative 0; Mismatches 0;
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83.2%; Score 258; DB 2; L
Best Local Similarity 89.1%; Pred. No. 5.8e-15;
Matches 49; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA
                                                                                                                                                            EMBL; AX007275; AAG38451.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20359389; PubMed-10899896;
                MEDLINE-21117018; PubMed-11179374;
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PRINTS; PRO1484; PRIACTNFAMLY.
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                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
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NCBI_TaxID=518;
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01-JUN-2001
01-JUN-2002
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NON_TER
SEQUENCE
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EMBL; AJ250089; CAB76443.1; -. InterPro; IPR004899; Pertact.sup.
InterPro; IPR002465; Perito.
Fign.; PF03212; Pertactin; Inferpro; IPR04812; Pertactin; InterPro; IPR04812; Pertactin; Inferpro; IPR04812; Pertactin; InterPro; IPR04812; Pertactin; INTERP04812; Pertact
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKVPPAPKPAPQPPQPPQPPQPPQPPQPQPQPQPPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 111;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                         Length 256;
                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 111 AA; 11453 MW; 9B67012D3B9AEECA CRC64;
                                                                                                                                                                                                                           26277 MW; 6A894FE6D48D52D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-ocr-2000 (TrEMBLrel. 15, Created)
01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                     86.5%; Score 26%; DB 2;
90.7%; Pred. No. 1.8e-15;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 265; DB 2;
Pred. No. 1.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AA
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InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20359389; Pubmed-10899896;
                                InterPro; IPR002965; Prich_exterpro; IPR03212; Pertactin; 1. PRINTS; PR01482; PERTACTIN; 1. PRINTS; PR01217; PRICHEXTENSN. NON_TER 1 1 1 1 NON_TER 256 SEQUENCE 256 AA; 26277 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 85.5%;
Best Local Similarity 84.5%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.7
Matches 49; Conservative
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Q9ALP5;
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Gaps

RESULT 7 Q9ALP5

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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250087; CAB76441.1;
"InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P. rich_extensn.
Pf03212; Pertactin; I.
                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.6%; Score 256; DB 2; Length 11
87.5%; Pred. No. 8.7e-15;
Live 0; Mismatches 5; Indels
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NON-TER 111 111 111 111 111 111 111 6 MW; 5140669692808F8E CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20359389; PubMed=10899896;
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Pertactin (P.68) (Fragment).
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hes 49; Conservative
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Best Local Similarity
Matches 49; Conserva
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01-OCT-2000 (
01-JUN-2002 (
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                                                                                                                                                                                                                                                                           Bordetella.
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SEQUENCE
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                                                09K5G9
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RESULT 11
Q9K5G9
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EMBL: AJJ45927; CABB2515.1; InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR003991; pertactin.vir.
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Mool F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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89.1%; Pred. No. 3.4e-14;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 83.2%; Score 258; DB 2; Length 200; Local Similarity 89.1%; Pred. No. 9.7e-15; nes 49; Conservative 0; Mismatches 2; Indels
                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                             Novel Genetic and Phenotypic Heterogeneity in Bordetella
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNEAMLY.
SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
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200 Aa; 20826 MW; 9F3AC6E4128942E6 CRC64;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 AA
                                                                                                                                                                                                                                                                                          bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL: AY007211. AAG38447.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                     MEDLINE-21117018; PubMed=11179374; Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1217; PRICHEXTENSN.
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  Pertactin (Fragment)
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Best Local Similarity
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                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=518;
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NON_TER
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Q9L4E2;
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Q9L4E2
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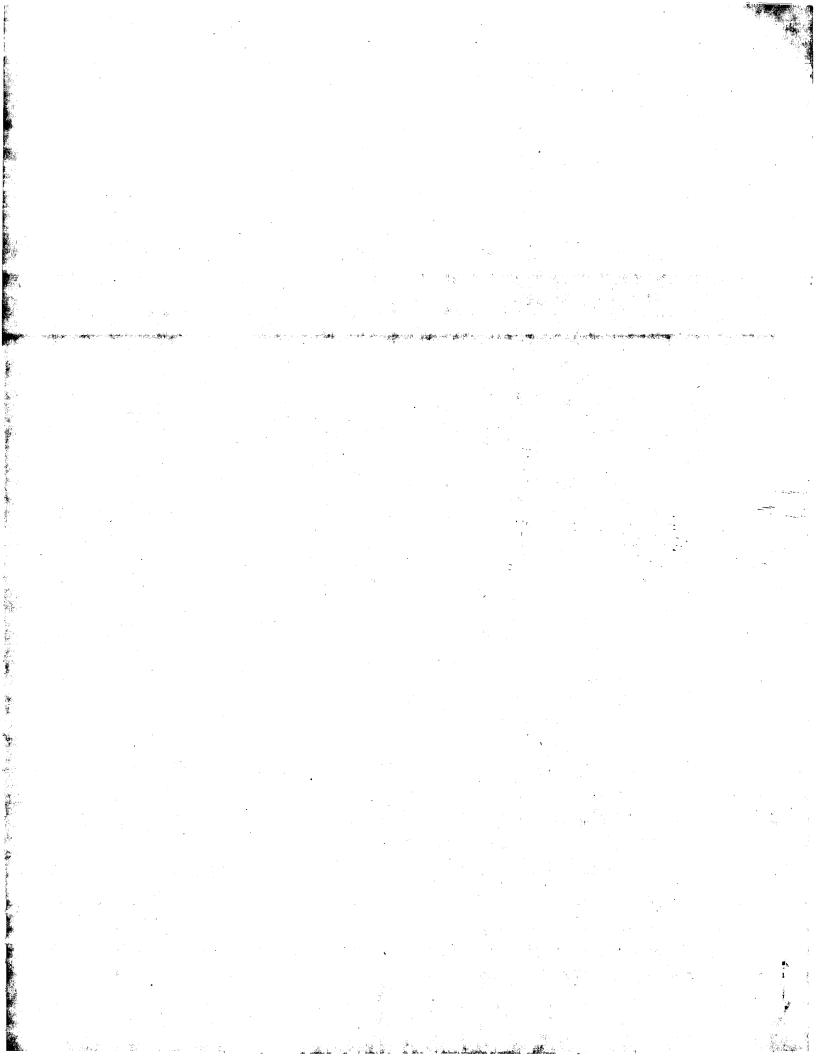
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Length 111;

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Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families camino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1;
1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                    Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.6%; Score 256; DB 2; Length 12
87.5%; Pred. No. 9.4e-15;
Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                           122 AA.
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Interpro; IPR002965; P_rich_extensn.
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115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
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         SEQUENCE
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                                                                                                                                                                                                                                                          RESULT 15
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250083; CAB76437:1; -.
Interpro: IPR004899; Pertact.sup.
InterPro: IPR002965; P.rich_extensn.
Pf03212; Pertactin; 1.
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID-518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 256; DB 2; Length 252;
Pred. No. 1.7e-14;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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26107 MW; 368C142508D77057 CRC64;
                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                         252 AA.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last sen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007265; AG38441.1; -
InterPro; IPR004895; Pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC19395;
MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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1 Similarity 87.5%;
49; Conservative
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       Pertactin (Fragment)
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NON_TER 252 3
SEQUENCE 252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=518;
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Q9K5H3
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immut. 68:4815-4817(2000).
EMBL; AJ250091; CAB76445.1;
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002065; P. Inf.
PF03212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                     Length 115;
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                                                            Indels
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
81.9%; Score 254; DB 2; L/81.7%; Pred. No. 1.3e-14;
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85.2%; Pred. No. 3.8e-14;
Live 0; Mismatches 2;
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Job time : 28.598 secs
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             Query Match
Best Local Similarity 81.75
Matches 49; Conservative
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Best Local Similarity 85.2
Matches 46; Conservative
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7, 2003, 16:53:34; Search time 16.1908 Seconds (without alignments) 306.927 Million cell updates/sec
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1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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1: //ggn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
2: //ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
3: //ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
4: //ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
5: //ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
6: //ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
7: //ggn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*
8: //ggn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*
9: //ggn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*
11: //ggn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*
11: //ggn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*
13: //ggn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.ppp:*
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14: //ggn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.ppp:*

Published_Applications_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 21, Appl Sequence 21, Appl Sequence 6, Appl Sequence 15, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 20, Appl Sequence 21, Appl Sequence 24, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 160, Appl Sequence 160, Appl Sequence 160, Appl Sequence 17, Appl Sequence 160, Appl Sequence 160, Appl Sequence 17, Appl Sequence 180, Appl Sequence 180, Appl Sequence 180, Appl Sequence 180, Appl
SUMMARIES	US-09-855-754-22 US-09-855-754-19 US-09-855-754-19 US-09-855-754-16 US-09-855-754-4 US-09-855-754-16 US-09-855-754-18 US-09-855-754-18 US-09-855-754-14 US-09-855-754-14 US-09-855-754-14 US-09-855-754-20 US-09-855-754-21 US-09-855-754-21 US-09-855-754-21 US-09-855-754-21 US-09-855-754-21 US-09-855-754-24 US-09-855-754-24 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-09-855-754-34 US-00-855-754
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Sequence 7, Appli Sequence 967, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 5, Appli Sequence 5, Appli Sequence 61, Appli Sequence 60, Appli Sequence 62, Appli Sequence 62, Appli Sequence 62, Appli Sequence 62, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 63, Appli Sequence 64, Appli Sequence 65, Appli Sequence 66, Appli	Sequence 35844, A Sequence 2, Appl1 Sequence 9, Appl1
	10 US-U9-864-/61-36844 9 US-10-020-215-2 10 US-09-823-240-9
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120 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	116.5
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ALIGNMENTS

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARABERTOSSIS, AND STATLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILLE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: 9206-0000
CURRENT FILLING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUTSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 54; Conservative 0; Mismatches 0;
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US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                             APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
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US-09-855-754-21
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LENGTH: 54
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CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHEELA PRAPARHICASSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHEEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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          REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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Pred. No. 6.2e-12;
0; Mismatches 5;
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Pred. No. 1.9e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BORDETELLA PARABERTUSSI TITLE OF INVENTION: BRONCHISEPTICA, THEIR UTITLE OF INVENTION: IMMUNGENIC COMPOSITION; FILE REFERENCE: 03495-0206-00000; CURRENT PELLCATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
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US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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L Similarity 84.5%;
49; Conservative
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1 Similarity 96.3%;
52; Conservative
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Best Local Similarity
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US-09-855-754-6
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: MANDHOSENIC COMPOSITIONS PILE REFERENCE: 03495-0206-00000
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR TELLIA DATE: 2001-09-10
PRIOR FILING DATE: 2001-05-25
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Pred. No. 5.8e-11;
0; Mismatches 5; Indels
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Pred. No. 1.7e-11;
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PRIOR APPLICATION NUMBER: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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US-09-855-754-15
                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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89.1%;
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1 Similarity 84.5%;
49; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
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APPLICANT: GUISO-MACLOF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPEATURING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA PERPEATURING INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR ELILING DATE: 2000-05-25
                                                                                                                                                                         1 GAKVPPAFKPAPQPGPQP----PQP-PQPPQPQPQPQPQPQPEAPAPQPPAGRELSAA
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
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                                                    Length 59;
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                                                  Score 249.5; DB 9;
Pred. No. 6.7e-11;
1; Mismatches 3;
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Pred. No. 7.2e-11;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
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PRIOR FILIND BATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VOT: 2.1
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US-09-855-754-14
                                                                                                                                                                                                                                                                                                              Sequence 20, Aprlication US/09855754
Publication No. US2002019237A1
GENERAL INFORMATION:
APPLICANT: BOUNSAUX: EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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85.2%;
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illarity 81.7%;
Conservative
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Best Local Similarity 85.2
Matches 46; Conservative
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SOFTWARE: Patentin Ver.
                                               Query Match
Best Local Similarity
Matches 49; Conserv
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US-09-855-754-16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2002-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                 Length 911;
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                                                                                                                                                                 Score 258; DB 9;
Pred. No. 1.7e-10;
0; Mismatches 2;
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US-09-855-754-18
                                                                                             ORGANISM: Bordetella bronchiseptica
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; Sequence 18, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
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ilarity 89.1%;
Conservative
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Best Local Similarity 87.5%;
Matches 49; Conservative
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SOFTWARE: Patentin Ver. 2.1
  SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
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US-09-855-754-16
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LENGTH: 56
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LENGTH: 59
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                      ID NO 4
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Matches
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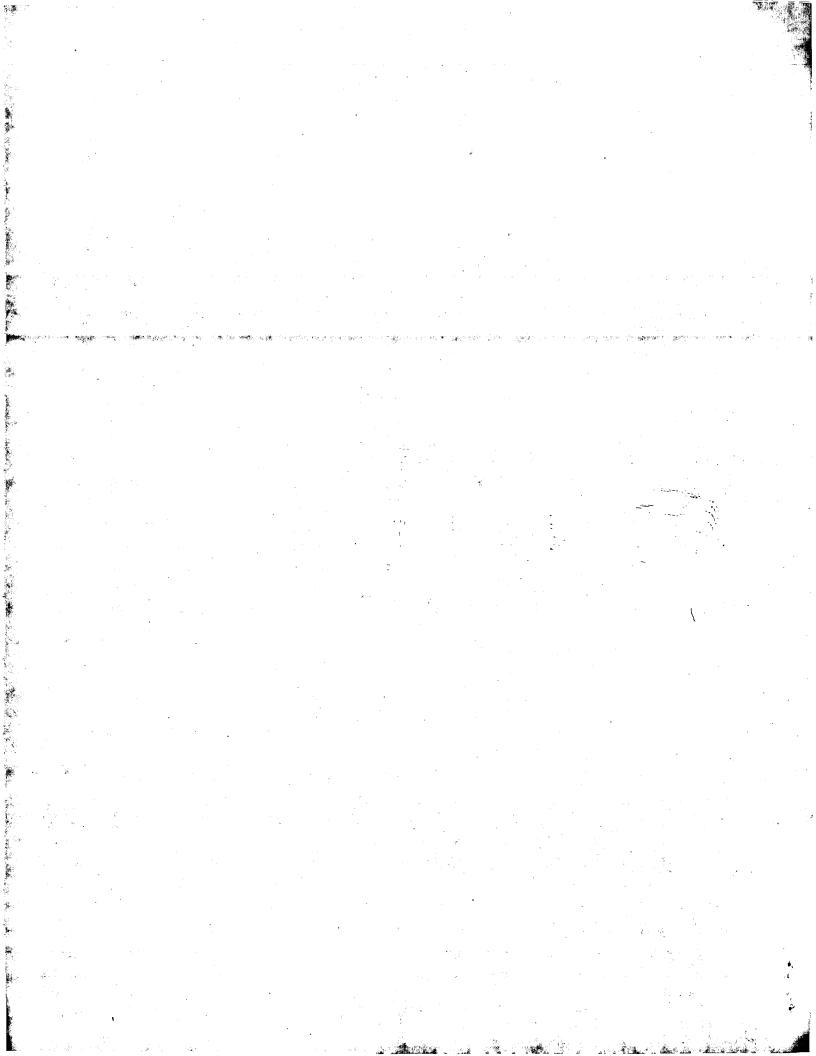
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RESULT 15
US-10-001-873-50
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LENGTH: 910
                        US-09-855-754-5
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTISSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MANUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
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Pred. No. 5.6e-10;
1; Mismatches 1
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Pred. No. 8.7e-09;
0; Mismatches 1
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                  Sequence 17, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
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75.9%;
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Best Local Similarity 85.7%;
Matches 48; Conservative
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Best Local Similarity
Matches 41; Conserv
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                                                                                                                            US-09-855-754-17
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISPETICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                           OF THE REPEATED
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                                                                                                      APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PITTLE OF INVENTION: BRONGHISPETICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
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11.1e-07;
1; Indels 12; (
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Best Local Similarity 70.4%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 216; DB
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUSSAUX EUDE, CAROLINE
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                                                                                  CAROLINE
Sequence 5, Application US/09855754
Publication No. US20020192237A1
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75.98;
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SEQ ID NO 24
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                                                   GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE,
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Best Local Similarity
Matches 41; Conserv
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us-09-855-754b-22.rapb
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APPLICANT: Sun, Yongming
APPLICANT: Library Sun, Yongming
APPLICANT: Library Compositions and Methods Relating to Lung Specific Genes and Prot
APPLICANT: Library Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0275
CURRENT PLING DATE: 2001-11-20
FRIOR PAPLICATION NUMBER: 60/252,055
PRIOR PAPLICATION NUMBER: 60/252,496
PRIOR PAPLICATION NUMBER: 60/252,496
PRIOR PELING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: 60/252,496
PRIOR PELING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,496
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,496
PRIOR STATE DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,496
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us-09-855-754b-22.rpr

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May 7, 2003, 16:41:02; Search time 10.1193 Seconds (without alignments) 513.008 Million cell updates/sec
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310
1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 54
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
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Perfect score:
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SUMMARIES

G	Description	pertactin - Bordet	Ë	outer membrane pro			UL36 protein - hum	pherophorin-S - Vo	sulfated surface q	chitinase (EC 3.2	hypothetical prote		Ψ	proline-rich prote	cysteine-rich exte	hypothetical prote			proline-rich prote		cysteine-rich exte	proline-rich prote	hydroxyproline-ric	extensin - Volvox	hypothetical prote		m	hypothetical prote		circumsporozoite p
SUMMARIES	ΙD	S15204	A47675	A32560	JC2301	T14355	WMBEH6	T10798	A33647	S51939	T48814	A34043	S42442	S16748	A48232	AE2295	T24470	B96534	S21961	A86335	B48232	T17547	T07907	S22697	T18281	T10340	S47538	F75518	E22364	OZZOMB
	DB	2	7	7	7	7	-	~	7	~	7	7	~	7	~	~	~	7	~	~	7	~	~	7	~	~	7	7	7	-
	Query Match Length	922	911	910	430	1494	3164	599	485	439	1952	141	487	449	209	383	165	464	534	1137	196	544	446	464	1474	875	431	839	320	335
æ	Query Match	85.5	83.2	69.7	55.3	52.3	50.8	49.7	49.4	49.0	48.9	48.7	47.7	47.6	47.4	47.1	46.9	46.5	46.3	46.1	46.0	45.5	45.3	45.3	٠	45.2	45.0	44.7	44.5	44.4
	Score	265	258	216	171.5	162	157.5	154	153	152	151.5	151	148	147.5	147	146	145.5	144	143.5	143	142.5	141	140.5	140.5	140.5	140	139.5	138.5	138	137.5
	Result No.	-	7	9	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	58

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Gaps

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1 GAKVPPAPKPAPQPGPQP-PQPPQPPPQPQPQPQPQPQPARAPAPQPPAGRELSAA 54

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Ouery Match

83.2%; Score 258; DB 2; Length 911;
Best Local Similarity 89.1%; Pred. No. 2.2e-10;
Matches 49; Conservative 0; Mismatches 2; Indels

circumsporozoite p pistil extensin-11 hypothetical prote hypothetical prote procyclic acidic r hypothetical prote proline-rich prote transcription fact transcription fact po-rich protein - glycaraldehyde-3-p AcOrf-66 protein - procyclic acidic r procyclic acidic r procyclin PSSA-1 - pneumococcal surfa regulatory factor	otein P70 on 07-Apr-1994 #text_change 08-Oct-1999 Charles, I.G. mbrane protein from Bordetella parapertussis: clo 51771; PMID:2041476 :939761; PIDN:CAA38419.1; PID:939762	Query Match Best Local Similarity 84.5%; Score 265; DB 2; Length 922; Best Local Similarity 84.5%; Pred. No. 7.8e-11; Matches 49; Conservative 0; Mismatches 5; Indels 4; Gaps 1; Qy 1 GARVPPAFRPAPQPGPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQP
OZZOBK JQ1696 S75138 S75138 S75138 AZ6036 AZ6036 AZ6201 S56201 S56201 S56201 S7858 AZ6918 AZ6918 AZ6918 AZ6918 AZ6918 AZ6918 AZ6013	ALIGNMENT slla parapertussis outer membrane protein P70 la parapertussis la fesquence_revision 07-Apr sl4659 G; Novotny, P.; Charles, 409-417, 1991 outin, an outer-membrane pr sl5204; MUID:91251771; PM LIL> EMBL:X54547; NID:939761;	Match Local Similarity 84.5%; Score 265; Local Similarity 84.5%; Pred. No. 7. 85.49; Conservative 0; Mismatche 1 GAKVPPARRPAPOPGPOPPOPPOPPOPPOPPOPPOPPOPPOPPOPPOPPOP
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	erti orati chy tny 1999 out	85.5%; 84.5%; 11ve OPGPOPP 11111 OPGPOPP 10chisep
348 426 1749 127 127 127 128 506 506 514 400 440 808 808 143 145 744	RESULT 1 S15204 pertactin Bordetella parapertussis pertactin Bordetella parapertussis (Alternate names; outer membrane pr C. Species: Bordetella parapertussis C. Date: 07-Apr-1994 Bequence_revisit C. Accession: 515204; 814659 R.Li, L.J. Dougan, G.; Novotny, P.; MOI. Microbloll. 5, 409-417, 1991 A. Title: P. 70 pertactin, an outer-me A. Reference number: 515204; MUID:912 A. Rocession: 515204 A. Residues: 1-922 CLIL> A. Residues: 1-922 CLIL> A. Corss-references: BMBL:X54547; NID A. Gene: prn C. Genetics: C. Genetics: C. Genetics:	Query Match Best Local Similarity Best Local Similarity Best Local A9; Conservative 1 GARVPPAFKPAPOPGPP
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RESULT 3

A32560

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R.M.Geoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; I. J. Gen. Virol. 69, 1531-1574, 1988
A.Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Reference number: A30083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: 130085
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-3164 < MCG>
A; Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeted to the
                   EMBL: AF077000; NID: 93598973; PID: 93598974; PIDN: AAC62959.1
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A; Residues: 1-599 <GOD>
A;Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to t
C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pherophorin-S - Volvox carteri
C;Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10799
B;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
ExGodl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
R;Godl, E.; 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The p
A;Reference number: 217154; MUID:97162277; PMID:9009264
A;Recession: T10798
A;Accession: T10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: I30085
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                                                                                                                                                                                                                                                                                              Gaps
                                               A) Experimental source: brain
C;Genetics:
C;Genetics:
C;Function:
A;Description: may be involved in regulating Ha-ras-dependent cell growt
C;Reywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                            Score 154; DB 2; Length 59
Pred. No. 0.00094;
1; Mismatches 17; Indels
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C,Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОР
                                                                                                                                                                                                                                   Score 162; DB 2;
Pred. No. 0.00058;
3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 157.5; DB Pred. No. 0.002; 2; Mismatches
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UL36 protein - human herpesvirus 1 (strain 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 24; Conservative
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ilarity 72.3%;
Conservative
                                                                                                                                                                                                                                        52.3%;
ilarity 65.3%;
Conservative
A; Residues: 1-1494 <CAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                    C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
R;Charles, IG;; Dougan, G; Pickard, D; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Fitle: Molecular cloning and characterization of protective outer membrane protein P-6
A;Reference number: A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine-phosphatase (EC 3.1.3.48) TD14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14355
R;Cao, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, K.R.; Graham, R.M.; Zhou, M.
A;Title: A novel putative protein-tyrosine phosphatase contains a BRO1-like domain and A;Reference number: Z18004; MUID:98361981; PMID:9694860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
Nakamura, Y.
1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A;Reference number: JC2299; MUID:96051989; PMID:8535973
A;Accession: JC2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-430 <WAD>
A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical 47.8K protein - Pneumocystis carinii
N/Alternate names: ORF-3
C.Species: Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054 A;Note: it is uncertain whether Met-1 or Met-3 is the initiator
  GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP---PQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Pred. No. 5.3e-05;
5; Mismatches 5; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKVPPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Reywords: membrane protein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-910/Product: outer membrane protein P6.9 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                      - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 216; DB 2; I
Pred. No. 1.2e-07;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                         outer membrane protein P.69 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.78;
75.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 55.3%;
1 Similarity 52.5%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 P 318
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Matches

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Best Loca Matches

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셤 ò RESULT T14355

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pherophori

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1;

Gaps

1;

Indels

47

Length 1952;

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hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
                    A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
                                                                                                                                                                                                                                                                                                                                                   5 фРАРКРА-РОРСРОРРОРРОРРОРРОРОРОРОРОР
                                                                                                                                                                                                                    Score 151.5; DB 2;
Pred. No. 0.0034;
4; Mismatches 14;
                                                                                                                                                                                                                    48.9%;
56.8%;
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Best Local Similarity 55.6%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                     Conservative
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A,Molecule type: DNA
A,Residues: 59-136 <BA2>
A,Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-141 <BAK>
A;Cross-references: GB:M32217
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Best Local Similarity
Matches 25; Conserv
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A; Residues: 1-487 <FAR>
                                                                                                                    A; Gene: NCSP:15E6.220
A; Molecule type: DNA
                                                                                                                                            A; Map position: 2
A; Introns: 281/3
                                                                                               C;Genetics;
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R;Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
C. Call Biol. 109, 3493-3501, 1889
A;Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A;Reference number: A33647; MUID:90094551; PMID:2689458
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48814
R;Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chitinase (EC 3.2.1.14) precursor - beet
C;Species: Beta vulgaris (beet)
C;Date: 28-0c-1996 *sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: S51939; S72315; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.
Plant Mol. Biol. 27, 211-216, 1995
A;Title: A prolline-rich chitinase from Beta vulgaris.
A;Reference number: S51939; MUID:95170004; PMID:7865792
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                                                                                        C;Species: Volvox carteri
C;Date: 11-Apr_1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
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A; Residues: 1-485 <ERT>
A; Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C; Keywords: glycoprotein
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A;Residues: 1-439 <BER>
A;Cross-references: EMBL:X79301; NID:g488730; PID:g488731
A;Note: the authors translated the codon TGC for residue 416 as Gly
A;Accession: S72315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 РРАРКРАРОРОРОРРОРРОРРОРОРОРОРОРОРОРОР 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: plant chitinase homology
C; Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26439/Product: chitinase #status predicted <MAT>
F;183-423/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 153; DB 2;
Pred. No. 0.00093;
1; Mismatches 17;
                                                                sulfated surface glycoprotein 185 - Volvox carteri
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il Similarity 57.1%;
24; Conservative
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A; Accession: T48814
A; Status: preliminary
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A; Residues: 191-397 <BER2>
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A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
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C;Accession: A34043; B34043
R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Blochem. Biophys. Res. Commun. 166, 66-73, 1990
A:Title: Presence in invertebrate genomes of sequences characterized by the repetitio A;Reference number: A90159; MUID:90147742; PMID:2105723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear protein EBNA2 - human herpesvirus 4
C;Species: |human herpesvirus 4, Epstein-Barr virus
C;Species: |human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 *Requence_revision 19-Mar-1997 *text_change 20-Jun-2000
C;Accession: S42442; S32988; S42447
R;Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: A;Reference number: S42440; MUID:86259739; PMID:3460083.
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R;Dambaugh; T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen A;Reference number: S42447; MUID:85063846; PMID:6209719
A;Accession: S42447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
C;Species: Owenta|fusiformis
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 151; DB 2;
Pred. No. 0.00048;
0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1.487 <SAM>
R;Farrell, p.J:
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S32998
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A; Residues: 1-88, 'PPP', 89-487 <DAM>
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Best Local Similarity
Matches 23; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary A; Molecule type: DNA
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Job time
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A;Description: Cloning and characterization of a proline-rich gene expressed specificall A;Reference number: S16748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1991
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:9341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :Title: Developmental expression of tobacco pistil-specific genes encoding novel extens: Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Keywords: cell wall: extracellular matrix; fertilization; glycoprotein F;1-19/Domain: signal sequence #status predicted <SIG> F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT> F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c; opecies: Nicotiana tabacum (common tobacco)
C; Date: 26-May-1994 *sequence_revision 26-May-1994 *text_change 01-Dec-2000
C; Accession: A48232; PQ0475; S24617
R; Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheunq, A.Y.
                                                                                                                                                                                                                                                                                                                                                         Species: Brassica napus (rape)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
A;Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extensin-like protein 1 precursor - common tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 147; DB 2; Length 209;
Pred. No. 0.0012;
6; Mismatches 12; Indels
                                                                      Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 39-209 <GOL>
A; Cross-references: EMBL:214020; NID:919918; PID:919919
A; Experimental source: stigma, style; strain Petit Havana SR1
                                                                                                                    Indels
                                                                                                                                                                                                4 VPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                    Score 148; DB 2;
Pred. No. 0.002;
1; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147.5; DB
Pred. No. 0.002;
4; Mismatches
                                                                                                                                                                                                                                                                                                                       proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 13-3n-11995 #sequence_revision
C;Accession: SiG'n Foster, G.D.; Blundell
R;Roberts, M.R.; Foster, G.D.; Blundell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.4%;
ilarity 42.4%;
Conservative (
                                                                      47.78;
53.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
                                                     Query Match
Best Local Similarity 53.2*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: glutelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-449 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA; Residues: 1-209 < WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S16748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A48232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: PQ0475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 QPP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteine-rich
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hypothetical protein all3916 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2295
R;Raneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUDD:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:BA000019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                            47
  -PPQPPQPQPQPQPEAPAPQPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 РРАРКРАРОРСРОРРОРРОРРОРРОРОРОРОРОРОР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 2;
Pred. No. 0.0022;
1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7, 2003, 16:55:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.1%;
54.8%;
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OM protein - protein search, using sw model

7, 2003, 16:31:28 ; Search time 28.0579 Seconds (without alignments) 256.453 Million cell updates/sec Мау Run on:

US-09-855-754B-22

Title: Perfect score:

310 1 Gakvppapkpapgpgpgppg.......... Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

/SIDS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1984.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1984.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDS/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDS/gcgdata/geneseqy/geneseqp-embl/AA1986.DAT:

SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989

/SIDS2/gcgdata/geneseq/genesegp-emb1/AA1990.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl

/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: /gcgdata/geneseq/geneseqp-embl/AA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 IDS2/gcgdata/geneseq/geneseqp-emb1/AA1995

/gcgdata/geneseq/geneseqp-embl/AA1999.DAT 'gcgdata/geneseq/geneseqp-emb1/AA1996.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT /gcgdata/geneseq/geneseqp-embl/AA19

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcqdata/geneseqp-embl/AA2001.DAT:/

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:

SUMMARIES

-										
Description	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Bordetella paraper	Bordetella paraper	B. bronchiseptica	Pertactin antigen	· prn proteins. Bor	Bordetella bronchi	B. bronchiseptica
) ;									
QI	AAE16201	AAE16200	AAE16198	AAR25578	AAE16185	AAE16194	AAR14320	AAR26503	AAE16183	AAE16197
90	23	23	23	13	23	23	12	13	23	23
% Query Match Length DB	54	52	28	922	922	52	911	911	911	26
& Query Match	100.0	92.6	85.5	85.5	85.5	83.2	83.2	83.2	83.2	82.6
Score	310	287	265	265	265	258	258	258	258	256
Result No.	н	7	Э	4	S	9	7	æ	6	10

Pertactin antigen B. bronchiseptica R. bronchisentica		Bordetella pertuss Bordetella pertuss Bordetella pertuss			Human ORFX ORF2085	human	beet c	Human polypeptide			.Human polypeptide	Human polypeptide	\rightarrow	opsis	human		Arabidopsis thalla		ser-Pro-Pro de	Mouse ischaemic co	Plasmodium berghei	Sugarcane proline	Streptococcus pneu		Arabidopsis thalia	CO
12 AAR14321 23 AAE16195 23 AAE16199			-		21 AAB42321 22 ABC00876	ABG0987		22 AAO04412 22 AAO02076		-				-	•			22 ABB67302	•						21 AAG36453	21 AAG36452
922 60 48	m on c	100			900	239												40.		261				749	1222	257
240	76.6		€		00		6	2 6				46.3	•			٠	٠	•	•	43.9		٠		43.5	43.4	43.4
255 254 248	247.5	216	195.5	156	155.5	155.5	152	151	149	~	144.5	ຕ	4.	4	141		139	136.5	2	£	135.5	35.	135	m	134.5	134.5
11 12 13	41 45 45	17	19	21	22	24	25.	25	28	29	30	31	32	E (ъ. 4 г	5	36	3/	9 6	66	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 **AAE16201**

AAE16201 standard; peptide; 54 AA

AAE16201;

26-MAR-2002 (first entry)

B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica.

W0200190143-A2.

29-NOV-2001.

23-MAY + 2001; 2001WO-EP06457.

25-MAY 2000; 2000US-206969P.

XXXXXXXXXXXX

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English. Seguence

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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pertactin outer membrane protein region II
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Gaps ö 1 GAKVPPAPKPAPQPEGPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA 54 Length 54; Indels 100.0%; Score 310; DB 23; 100.0%; Pred. No. 8.8e-17; iive 0; Mismatches 0; 54; Conservative Query Match Best Local Similarity Matches g å

54 AA;

AAE16200 standard; peptide; 52 AA 26-MAR-2002 (first entry) AAE16200; AAE16200 RESULT

bronchiseptica strain II-8 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2 29-NOV-2001. 23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Suiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods claim 26; Fig 1c; 47pp; English.

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1;
                                                                                                                                                                                         B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                           Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\rm II}\,.
                                                           5
                                                                          54
                                                                           1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                    Length 52;
                                                           Indels
                                                          . ;
                                          , DB 23;
4.4e-15;
                                         Score 287; DB
Pred. No. 4.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                        AAE16198 standard; peptide; 58 AA.
                                         Match 92.6%;
Local Similarity 96.3%;
hes 52; Conservative
                                                                                                                                                                                                                                                                                        23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                      25-MAY-2000; 2000US-206969P.
                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                      Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                     WO200190143-A2.
                                                                                                                                                                                                                                                                      29-NOV-2001.
                                                                                                                                                          AAE16198;
                             Sequence
                                             Query Match
                                                     Best Loca
                                                                                                                                  AAE16198
                                                                                                                         RESULT
                                                                                                                                                           ð
                                                                                              g
   ប្បប្បវន្តិ
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 41yoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as bloodgical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

WPI; 2002-097639/13.

Claim 26; Fig 1c; 47pp; English.

58 AA; Sequence

Gaps 4, DB 23; Length 58; Query Match 85.5%; Score 265; DB 25 Best Local Similarity 84.5%; Pred. No. 2e-13; Matches 49; Conservative 0; Mismatches

ä

54

õ

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.

Bordetella parapertussis.

Region Region

Location/Qualifiers
254..304
/note= "Pertactin region I" .
564..621
/note= "Pertactin region II"

WO200190143-A2 29-NOV-2001

Bordetella parapertussis pertactin outer membrane protein, p.70.

26-MAR-2002 (first entry)

AAE16185;

AAE16185 standard; Protein; 922 AA.

RESULT 5 AAE16185

RESULT AAR2557

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A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pBC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
35..643
/label- P70
260..262
266..285
/note= "motif associated with cell-cell adhesion"
266..285
/note= "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575..612
/note= "contains 9 direct repeats of Pro-Gln-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "contains 9 direct repeats of Pro-Gln-Pro"
712..714
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acellular vaccine for immunisation against whooping cough -comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                           Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 85.5%; Score 265; DB 13; Length 92
1 Similarity 84.5%; Pred. No. 1.5e-12;
49; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                  Bordetella parapertussis P95 antigen precursor.
AAR25578 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-GB02302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90GB-0027901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WELL ) WELLCOME FOUND LTD.
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                        Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-250033/30.
N-PSDB; AAQ26509.
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                     08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles IG;
                                                            AAR25578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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for

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

N-PSDB; AAD25442

25-MAY-2000; 2000US-206969P 23-MAY-2001; 2001WO-EP06457

(INSP) INST PASTEUR

Disclosure; Page 34; 47pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affility chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKVPPAPKPA ---- PQPGPQPPQPPQPPQPPQPQPQPQPPQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 265; DB 23;
Pred. No. 1.5e-12;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16194 standard; peptide; 52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%;
84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.59
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16194;
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Gaps

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapartussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3354-3448 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. bronchiseptica; P.68; outer membrane protein; piglet; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 258; DB 12;
Pred. No. 4.8e-12;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atrophic rhinitis; alternative cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35..632
/label= P.68
266..279
/label= Repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR26503 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1B; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WELL ) WELLCOME FOUNDATION LTD.
570..572
/label= repeat
574..576
/label= repeat
                                                                                    578..580
/label= repeat
                                                                                                                                   581..583
/label= repeat
                                                                                                                                                                                                                         587..589
/label= repeat
                                                                                                                                                                                                                                                                      599..601
/label= repeat
                                                                                                                                                                                                           repeat
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                                                                                                                                                                               584..586
/label- re
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Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prn proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-1990;
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                                                                                                                                                                                                                                                                                                                                          WO9115571-A
                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-1991,
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    Peptide
                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as blological fluids, such as human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                          B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                      Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 258; DB 23;
89.1%; Pred. No. 6.2e-13;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Fig 1c; 47pp; English.
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/label= repeat
271..275
/label= repeat
                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001WO-EP06457
26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-1992 (first entry)
                                                                                                                                                        Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.1<sup>1</sup>
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AA;
                                                                                                                                                                                                    WO200190143-A2
                                                                                                                                                                                                                                                 29-NOV-2001
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Gaps

Indels

AAR14320;

AAR14320 RESULT

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Peptide Peptide

Sequence

Length 911;

for

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Courter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens and infinity chromatographic columns. Pertactin is useful as antigens and infinity chromatographic columns. Pertactin is useful as antigens and infinity chromatographic columns. Pertactin is useful as antigens and all tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                               Polypeptides, containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                     The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPP—--PQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPQPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.2%; Score 258; DB 23;
89.1%; Pred. No. 4.8e-12;
ive 0; Mismatches 2;
                                                                                                   ΰ
                                                                                                                                                                                                                                                                             Disclosure; Page 28; 47pp; English
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                                                                                              Guiso-maclouf N. Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16197 standard; peptide; 56
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                  25-MAY-2000; 2000US-206969P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.1
Matches 49; Conservative
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                                                           (INSP ) INST PASTEUR
                                                                                                                                    WPI; 2002-097639/13.
N-PSDB; AAD26440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica pertactin outer membrane protein, p.68
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2%; Score 258; DB 13; Length 911;
llarity 89.1%; Pred. No. 4.8e-12;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Pertactin region II"
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/note= "Pertactin region I"
559..610
                               260.262
/label- RGD_tripeptide
701..703
/label- RGD_tripeptide
                  Repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                        91GB-0006568
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                                                                                                                                                                                                                  92WO-GB00561
                                                                                                                                                                                                                                                                                                (WELL ) WELLCOME FOUND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-366258/44.
N-PSDB; AAQ34566.
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les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911 AA;
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                                                                                                                                                                                                                  27-MAR-1992;
                                                                                                                                                                                                                                                        27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                          15-0CT-1992.
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                                                                                                                                  WO9217587-A
                                                                                                                                                                                                                                                                                                                                      Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                 Peptide
                                                                         Pept1de
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91WO-GB00487.

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                 The 46 Xs represent amino acids missing in the specification
                                                                                                                                         Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                         Disclosure; Fig 1C; 38pp; English.
                                                           (WELL ) WELLCOME FOUNDATION LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 26; Fig 1c; 47pp; English.
                                                                                  Clare JJ, Romanos MA;
                                                                                                      WPI; 1991-325214/44.
N-PSDB; AAQ14320.
              28-MAR-1991;
                                     02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16195;
                                                                                                                                        Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                          Couter membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                  Score 256; DB 23; Length 56;
Pred. No. 9.2e-13;
0; Mismatches 5; Indels
                                  present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                                                                                        pertactin outer membrane protein region II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/label= -
          26; Fig 1c; 47pp; English.
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610..612
/label= repeat
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/label= repeat
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Best Local Similarity 87.5%;
Matches 49; Conservative (
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'label=
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/label= re
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'label= re
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Tabel- re
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label- r
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                                                                                                                                                                                             56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                     Gaps
                                                                                                                                                                      54
                                                                                                                                      1 GAKVPPAPKPAPQPGPQP-PQPPQPPQP---PQPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                     4
                                               Length 922;
                                                                                                Indels
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                                               Score 255; DB 12;
Pred. No. 8.2e-12;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                            AAE16195 standard; peptide; 60 AA
                                            Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica.
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922 AA;
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as

17-0CT-1991

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and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal calls, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
  Pertactin antibody is useful for treating Bordetella infections
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60 AA; Sequence

Gaps ; 9 Length 60; Indels Score 254; DB 23; Pred. No. 1.4e-12; 0; Mismatches 5; 81.9%; ilarity 81.7%; Conservative Local Similarity 49; Query Match Matches

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1 GAKVPPAPKPAPQPGPQP----PQP-PQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA a ö

RESULT 13

AAE16199 standard; peptide; 48

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AAE16199;

(first entry) 26-MAR-2002 B. bronchiseptica strain II-7 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica,

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic composition

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica present invention relates to Bordetella bronchiseptica pertactin pertactin outer membrane protein region II. The

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Gaps

54 ., 2

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AAE16193 standard; peptide; 49

RESULT 15

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AAE16193 ID AAE1

1 GAKVPPAPRPAPQPGPQP-PQP-PQPPQPPQPQPQPQPEAPAPQPPAGRELSAA

48 AA; Sequence

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                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                 Gaps
                                             9
                                                                                           1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
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                Length 48;
                                             Indels
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Pred. No. 3.8e-12;
0; Mismatches 2;
                DB 23;
Score 248; Db 2.,
                                Pred. No. 3.2e
0; Mismatches
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                                                                                                                                                                                        AAE16196 standard; peptide; 53
             85.2%;
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87.5%;
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                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica,
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Best Local Similarity 87.5
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                           Best Local Similarity
Matches 46; Conserv
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               Query Match
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AAE16193;
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26-MAR-2002 (first entry)

B. bronchiseptica strain II-1 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II

49 AA; Sequence

Gaps 76.6%; Score 237.5; DB 23; Length 49; 83.6%; Pred. No. 2e-11; 1ve 0; Mismatches 2; Indels 7; Conservative Query Match Best Local Similarity Matches 46; Conserv

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1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPPQPEAPAPQPPAGRELSAA 54

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Search completed: May 7, 2003, 16:47:11 Job time: 29.0579 secs

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              APPLICANT: CLARE,
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Sequence 4, Appli
Sequence 2, Appli
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US-08-929-417-2
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US-08-453-265-6
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US-08-277-16-11
US-08-277-16-11
US-08-277-16-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2,
Sequence 2,
Sequence 2,
Sequence 2,
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                                                                Sequence Seq
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FLING DATE: 02-Unn-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEDOVIZZ, Richard M.
REFERENCE/DOCKET NUMBER: 37,067
REFERENCE/DOCKET NUMBER: 37,067
TELECHOM/UCATION INFORMATION:
TELEPRAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
TYPE: Innear
TOPOCLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER: READSALE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                 0S-09-179-558-66
0S-09-179-558-66
0S-09-114-266-149
0S-09-14-5698-4
0S-08-476-5098-4
0S-09-027-420-4
0S-08-465-746-2
0S-08-465-746-2
0S-08-465-746-2
0S-08-465-746-2
0S-08-477-4914-3
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Pred. No. 4e-16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-08-312-949-2
S-08-072-070-2
S-08-469-434-2
                                                                                                                                                                                                                                                                                                                                                                                                US-08-319-795-2
US-08-468-985-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MAUGH, KATHY J.:ANDERSON, DAVID M.:STRAUSBERG, SUSAN L.:MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,;SGAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PPAP--KPAP----QPGPQPPQPPQPPQPPQPQP--QPQPEAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.1e-05;
1; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 216; DB 4;
Pred. No. 7e-12;
0; Mismatches
APPLICATION NUMBER: US/08/460, 269C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.1%; Score 133.5; 51.0%; Pred. No. 4.1
                                                                                                                    REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
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APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOY-1986
APPLICATION NUMBER: 650,128
                                                                     NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 93,456
APPLICATION NUMBER: 933,945
                                                                                                                                                                                         (703) 243-6410
                                                                                                                                                                                                                                                                   LENGTH: 910 amino acids
                           FILING DATE: 02-Jun-19
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.7%;
Best Local Similarity 75.9%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-SEP-1984
                                                                                                                                                              TELEPHONE: (703)
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5202236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO:37:
LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5202236-37; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5202236-37
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                                       Sequence 4, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAREL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.2%; Score 258; DB 4; Length 911;
1larity 89.1%; Pred. No. 1.6e-15;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 911 amino acids
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                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                         USA
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                   STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
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Gaps

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US-08-929-417-2
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                     Sequence 160, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCE: 452
CORRESPONDENCE: ADDRESS:
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 641;
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Pred. No. 4.6e-05;
1; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Burnham, Martin K.
TITLE OF INVENTION: No. 5928895el IgA Fc Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 PAPKP-APQPGPQPPQPPQPPQPQPQPQPQPEAPAPQP--PAGRELSA
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                                                                                                                                                                                             5 РРАРКРАРОРОРОРРОРРОРОРОРОРОРОРОРОРОР 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCLI Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 132.5; DB Pred. No. 9e-05; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Human Genome Sciences, Inc.
F: 9410 Rey West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08929417
Patent No. 5928895
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.78;
52.98;
                                                                                          Ouery Match 42.9%;
Best Local Similarity 51.2%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 641 amino acids
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9°
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-961-083-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20820
                                      LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                       JS-08-961-083-160
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US-08-929-417-2
                SEQ ID NO:3
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Gaps
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APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER! OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKVPPARKPAPQPGPQP------PQPPQPPQPPQPQPQPQPQPEAPAPQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: MAY 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 132; DB 2;
Pred. No. 5.8e-05;
6; Mismatches 13
                                                                                                                                                                                                        OPERATION SYSTEM: DOS
SOFTWARE: FESTSED for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/929,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28,354
ER: P50545
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                                                                                                                                                                                                                                                                                                                                                               60/027,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PETELEBENMUNICATION INFORMATION: TELEPHONE: 215/994-2252 TELEFAX: 315/994-2222
                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICAȚION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027
FILING DATE: 24-SEP-1996
APPLICATION NUMBER: 60/040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%;
48.1%;
                                                                                                                                                                       3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Q. Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.6
Best Local Similarity 48.1
Matches 25; Conservative
                                                           CITY: Philadelphia
STATE: PA
COUNTY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-246-982A-16
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25 РРРОРРРРРРРОРООРРОСОРРРРРРРР - СРАБЕРГИКРККЕЦSА 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                        Score 131.5; DB 1; Length 3119;
Pred. No. 0.00044;
3; Mismatches 17; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PAPKPAPQPGPPQPPQPPQPPQPQPQPQPEAPAPQP--PAGRELSA 53
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                                                                                                                                                                                                                                                                                                                                                                                            6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPGPEAPAPQP--PAGRELSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                  0609.3880002
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30-MAY-1995
314
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-453-265-16; Sequence 16, Application US/08453265; Patent No. 5693757; Patent INFORMATION:
                      ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTATION TUMBER: 29,021
REPRENCE/POCKET UNMER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHOR: (202) 371-2600
TELEFRAX: (202) 371-2500
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                              42.4%;
Best Local Similarity 54.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3119 amino acids
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.49
Best Local Similarity 54.09
Matches 27; Conservative
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                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-246-982A-16
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                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                         TOPOLOGY:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRE 50
                                                                                                                  TITLE OF INVENTION: Proapoptotic Peptides, Dependent TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                         E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131; DB 4;
Pred. No. 9.9e-05;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz
; Sequence 28, Application US/09041886; Patent No. 6235872; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carthryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
                                                                            APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-904 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 513 amino acids
amino acid
                                                                                                                                                                                                                                                                         CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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Gaps
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APPLICANT: Ambrose, Christine M.
APPLICANT: Ambrose, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES. 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 589;
         Indels
                                                                                                                                                                                             Sequence 31, Application US/09041886

Patent No. 6233372
GENERALITRORMATION
TO SPECIAL TROPAMATION
TITLE OF INVENTION: Proapototic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San.Diego
STATE: California
                                                6 PAPKPAPUPGPQPPQPPQPPQPQPQPQPQPGPEAPAPQPPAGRE 50
                                                                                         6 PAPKPAPOPGPOPPOPPOPPOPOPOPOPOPOPOPOPEAPAPOPPAGRE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 РРРРРРРРОПРОПРОВРОДОР ПРОВРОВРРРРР В 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131; DB 4;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08246982A Patent No. 5686288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
TELEFAX: (619) 535-901
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sterne, Kessler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 589 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
      Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-041-886-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                US-09-041-886-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-246-982A-6
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                                                                                                                                                           RESULT 13
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42.3%; Score 131; DB 4; Length 530;
Best Local Similarity 53.3%; Pred. No. 0.0001;
Matches 24; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 131; DB 4; Length 552;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PAPKPAPQPGPPQPPQPPQPPQPQPQPQPPAPAPQPPAGRE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 PPPPPPPPPPQLPQPPPQAQPLLPQPQPPPPPPPPPAAAE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
WUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/041,886
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                         ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 2626
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-041-886-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-041-886-30
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Search completed: May 7, 2003, 16:57:30 Job time: 12.0142 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 131; DB 1; Length 3144;
Pred. No. 0.00049;
0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUNTRY: U.S.A.

ZIATE: D.C.
COUNTRY: U.S.A.

ZIP: 20005
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC COMPATIAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3880003
TELEFOND: (202) 371-260
TELEFOND: (202) 371-260
TELEFOND: (202) 371-254
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 РАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРЕАРАРОРРАСТЕ 50
                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
NTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08453265
Patent No. 5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Sterne, K
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-246-982A-6
COUNTRY:
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Gaps
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                                                               Score 131; DB 1; Length 3144;
Pred. No. 0.00049;
0; Mismatches 21; Indels
                                                                                                                                                                 6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPQPQPEAPAPQPPAGRE 50
                                                                     Query Match 42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-453-265-6
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49; Search time 5.0494 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-855-754B-21
298
1 GAKVPPAPKPAPGPGPQPPQ......QPQPEAPAPQPPAGRELSAA 52

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMAKIES		
Result		Query					
NO.	Score	Match	Length	88	ID	Description	ption
-	. 259	86.9	911	п	PERT_BORBR	003035	bordetella
7	256		922	Н	PERT_BORPA	P24328	bordetella
m	217	72.8	910	-	PERT_BORPE	· P14283	bordetella
4	14	49.3	485	7	SSGP_VOLCA	P21997	volvox cart
S	145.5	48.8	3164	Н	TEGU_HSV11	P10220	herpes simp
9	145	48.7	141	-	YPRO_OWEFU	P21260	
7	•	48.5	449	П	APG_BRANA	P40603	brassica na
60	142	47.7	2004	-	MOZ_HUMAN	092794	homo sapien
	141	47.3	487	Н	EBN2_EBV	P12978	•
10	133.5	•	426	٦	EXLP_TOBAC	003211	
11	132.5	٠	431	-	ACRO_RABIT	P48038	oryctolagus
	32	44.5	534	Т	APG_ARATH	P40602	
13	131.5	44.1	3110	-	HD_RAT	P51111	
	131	٠.	440	-	G3PT_MOUSE	064467	mus musculu
15	13	•	875	-	Y066_NPVOP	083949	orgyia pseu
16			339	-	CSP_PLABE	P06915	
17	129.5	43.5	347	-	CSP_PLABA	P23093	
18	129.5	43.5	555	-	GP1_CHLRE	09fpq6	chlamydomon
19	_	•	3144	-	HD_HUMAN	P42858	
20	127.5		565	-	MOT8_MOUSE	070324	mus musculu
21	127	•	282	-	GDA3_WHEAT	P04723	triticum ae
22	127	42.6	808	-	Y066_NPVAC	P41467	autographa
23	126	42.3	421	-	ACRO_HUMAN	P10323	homo sapien
24	126	42.3	3119	-	HD_MOUSE	P42859	mus musculu
25	125.5	42.1	919	-	RFX1_HUMAN	P22670	homo sapien
26	125.5	٠	1790	-	SEPA_EMENI	P78621	emericella
27	125	٠	224	7	Y091_NPVAC	P41479	autographa
28	125	41.9	232	-	- 1	P58840	homo sapien
53	125	•	415	_	- 1	P08001	sus scrofa
30	N	41.9	1362	-	BRD4_HUMAN	060885	homo sapien
31	124.5	41.8	129	-	PARB_TRYBB	P09791	trypanosoma
32	124.5	41.8	722	-	- 1	Q9p2y4	homo sapien
33	124.5	41.8	1206	٦	FM14_MOUSE	005859	mus musculu

	PO8469 trypanosoma Q06084 trypanosoma P14918 zea mays (m			
FMN1_MOUSE GDA6_WHEAT	PARI_TRYBB PARC_TRYBB EXTN_MAI2E	KPC1_TRIRE HXA3_MOUSE	TKAZ_HUMAN PRP2_MOUSE TONB_NEIGO	PRP3_MOUSE MEFD_MOUSE
				т т
1468 296	143 145 267	1139	261 261 283	296 514
41.8	111 444	1.04	4.4.	4.04
124.5	123.5 123.5 123.5	122.5 121.5	120.5 120.5 120.5	120.5
34 35	36 37 38	98 4 4	4 4 4 4 3 3 4 4	4 4 4 5

ALIGNMENTS

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EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                              Query Match
                                                                                         SEQUENCE
                                                                                                                        Local
                      DOMAIN
REPEAT
                                                       REPEAT
REPEAT
                                                                            DOMAIN
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                                                                                                                                                                                                                       PERT_BORPE
                                                                                                                                   Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                           STRAIN-CN2591;
MEDIJUE-91251771; PubMed-2041476;
Li L.J., Dougan G., Novotny P., Charles I.G.;
Li D. O pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                            MICTOBIOL 5:409-417(1991).
FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-6-D SEQUENCE. PRETACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Outer membrane.
DISERSE: MAY COMPRIBUTE TO THE DISERSE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                              ?
                                                                                                                                   1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 52
                                                                                       Score 259; DB 1; Length 911;
Pred. No. 9.8e-10;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95)
                                           3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.95.
PERTACTIN (P.70).
                                                                                                                                                                                                                922 AA
                                                                                                   Pred. No. 9.86
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S15204; S15204.
PIR; S14659; S14659.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03212; Pertactin; 1.
                                                                                         86.9%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X54547; CAA38419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                  93995
                                                                                                               Conservative
                                                                                                                                                                                                               STANDARD;
                                                                   911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONCENTRATIONS
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane;
                                                                                                                                                                                                              PERT_BORPA
P24328;
                                                                                                               49;
                                                                                                                                                                                                                                                                                                                 Bordetella
                                                                  SEQUENCE
                                                                                          Query Match
                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
PROPEP
SITE
                                 REPEAT
REPEAT
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            DOMAIN
                                                        DOMAIN
                        REPEAT
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PERT_BORPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                               Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89264462; PubMed-2542937; Charfield S., Smith M., Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.; "Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetalla pertussis."; Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Outer membrane.
-i- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                              X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         52
                                                         4 X 5 AA TANDEM REPEATS OF G-A-V-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPP--QPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                     ;
9
                                                                                                                                                                                                                                                                                           Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-7AN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRN OR OMFGE
                                                                                                                                                                                                                                                                                           Score 256; DB 1; Length 92
Pred. No. 1.5e-09;
0; Mismatches 3; Indels
                                                                                                                                                                             (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                 LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 264 AND 332.
MEDLINE-92407514; Pubmed-1527510;
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                                                                                                                                                                                                                                    95178 MW;
                                                                                                                                                                                                                                                                                           85.98;
                                                                                                                                                                                                                                                                                                                       84.5%;
                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                         290
270
275
285
603
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                                                                                                                                         276
281
575
922 AA;
                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CN2992
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P14283;
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PRO-RICH.

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Query ...
Best Local Similary
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P10220;
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                         SEQUENCE
                                                Query Match
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                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
   FT
SO
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS.
RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
I. PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
The extracellular matrix of Volvox carteri: molecular structure of
                                                                                                                                                               LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                     CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                           Score 217; DB 1; Length 910;
Pred. No. 3.4e-07;
0; Mismatches 1; Indels 10;
                                                                                                                                                                                                                                  (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                       1 GAKVPPAPKPAPQPPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
                                                                                                                 PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                      (APPROXIMATE).
                                                                               Outer membrane; Signal; Virulence; Repeat.
SIGNAL 1 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-f. Nagariensis / HK10; MEDLINE-90094551; PubMed-2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Sulfation; Hydroxylation.
                                                                                                                             POTENTIAL
         InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                     PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRIACTNFAMLY.
                                                                                                                                                                                                                                                       93452 MW;
                                                                                                                                                                                                                                                                              72.8%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROXYPROLINE RESIDUES.
                                           Pfam; PF03212; Pertactin; 1
                                                                                                                                                                                                                                                                                                    41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                     285
290
593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volvocaceae; Volvox.
NCBI_TaxID=3067;
PIR; A32560; A32560.
                                                                                                                                                                                                        276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                        SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A33647
                                                                                                                                                                                                                              REPEAT
DOMAIN
SEQUENCE
                                                                                                              CHAIN
PROPEP
SITE
                                                                                                                                                                        DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                           REPEAT
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                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               SSGP_VOLCA
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                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88274327; PubMed-2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-i- FÜNCTION: TEGUMENT PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                       Length 485;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
: A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPKPAPQPGPQP-PQP-PQP-PQPQPQPGPEAPAPQPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus (type 1 / strain 17).
Viruses; dsbNA viruses, no RNA stage; Herpesviridae;
Alphaherpesytrinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%; Score 145.5; DB 1;
71.1%; Pred. No. 0.017;
tive 2; Mismatches 6;
                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                      5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРР 44
                                                                                                    Score 147; DB 1;
Pred. No. 0.0036;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPRO_OWEFU STANDARD; PRT; 141 AA. P21260; P21201; Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-MAY-1995 (Rel. 32, Last annotation update) 4ypothetical|proline-rich protein (Fragment). Wenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                      PRT; 3164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; 193005210; Herpes_UL36.
Pfam; PF03585; Herpes_UL36; 1.
                                                  50436 MW;
                                                                                                    1 49.38;
Similarity 57.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
228
260
285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMBEH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCBI_TaxID=10299;
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                            RESULT
                                                              q
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                           Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TaxID-3708;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                           Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.; "Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine."; Blochem. Blophys. Res. Commun. 166:66-73(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                ol-rEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
APG OR CEX.
                                                                                                                                                                                        ö
                                                                                                                                                                   Score 145; DB 1; Length 141;
Pred. No. 0.002;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                   15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                  H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                          5 PPAPKPAPQPGPPQPPQPPQPPQPQPQPGPEAPAPQPPAGR 47
                                                                                                                                                                                                                            Pred. No. 0.002
0; Mismatches
                                                                                                                                                                                                                                                                           449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                        POLY-PRO
                                                                                                      protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001087; Lipase_GDSL.
                                     MEDLINE-90147742; PubMed-2105723;
                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                      48.7%;
55.8%;
Oweniidae; Owenia
                                                                                                                                                                                       24; Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428
                                                                                 PIR; A34043; A34043.
PIR; B34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
428
449 AA;
                                                                                                                                                     141 AA;
                                                                                                                                                                              Best Local Similarity
Matches 24; Conserv
                            SEQUENCE FROM N.A.
          NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATURATION.
                                                                                                      Hypothetical
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S16748;
                                                                                                                                                                                                                                                                          APG_BRANA
P40603;
Sabellida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                  DNA_BIND
NON_TER
                                                                                                                                                     SEQUENCE
                                                                                                                                                                       Query Match
                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                  APG_BRANA
                                                                                                                                                                                                                                                         RESULT
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                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOLTOW J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman U., Mitelaman F., Volinia S., Watmore A.E., Housman D. E.; Housman P., Willias S., Watmore A.E., Housman D. E.; Wrhe translocation t(8;16/pl1;pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).

1- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.

1- SUBCELLULAR LOCATION: Nuclear:

1- DISEASE: PARTICIPATES IN A T(8;16)(PI1;P13) CHROMOSOMAL TRANSLOCATION THAT PRODUCES A MOS.CBP CHIMAERA OBSERVED IN THE M./MS SUBTYDE OF ACUTE MYELOID LEUKERIA.

1- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.

1- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                           Gaps
                                                                                                               46
                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                           ------PPQPPQPQPQPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translocation; Zinc-finger; Repeat;
                                                      15;
     Length 449;
                                                         Indels
     DB 1;
Score 144.5; DB.
Pred. No. 0.0049;
); Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHD-TYPE 1.
PHD-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C2HC-TYPE.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLU.
POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR0012717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Ffam; PF00628; PHD; 2.
Ffam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00549; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS00165; ZF_PHD_2; 2.
Proto-oncogene; Chromosomal transloca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96376968; PubMed-8782817;
                                                         3;
                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U47742; AAC50662.1; -. Genew; HGNC:13013; ZNF220.
     48.5%;
48.3%;
                                                                                                               3 KVPPAPKPAPQPGPQPPQ-
                                                           Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1150
1242
1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
     Query Match
Best Local Similarity
Matchės 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                      MOZ_HUMAN
Q92794;
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Ouery Match
                                                                                                                       EXLP_TOBAC
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                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glbson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF LMP-1.
-1- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90266473; PubMed-2161150;
PETÍ L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                               BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen J.I., Wang F., Kleff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
J. Virol. 65:2545-2554(1991).
                                                                                                                       4
                                                                                            Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X 2 AA TANDEM REPEATS OF R-G. DEF40D7F8ED61D1A CRC64;
                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                         Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                      MW; 9FFBBAC3792854BA CRC64;
                                                                                                                                                        5 PPAPKPAPQPGPQPPQP-PQPPQP---PQPQPQPGPEAPAPQPP 44
                                                                                            Score 142; DB 1;
Pred. No. 0.02;
                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last annotation update)
EBNA-2 nuclear protein.
                                                                                                                                                                                                                            487 AA
                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
                                                                                                                   1; Mismatches
                      GLN/PRO-RICH.
                                    MET-RICH
                                                            MOZ-CBP
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; V01555; CAA24877.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52544 MW;
                                                                                                      Similarity 61.4%;
27; Conservative
                                                                    2004 AA; 225054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Repeat.
DOMAIN 345 356
SEQUENCE 487 AA; 5254
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - I - PTM: PHOSPHORYLATED.
1414
1597
1704
1977
                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10377;
1411
1593
1643
1897
1546
                                                                                                                                                                                                                          EBN2_EBV
P12978;
                                                                    SEQUENCE
                                                                                            Query Match
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                     DOMAIN
DOMAIN
SITE
                                                                                                                                                                                                                                                                                                 BYRF1.
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                           PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
51A495CC94017812 CRC64;
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AKVPPAPKPAPKPAPQPGPQPPQPP-----QPPQPPQPQPQPQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 426;
 Score 141; DB 1; Length 487;
                                                                                        23; Indels
                                                                   1 GAKVPPAPKPAPQPGPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRE 48
                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000419; Pollen_Ole_e_I.
Pfam; PF01199; Pollen_Ole_e_I; I.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                  Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 133.5; DB 50.9%; Pred. No. 0.022; ive 1; Mismatches
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                                  1; Mismatches
                                                                                                                                                                                            426
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                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                           Created)
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47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z14019; CAA78397.1; -.
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                          STANDARD;
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310
426 AA;
                Best Local Similarity
Matches 24; Conserv
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Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-4097;
                                24;
                                                                                                                                                                                     EXLP_TOBAC
Q03211;
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                                                                                                                                                                                                                           01-JUN-1994
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P48038;
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REPEAT
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534 AA

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana.";
                                                                       APG_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
-!- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                 STRAIN-New Zealand white; TISSUE-Testis;
MEDLINE-9436861; Pubmed-8086468;
Richardson R.T., O'Rand M.G.;
Richardson R.T., O'Rand M.G.;
Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
preproacrosin-related cDNA.";
Biochim. Biophys. Acta 1219:215-218(1994).
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAYAGE SPECIFICITY, IT
IS SINTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
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N-LINKED (GLCNAC. . ) (POTENTIAL)
CHARGE RELAY SYSTEM (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM (BY SIMILARITY CHARGE RELAY SYSTEM (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 132.5; DB 1; Length 431;
Pred. No. 0.025;
); Mismatches 19; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1C015A4E0BC0C668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
               01-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY
Created)
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          ACROSOME
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CARBOHYD
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ACT_SITE
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Theologis A., Ecker J.R., Palmo, J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palmo, J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Conway A.B., Frujii C.Y.,
Chun P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Chun P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Chun P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Haykan E.,
Chun P., Etqu P., Feldblyum T.V., Lenz C.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Lucs J.S., Maiti R., Marzalai A.,
Lin X., Liu S.X., Lucs J.S., Maiti R., Marzalai A.,
Chun Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Saxano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Saxano H., Tambunga G., Toriumi M.J., Town C.D.,
Wu Utterback T., Van Aken S., Vaysbers M., Vysotskaia V.S., Walker M.,
Chillian C.M., Venter J.C., Davis R.W.;
Fegenence and analysis of chromosome I of the plant Arabidopsis
P40602; 093214; 09LNT8;
01-FEB-1995 (Rel. 31, Created)
115-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
APG OR ATIG20130 OR T20H2.9.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocks; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES. CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis all length cDNA clones (RAFLs) sequenced by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSP consortium (Salk/Stanford/PGEC).";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-1- TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.

-1- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE=94004980; PubMed=8401599; Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene."; Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     eurosids II; Bra
NCBI_TaxID=3702;
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EMBL; X60377; CAA42925.1; -.

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Gaps

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2 AKVPPAPKPAPQPGPQ-----PPQPPQPPQPPQPQPQPQPQPQPAPQPPA 45

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25; Conservative

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POLY-PRO
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                                                                                                                              EMBL; U18650; AAA90987.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CD-1; TISSUE-Testis;
MEDLINE-92273722; PubMed-1375514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ICR Swiss; TISSUE-Testis;
MEDLINE-95254745; Pubmed-773666;
                                                                                                                                                         InterPro; IPR000091; Huntingtin. Pfam; PF03541; Huntingtin; 1.
                                                                                                                                                                                                                                                                                                                                                          44.18;
59.28;
                                                                                                                                                                                     PRINTS; PR00375; HUNTINGTIN.
                                                                                                                                                                                                                                                                                                                               343757
                                                                                                                                              : AAC52133.1;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                   1411
2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GAPDH)
                                                                                                                                                                                                                                                                                                                               AA:
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                   1408
2506
3110
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GAPDS OR GAPD-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                              U01022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G3PT_MOUSE
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
G3PT_MOUSE
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLOLAR LOCATION: Cytoplasmic (By similarity).
-i- TISSUE SPECIFICITY: EXPRESSED TO A HIGH DEGREE IN ALL THE REGIONS
OF THE BRAIN OF ADULTS AND IN MEIOTIC CELLS OF THE TESTIS. IN
ADDITION, VERY LOW LEVELS AND IN MEIOTIC CELLS OF THE TESTIS. IN
TISSUES (HEART, MUSCLE, LIVER, LUNG AND KIDNEY).
-i- DEVELOPMENTAL STAGE: IDENTIFIED AT HIGH LEVELS. IN NEURONAL TISSUES
OF EMBRYOS AS EARLY AS DAY 14.5. THIS EXPRESSION REMAINS CONSTANT
IN ALL FURTHER DEVELOPMENT STAGES (UP TO THE ADULT). ON THE OTHER
HAND THE EXPRESSION IN NON-NEURONAL TISSUES IS DOWN-REGULATED FROM
STAGE 17.5 DAY OLD EMBRYOS.
-i- POLYMORPHISM: THE POLY-CLN REGION DOES NOT APPEAR TO BE
POLYMORPHIC, EXPLAINING THE ABSENCE OF A ROBENT HD-LIKE DISORDER.
-i- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hamelster H., Epplen J.T., Raess O., F. Bression of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.L.;
Huntington's disease gene
                                                                                                     ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strong T.V., Tagie D.A., Valdes J.M., Elmer L.W., Boehm K., Swaroop M., Kaatz K.W., Collins F.S., Albin R.L.;
"Widespread expression of the human and rat Huntington's disease ge in brain and nonneural tissues.";
Nat. Genet. 5:259-265(1993).
-i- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR VESICLE FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                            DB 1; Length 534;
                                                                                                                                                                                                                                       Pred. No. 0.029;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                 139 PPEPKPAPPAPKPVPCPSPPKPPAPTPKPVPPHGPPKPAPAPTP 184
                                                                                                                                                       S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                   PPAPKPAPQPGPQPPQPPQPPQPQPQPQP-----EAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3110 AA.
                                                                                                                                                                                                                            Score 132.5;
                                                                                                  POTENTIAL
                                                                    PROSITE; PS01098; LIPASE GDSL SER; 1.
EMBL: AC022472; AAF79900.1; ALT_SEQ.
EMBL: AY0S0847; AAL24235.1; -..
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Mol. Genet. 4:1173-1182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96133292; PubMed-8528205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94100980; Pubmed-8275091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1773-1926 FROM N.A.
                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                          44.58;
52.28;
                                                                                                                                                                                                 58007
                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                        Lipase
                                                                                                                                                      77
141
325
534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development.
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                       Pfam; PF00657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                                                                                                           ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                  HD_RAT
P51111;
                                                                                                                                                                                                                                          Local
                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       during
                                                                                                               CHAIN
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                             Query
                                                                                                                                                                                                                                                                                                                                                                      HD_RAT
 STATETTERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Welchij.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-melotic spermatogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus mūsculus<sub>i</sub> (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaļia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.;
"Expression of a glyceraldehyde 3-phosphate dehydrogenase gene
specific to mouse spermatogenic cells.";
Blol. Reprod. 46:869-878(1992).
                                                                                                                                                                                                                                                                                                                                                                                                        Length 3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  064467; 060650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KPAPQPGPQPPQPPQPPQPQPQPQPGPAPAPQP---PAGR---ELSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 ОРРРОРРРРРРРОРОРОР-РОСОРРРРРРРРВЕР 65
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                       MW; 33C357E8FC141550 CRC64;
                                                                                                                                                                                                                                     REPEATS DOMAIN
REPEATS DOMAIN
REPEATS DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     Score 131.5; DB 1;
Pred. No. 0.12;
1; Mismatches 12;
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                                                                                                                                                                                                                                                                                    POLY-GLN.
POLY-PRO.
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POLY-GLU.
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Search completed: May Job time: 7.0494 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
TISSUE SPECIFICITY: TESTIS-SPECIFIC.
DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC GERM CELLS. LEVELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATES THIOL GROUP DURING CATALYSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PPAPKPAPQPGPQPPQPPQ-----PPQPPQPQPQPEAPAPQPPAGRELS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ODMINEV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 131; DB 1; Length 440;
Pred. No. 0.031;
1; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCERALDEHYDE 3-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                             SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN REF. 2).
L -> V (IN REF. 2).
05FF0A093D1ABD9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 AA
                                                                                                                                                                                                                                                                                                                                                                              CYS/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                            POLY-PRO
                                                                                                                                                                                                                                                       HSSP, P56649; IDSS.
MGD; MGI:95653; Gapds.
Interpro: IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gen. Virol. 77:825-837(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   083949; 065364; 010323;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                  Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%;
49.1%;
                                                                                                                                                                                                                            EMBL; M60978; AAA53033.1; -. EMBL; U09964; AAA80276.1; -.
                                                                            DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       283
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                                              DURING MATURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I_TaxID-164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                 Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOGG_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                           "Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PPAPKP------APQPGPQPPQPPQPP-QPPQ--PQPQPPQPEAPAPQPP 44
                                                                                                                                                        Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.0%; Score 131; DB 1; Length 87;
51.9%; Pred. No. 0.052;
tive 1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 91 POLY-PRO.
875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
                                    Carlson C., Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (
or send an email to license@lsb-sib.ch)
PubMed=7618274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U75930; AAC59070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D45397; BAA08236.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U39145; AAB04047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.9 Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01100; 1FOS
                                                                                                                          replication.
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bordetella bordetella bordetella bordetella

bordetella bordetella

bordetella bordetella bordetella

bordetella bordetella

bordetella

0.09a1q4 0.09k5h9 0.09k5h7 0.09k1y1 0.09k1y1 0.09a1y0 0.09a1y0 0.09s6n1 0.09s6n1

pneumocysti pneumocysti pneumocysti

pneumocyst

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P!68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                              107 A.A.
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                           Q96VI4
Q9UVD0
Q9UVD1
Q9JLE9
Q8W158
Q8T1Y6
Q9SBM1
                                                                                                                                                                                                                                                 Q96VJ1
O88902
Q9ULL5
Q08194
Q69023
                                                                                                                        088143
093198
069257
08RSU0
                                       Q9KJY0
Q9AHP0
Q9AIX8
                                                                      0986M9
0983M8
0986N0
0986N1
069259
                    Q9K5H7
Q9KJY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella.
NCBI_TaxID=518;
                                                                                                                                             196.5
162.5
158.5
154.5
151.5
149
148.5
                                                                                                                                                                                                                                                                                                                                                                            Q9K5G4
Q9K5G4;
                                                                                                                                                                                                                                                                                                                                                       RESULT 1
Q9K5G4
 Q9k594 bordetella
Q9k591 bordetella
Q9alp7 bordetella
Q9alp3 bordetella
Q9alp5 bordetella
Q9alp5 bordetella
Q9k59 bordetella
Q9k59 bordetella
Q9k59 bordetella
Q9k59 bordetella
Q9k59 bordetella
Q9k57 bordetella
Q9k57 bordetella
Q9k595 bordetella
Q9k595 bordetella
Q9k595 bordetella
                                                                  7, 2003, 16:38:52; Search time 26.5758 Seconds (without alignments) 403.166 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                      298
1 GAKVPPAPKPAPQPGPOPPQ......OPOPEAPAPQPPAGRELSAA
        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein – protein search, using sw model
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09K5G1
09ALP7
09ALP3
09ALP5
09KSH5
09L4E2
09K5G9
09K5G9
09K5G7
09K5G7
                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:*
sp_nammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fung1:*
                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                            US-09-855-754B-21
                                                                                                                                                                                                                                                                                                                                                                                                         sp_plant:*
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                                                                                                                                                                                                                                                                                                    SPTREMBL_21:*
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Jatabase

Q96v11 pneumocysti 088902 rattus norv Q9ulls homo saplen 008194 nicotiana t Q69023 human herpe

09)1e9 rattus norv Q8w158 brassica ol Q8t1y6 dictyosteli Q9sbml volvox cart

ö Boursaux-Eudé C., Guiso N.;

Boursaux-Eudé C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

Infect. Immut. 68:4815-4817(2000).

EMBL; AJ250092; CAB76446.1; ...

EndL; AJ250092; CAB76446.1; ...

InterPro; IPR001899; Pertact. sup.

InterPro; IPR002965; P_Ich_extensn.

PRINTS; PR01217; PRICHEXTENSN.

NON_TER 10 107

NON_TER 107

NON_TER 107

NON_TER 107

SEQUENCE 107 AA; 11076 MW; C32F321161C9E400 CRC64; Gaps ö 25 21 GAKVPPAFKPAPQPGPGPPQPPQPPQPPQPQPQPQPGPEAPAPQPPAGRELSAA 72 Length 107; 1 GAKVPPARKPAPQPGPPQPPQPPQPPQPPQPQPPAPAPAPAPAPARKELSAA Indels 100.0%; Score 298; DB 2; 100.0%; Pred. No. 2.2e-18; ive 0; Mismatches 0; Ouery Match Best Local Similarity 100.0 Matches 52; Conservative ð g

Query

Score

Result

1000 9663 9723 86723 86723 86629 86629 86628 8636 8836 8836 8836

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92.3%;
96.2%;
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                                      51; Conservative
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                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AA;
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                 Best_Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella.
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NON_TER
SEQUENCE
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Query Match
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                                                                                                                                                                                RESULT 4
Q9ALP3
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                                                                                                                                                                                                                                                                                                                                            Poursaux Ende C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4615-4817(2000).
EMBL; AJ250095; CAB76449.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Pirtoc_tatensn.
Pfon; PF00212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPQPGPEAPAPQPPAGRELSAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKVPPAPKPAPQPPQPPQPPQPPQP--PQPQPQPPAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
Local Similarity 96.3%; Score 287; DB 2; Length 10
Local Similarity 96.3%; Pred. No. 1.8e-17;
es 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31759 MW; 3B120CB158FD7474 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 107
107 AA; 11073 MW; AOA339BFF0EABBC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                          107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchiseptica Pertactin.;
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007273. AAG38449.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE-21117018; PubMed-11179374;
                                          PRT;
                                                                                                                                                                                                                                                                                                                             MEDLINE-20359389; PubMed-10899896;
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NON_TER 1 1
NON_TER 107 107
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01484; PRTACTNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03212; Pertactin; 1.
                                                                                                                                              Pertactin (P.68) (Fragment).
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                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 AA;
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                    01-OCT-2000
01-JUN-2002
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SEQUENCE
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                                                                    09K5G1;
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                                            Q9K5G1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AYO707267; AAG38443.1;
InterPro; IPR003992; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKVPPAPKPAPQPGPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                       1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 275; DB 2; Length 23
Pred. No. 3.4e-16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23930 MW; 5FB281B95E74678C CRC64;
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01-JUN-2001 (TrEWBLrel. 17, Created)
01-JUN-2001 (TrEWBLrel. 17, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
     DB 2;
94.1%; Score 280.5; DB 2;
98.1%; Pred. No. 1.5e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007277; AAG34653.1;
Interpro; IPR003992; pertactin.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002965; P. rich_extensn.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MBORD591;
MEDLINE=21117018; PubMed=11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21117018; PubMed=11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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09ALP9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq.
01-JUN-2002 (TrEMBLrel. 21, Last ann
Pertactin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0914E2;
01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                               MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.59
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 92.5
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=518;
            NCBI_TaxID=518;
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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Q9L4E2
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Linfert. Immun. 69:1917-1921(2001).

Linfert. Immun. 69:1917-1921(2001).

RinterPro; IPR003992; pertactin.

RinterPro; IPR003993; pertactin.vir.

InterPro; IPR004993; Pertactin.vir.

RinterPro; IPR004993; Pertactin.vir.

Refam: PF03212; Pertactin. 1.

RRINTS; PR01482; PRICHEXTENSN.

RRINTS; PR01484; PRIACTNEAMLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                          Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.2%; Score 260; DB 2; Length 347; ilarity 92.3%; Pred. No. 8.4e-15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                              347 AA; 36015 MW; D9A4B719E54842EB CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
                                                                                                                                                                                                                                                                 Score 263; DB 2;
Pred. No. 3.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA.
                                                                                                                                                                                                                                                                                                                          0; Mismatches
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE-21117018; PubMed-11179374;
                                                                                          PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                               Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                    88.3%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Best Local Similarity
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es 48; Conserv
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Q9K5H5;
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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1; ...
InterPro; IPR001899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                              Length 107;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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bronchiseptica Pertactin.";
EMBL, AVO70221; AAG38447.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004999; Pertact.sup.
InterPro; IPR0040965; P.rich_extensn.
PF03212; Pertactin; 1.
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107 AA; 11036 MW; 1AC13209D0238107 CRC64;
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200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
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Last annotation update)
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92.5%; Pred. No. 3.9e-15;
tive 0; Mismatches 2;
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Keil D.J., Fenwick B.; "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1; -.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
PF03212; Pertactin; 1.
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122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
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-JUN-2001 (TrEWBLrel. 17, Last sequence update)
-JUN-2002 (TrEWBLrel. 21, Last annotation update)
                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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86.0%; Pred. No. 6.3e-15;
iive 0; Mismatches 2,
                                                                                       Created)
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MEDLINE=21117018; PubMed=11179374;
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PRINTS; PRO1217; PRICHEXTENSN.
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                                                                                    -OCT-2000 (TrEMBLrel. 15,
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Best Local Similarity
Matches 49; Conservat
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49; Conserv
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RESULT 11
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MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
FPOLYMORPHISM of Repeated Regions of Pertactin in Bordetella pertuppertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL, AJZ50087; CAB7641.1.;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                      "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (Ang-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ445927; CAB82515.1; -.

InterPro; IPR003992; pertactin.

InterPro; IPR003991; pertactin.

InterPro; IPR003991; pertactin.

Penny: PR003912; Pertactin; 1.

PRINTS; PR01489; PERTACTIN:

PRINTS; PR01484; PERTACTINALY.

SEQUENCE 911 Aa; 94093 MW; DF531A9EB4383A32 CRC64;
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Mooi F.R.;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Pred. No. 5.8e-15;
0; Mismatches 2; Indels
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PRINTS; PR01217; PRICHEXTENSN.
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86.0%;
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Matches 49; Conservative
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NCBI_TaxID=518;
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                                               Pertactin.
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SEQUENCE
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815.4817(2000).
EMBL; AJ550089; CAB76443.1; -.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR004899; Pertact_sup.
PinterPro; IPR004899; Pertact_sup.
PinterPro; IPR01912; Pertactin: 1.
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Polymorphism of Repeated Regions of Pertactin in Bordetella
Ppertussis, Brodetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250083; CAB76437.1;
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03212; Pertactin;
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DEL;
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                                                                                                                                 RESULT 13
Q9K5G7
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09K5H3
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Boursaux-Eudé C., Guiso N.;
Boursaux-Eudé C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815.4817 (2000).

EMBL; AAZSOQ31, CAB76445.11.
InterPro; IPRO04689; Pertact_sup.
InterPro; IPRO02965; P_ICh_extensn.
Pfam; PPO03212; Pertactin; InterPro; IPRO02965; P_ICh_extensn.
                                                                                                             Gaps
                                                                                                                                                    1 GAKVPPAPPAPAPQPGPQP-----PQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSA 51
                                                                                                                                                                                      Gaps
                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
                                               Query Match 85.6%; Score 255; DB 2; L
Best Local Similarity 80.3%; Pred. No. 8.8e-15;
Matches 49; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CAT1;
MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:41:51; Search time 8.59284 Seconds (without alignments) 178.054 Million cell updates/sec Run on:

US-09-855-754B-21 298 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 52 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 segs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	•
			-269C-4	-269C-6	-269C-2	-716-11	-083-160	-886-28	-886-29	-886-30	-886-31	-982A-6	-265-6	-273B-42	-419-21	-886-15	_	-273B-8		-982A-16	-265-16	-624-11	-269C-8	-417-2	-841-2	-558-66	-661-2	-112-143	
	DI		US-08-460-269C	US-08-460-269C-6	US-08-460-269C-2	US-08-237-716-11	US-08-961-083-16	US-09-041-886-28	US-09-041-886-29	US-09-041	US-09-041	US-08-246	US-08-453-265-6	US-08-457-273B-4	US-08-556	US-09-041	5202236-37	US-08-457-27	5202236-3	US-08-246-982A-16	US-08-453-265-16	US-08-750-624-1	US-08-460-269C-8	US-08-929	US-09-109	US-09-179-558-66	US-08-718-661	US-08-818-	
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	Match		86.9	85.9	72.8	44.0	43.5	43.0	43.0	43.0	43.0	43.0	43.0	43.0	43.0	43.0	42.4	42.3	42.1	42.1	42.1	41.9	40.9	40.9	39.1	38.8	38.1	37.8	
	Score	1 1 1 1 1 1	259	256	21.7	131	129.5	128	128	128	128	128	128	128	128	128	126.5	126	125.5	125.5	125.5	125	122	122	116.5	115.5	113.5	112.5	
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	ALIGNMENTS BALIGNMENTS OB460269C WHICHAEL A. EXPRESSION OF HETEROLOGOUS TA SS: EN White, Zelano & Branige EN, White, Zelano & Branige En SS: En SS (Compatible) En SS: En SS (Compatible) En SS: En SS (Compatible) En SS (Compatib	tch al Similarity 92.5%; Score 259; DB 4; Length 911 al Similarity 92.5%; Pred. No. 1.8e-15; 49; Conservative 0; Mismatches 2; Indels GAKVPPAPRAPAPPEPOPP-POPPOPPOPPOPPAPAPAPAPARELSAA
44 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ROLOGOU f Brani te 1400 C	4; -15 APAI
66-1 118-1 118-2 118-2 118-2 118-2 15-2 15-2	TS ETEROI Suite 269C -2	DB 4 8e-1. ies QPEAP
2.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	mENTS P. HETI P. Su. 1.0, #1.0, 60,266	259; No. 1 mmatch PPQPQP
11477777777777777777777777777777777777	ALIGNMENT ALIGNMENT A. A. ION OF HE Blvd., S Sk tible cos/MS-Dos cos/MS-Dos cos/MS-Dos d M. 7,067 R: Popov- ON: S S	re 259; D d. No. 1.8 Mismatches PPQPQPQPQP
US-09-056-556-143 US-09-072-596-138 US-09-142-551A-4 US-09-142-551A-3 US-09-142-551A-3 US-09-095-443-2 US-09-095-443-2 US-09-323-735-2 US-09-323-735-2 US-08-476-5098-4 US-08-476-5098-4 US-08-46-636-3 US-08-46-636-3 US-08-149-14-3 US-08-149-14-3 US-08-149-14-3 US-08-149-14-3 US-08-149-14-3 US-08-149-14-3 US-08-146-636-2 US-08-119-14-3 US-08-119-14-3 US-08-119-14-3 US-08-119-14-3 US-08-119-14-3 US-08-119-14-3 US-08-119-14-3	AL 37 (69C 169C 16 16 16 16 16 16 16 16 16 16 16 16 16	Score Pred. ; Mis PPQPPC
800 800 800 800 800 800 800 800 800 800	PEFREY J. MICHAEL A MICHAEL A LEPRESSIO EXPRESSIO LA	8 0 0 0 0 0
444446046611000000	US/08460269C US/08460269C S, MICHAEL A N: EXPRESSIO ES: 17 DIRES: 111en, White Clarendon B TON W PC Compati STEN: PC-DOS TON ON DATA: UNDER: US/O UD ATA: UNDER: US/O UD ATA: UNDER: 343-643 NOW BA: TINPORMATION: TON: 4: Addinguishment of the control of the cont	98; 58; 100 100 100
174 174 174 174 174 174 174 174 174 174	ALIGNME -269C-4 e 4, APPLICATION US/08460269C NO. 6197548 APL INFORMATION: APPLICANT: CLARE, JEFFREY J. APPLICANT: CLARE, JEFFREY J. APPLICANT: CLARE, JEFFREY J. APDRESSION OF TEAST CORRESPONDENCE ADDRESS: ADDRESS: 17 CORRESPONDENCE ADDRESS: CITY: ARLINGTON STREET: 2200 CLATENDON Blvd., STREET: 1200 CLATENDON Blvd., OFFRATING SYSTEM: PC-DOS/MS-DOFFRATION UNDRER: 105/08/460 FILLING DATE: 02-JUN-1995 ATTORNEY/AGENT INFORMATION: TELEFAX: (703) 243-6410 MATION PON SEQ ID NO: 4 TELEFAX: (703) 243-6410 TELEFAX: (703) 243-6410 TTELEFAX: (703) 243-64333	86.90 Similarity 92.55 49; Conservative KVPPAPKPAPQPGPQP-PC
	-269C-4 NO. 619748 NO. 619748 APLICARTIC IN US, APPLICARTIC CLARE, J ROMANOS, TITLE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADR. ADDRESSE: MILL STREET: 2200 C TIT'R ARLINGTO STATE: VA COUNTRY: USA ZIP: 2201 COMPUTER: IBM OPERATING SYST COMPUTER: PACE COMPUTER: PAC	y rva: QPG
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	-269C-4 e 4, Apelication No. 6197548 AL INFORMATION: APPLICANT: CLARK ADDRICANT: CLARK ROMAN TITLE OF INVENT TORRESSEE: STREET: 22C STREET: 22C STREET: 22C STREET: 22C STREET: 22C STREET: 22C COMPUTER: TELECOMMUNICATICATICATICATICATICATICATICATICATICAT	nije Cc Papr
	-269C-4 -6 4, App. NO. 6137; APLICANTA APLICANTA CORRESPO CORPUTER COMPUTER MEDION COMPUTER MEDION COMPUTER MEDION COMPUTER MATION TELECOMM TOTOM T	Str. 849; KVPI
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•	ULT 1 08-460-269C-4 equence 4, Aprilcation (atent No. 6197548 GENERAL INFORMATION: APPLICANT: CLARE, ROMANOS TITLE OF INVENTION NUMBER OF SEQUENCY CORRESPONDENCE ADD STREET: 2200 CITY: ARLING STREET: 2201 COUNTRY: VAR COUNTRY: VAR COUNTRY: NED STREET: 2201 COMPUTER: 1B COMPUTER: 1B COMPUTER: 1B CORPUTER: 1B COMPUTER: 1B COMPUTER	Tool Tool Tool Tool Tool Tool Tool Tool
22000000000000000000000000000000000000	RESULT 1 US-08-460-269C- Sequence 4, A Patent NO. 61 GENERAL INF GENERAL INFORMATION NUMBER CORRES S S CORPES S COMPUT TELECO S COMPUT TELECO S S S COMPUT TELECO S S S S S S S S S S S S S S S S S S S	Query Ma Best Loc Matches
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Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/AS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ADPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         Score 217; DB 4;
Pred. No. 7.4e-12;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
                                   ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08237716 Patent No. 5589384
                                                                                                                                                               TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,955
                                                                                                                                                                                                                                                                                                                                                                             72.8%;
78.8%;
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                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.8
Best Local Similarity 78.8
Matches 41; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-237-716-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                         APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 922;
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 256; DB 4;
Pred. No. 3.3e-15;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                         Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.9%;
illarity 84.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS
                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                             ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                        22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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CURRENT APPLICATION DATA:

Region

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FILING DATE
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                                                                                                                                 JS-09-041-886-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
WUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.5%; Score 129.5; DB 4; Length 641; llarity 52.9%; Pred. No. 0.00019; Conservative 3; Mismatches 16; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= P69 BB05 epitope of Bordetella pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PAPKP-APQPGPQPPQPPQPPQPPQPQPQPEAPAPQP----PAGRELSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.0%; Score 131; DB 1; Length 33; Best Local Similarity 63.2%; Pred. No. 1e-05; Matches 24; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 РАРКРАРОРБРОРРОРРОРРОРРОРОРОРОРОРОР 43
                                                                OTHER INFORMATION: /label = LTB sequence
                                                                                                                                                                                                                                                  /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREEF: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 160, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                      LOCATION: Region
LOCATION: 10.31
COTHER INFORMATION: POTHER INFORM
                                                                                                                                                                                                      LOCATION: 4..7
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 27; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                               NAME/KEY: Region
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NAME/KEY:
LOCATION:
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Indels 14; Gaps
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                                                                                                                                  APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz Sharroz TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 128; DB 4;
Pred. No. 0.00021;
1; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 PAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAG-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 28, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.3%;
Matches 28; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELEFRA: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 513 amino acids
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CITY: San Diego
STATE: Callfornia
COUNTRY: United States
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MOLECULE TYPE: peptide
US-09-041-886-28
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                                                                                             GENERAL INFORMATION:
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US/09/041,886
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Patent No. 5686288
                                                                                                                                      Sequence 31, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31:
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Best Local Similarity 48.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       United States
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                                                                                                                                                                                                                                                                                                                                              CITY: San Dies STATE: California COUNTRY: United State 1P: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                        US-09-041-886-31
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%; Score 128; DB 4; Length 552;
48.3%; Pred. No. 0.00022;
tive 1; Mismatches 15; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                       Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bradesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR: STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                               6 РАРКРАРОРСРОРРОРРОРРОРОРОРОРОРЕАРАРОРРАG--
                                                                                                                                                                                                                                                                                                                                                                       ; DB 4;
0.00021;
                                                                                                                                                                                                                                                                                                                                                                     43.0%; Score 128; DB 4
48.3%; Pred. No. 0.0005
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDHER: 31,815
REFERENCE/DOCKET UNDHER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                           REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 amino acids
                                                                                                                                                                                                                                                              530 amino acids
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                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                              LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: MacConald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
CORRESPONDENCE: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                       ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 раркрарореоррорроррорророророророр
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Pred. No. 0.00023;
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41 PPPPPPEPPPEPPQPPPQAQPLLPQPQPP--PPPPPPPPPPPEPLHRPKKELSA 96
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                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mouse Model for Huntington's Disease and TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 5849995th Carolina
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
                                                                                                                                                   6 PAPKPARQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 РАРКРАРОРСРОРРОРРОРРОРРОРОРОРОРОРОР
                                                             Score 128; DB 1
Pred. No. 0.001;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                               Sequence 42, Application US/08457273B
Patent No. 5849995
GENERAL INFORMATION: Abplicant: Hayden, Michael
APPLICANT: Lin, Biaoyang
APPLICANT: Lin, Biaoyang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08556419C Patent No. 6093549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BENGET, VITGINIA C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEPHONE: 919-854-1401
                                                             43.08;
                                                                                 Best Local Similarity 48.33
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
; MOLECULE TYPE: protein US-08-453-265-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacConnaid, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 128; DB 1; Length 3144;
Pred. No. 0.001;
                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILIGN DATE: May 20, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3E: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 48.39
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
               READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-246-982A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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5202236-37; Patent No.
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                                                                                                                                                                                                                                                                                                                                                   --RELSA 51
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Pred. No. 0.001;
1; Mismatches 15; Indels 14
                                                                                                                                                                                                                                                                          Score 128; DB 3; Length 3144;
Pred. No. 0.001;
1; Mismatches 15; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence.
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                   6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPEAPAPQPPAG--
                                                  TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILLING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 РАРКРАРОРБРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРРАG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDRER: 31,815
REFERENCE/DOCKET UNDRER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%;
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Best Local Similarity 48.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                             Best Local Similarity 48.3
Matches 28; Conservative
Lanahan, Anthony
                                      Solomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-09-041-886-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                      SEQ ID NO 21
TRNGTH: 3144
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US-09-041-886-15
                                                                                                                                                                                                                                         US-08-556-419-21
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                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                              Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PPAPAFAPAPALAPAPALAPAPNPNPSPPSPPSPPSPPTPPTPPSPPAPAPAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPAPATAPATAPATAPAPATAPAPATAPAPATAPATAPATAPAPATAPAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATAPATA
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                                                                           APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 126.5; DB 6;
Pred. No. 0.00019;
1; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
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Job time: 11.6838 secs
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
5202236
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5202236-37
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein 7, 2003, 16:53:34 ; Search time 15.5911 Seconds Run on:

(without alignments) 306.927 Million cell updates/sec

US-09-855-754B-21 298

Perfect score:

Sequence:

1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

349150 seqs, 92025710 residues Searched:

349150 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: /ptodata/2/pubpaa/US06_NEW_PUB.pep: /ptodata/2/pubpaa/US06_PUBOMB.pep: /ptodata/2/pubpaa/US07_PUBCOMB.pep: /ptodata/2/pubpaa/US07_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep

SUMMARIES

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Description	Sequence 21, Appl		Sequence 15, Appl	4 . A	18,	Sequence 19, Appl	, A	ò	16,	14,	17,	23,	5,	24,	Sequence 3, Appli	91	7. At		
ID	US-09-855-754-21	US-09-855-754-22	US-09-855-754-15	US-09-855-754-4	US-09-855-754-18	US-09-855-754-19	US-09-855-754-6	US-09-855-754-20	US-09-855-754-16	US-09-855-754-14	US-09-855-754-17	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-10-171-384-3	US-09-765-272-160	US-09-904-987-7	US-10-001-873-50	US-10-077-584-9
DB	6	6	6	ڼ	6	6	6	6	6	6	6	δ	σ	6	6	10	10	6	0
Query Match Length DB	52	54	52	911	26	28	922	48	29	49	25	42	910	39	827	641	1543	1134	68
Query Match	100.0	96.3	86.9	86.9	86.2	85.9	85.9	83.6	81.4	80.0	79.2	72.8	72.8	62.9	47.0	43.5	43.0	42.8	41.9
Score	298	287	259	259	257	256	256	249	242.5	238.5	236	217	217	196.5	140	129.5	128	127.5	125
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Sequence 4, Appl1 Sequence 2, Appl1 Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 1, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 60, Appl Sequence 60, Appl Sequence 7, Appl Sequence 1, Appl Sequence 2, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 2, Appl1 Sequence 34, Appl1 Sequence 36, Appl1 Sequence 34, Appl1 Sequence 34, Appl1 Sequence 34, Appl1 Sequence 34, Appl1
9 US-10-077-584-4 10 US-09-764-864-967 11 US-09-76-740-2 9 US-09-976-740-43 12 US-10-023-523-43 12 US-10-023-523-43 13 US-10-023-523-43 14 US-10-023-523-47 15 US-10-023-523-47 16 US-10-023-523-47 17 US-10-023-523-47 18 US-10-023-523-47 19 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-298-5238-1 10 US-09-864-761-5848 10 US-09-864-761-5844 10 US-09-864-761-3498 10 US-09-864-761-3498
171 802 838 538 538 824 824 825 691 691 707 701 701 701 701 701 701 701 701 70
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124.5 124.5 121.2 121.2 121.2 121.2 121.2 120.0 110.0 110.0 111.0 110.0
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ALIGNMENTS

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APPLICANT: GUISO-MACLOF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTACTSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPETICAL PARAPETER PARAPE
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Score 298; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
Sequence 21, Application US/0985554 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                                                                                                                                                                        APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
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SOFTWARE: Patentin Ver.
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LENGTH: 52
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CURRENT APPLICATION NUMBER: US/09/855,754
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Best Local S
Matches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF INVENTION: POLYPEPTIDE CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACUTIN IN BOLDSMING.
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                                               BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IMMUNOGENIC COMPOSITIONS
  REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPQPGPAPAPQPPAGRELSAA
                           ORDETELLA PARAPERTUSSIS, AND BORDETELLA
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Pred. No. 7.5e-12;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length 54;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 287; DB 9;
Pred. No. 9.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                            FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOURSAUX-EUDE, CAROLINE
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Publication No. US20020192237A1
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Best Local Similarity 92.5%;
Matches 49; Conservative
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Matches 52; Conservative
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                         INVENTION:
INVENTION:
INVENTION:
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US-09-855-754-15
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LENGTH: 54
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGRAIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                              Length 911;
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                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                Score 259; DB 9;
Pred. No. 7.8e-11;
0; Mismatches 2
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CURRENT APPLICATION NUMBER: US/09/855,754
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
PRIOR APPLICATION NUMBER: 60/206,969
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Publication No. US20020192237A1
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86.0%;
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ilarity 92.5%;
Conservative
                   2000-05-25
              PRIOR FILING DATE: 2000-05-2
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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APPLICANT: BOURSAUX-EUDE,
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Matches 49; Conserv
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; ORGANIŜM: Bordetella bronchiseptica
US-09-855-754-16
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUISAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                US-09-855-754-16
Sequence 16, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION
APPLICANT: BOURSAUY-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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81.4%;
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88.5%;
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                                       Query Match
Best Local Similarity 88.5
Matches 46; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 81.4
Matches 48; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.
US-09-855-754-20
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LENGTH: 59
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TITLE OF INVENTION: PEGIONS OF PERFACTIN IN BONDEPELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BONDEFELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUGSIS, TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA PREFILE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGRIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                        Score 256; DB 9; Length 58; Pred. No. 1.3e-11; 0; Mismatches 3; Indels
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Pred. No. 1.3e-10;
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                                                                               ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
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Publication No. US20020192237A1
GENERAL INFORMATION:
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1 Similarity 84.5%;
49; Conservative
                                                                                                                                           85.9%;
ilarity 84.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver. 2.
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Best Local Similarity
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US-09-855-754-20
                                                                                                                                                                                     49;
               SEQ ID NO 19
LENGTH: 58
TYPE: PRT
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Best Local S:
Matches 49
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA
FITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORNOHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REFRENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNICABLIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                       Length 59;
     Length 48;
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86.8%; Pred. No. 1.8e-10;
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0; Mismatches 2;
Score 249; DB 9;
Pred. No. 3.4e-11;
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Pred. No. 1.1e-10;
1; Mismatches 3
                                                       0; Mismatches
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Matches 46; Conservative
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APPLICANT: GUISO-MACLOUF, NICCLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGGRUC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/4855,754
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PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                        Sequence 5, Application US/09855754; Publication No. US20020192237A1; GENERAL INFORMATION:
                                                                                                                     CAROLINE
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US-09-855-754-5
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ilarity 73.1%;
Conservative (
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Matches 38; Conserv
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Matches 41; Conserv
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US-10-171-384-3
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LENGTH: 39
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TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSELLA PERPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                            APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYEPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERIUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERIUSSIS,
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR ELLING DATE: 2000-05-25
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                              1 GAKVPPAPKPADQPGPQP-PQPPQPPQPPQPQPQPQPGPAPPQPPAGKELSAA 52
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4.4e-09;
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Pred. No. 2.7e-10;
1; Mismatches 1
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Pred. No. 4.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-855-754-23; Sequence 23, Application US/09855754; Publication No. US20020192237A1
                                                                                                                                                                Sequence 17, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 72.8%;
1 Similarity 78.8%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.2%;
Best Local Similarity 88.9%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver.
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Best Local Similarity
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                                                                                                                                            US-09-855-754-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 17
LENGTH: 52
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Matches

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                             10;
                                                                                                                                       ------PQPQPEAPAPQPPAGRELSAA 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 39;
  Length 910;
                                                                                             1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
72.8%; Score 217; DB 9; 78.8%; Pred. No. 5.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 196.5; DB Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
```

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; GENERAL INFORMATION:

APPLICANT: The Brigham & Women's Hospital, Inc.

APPLICANT: Beler, David

APPLICANT: Beler, David

APPLICANT: Beler, David

APPLICANT: Rao, Cherie

TITLE OF INVENTION: p53 Binding Protein-Related Protein in Cardiomyopathy

FILE REFERENCE: 81994/275368

CURRENT APPLICATION NUMBER: US/10/171,384

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 3

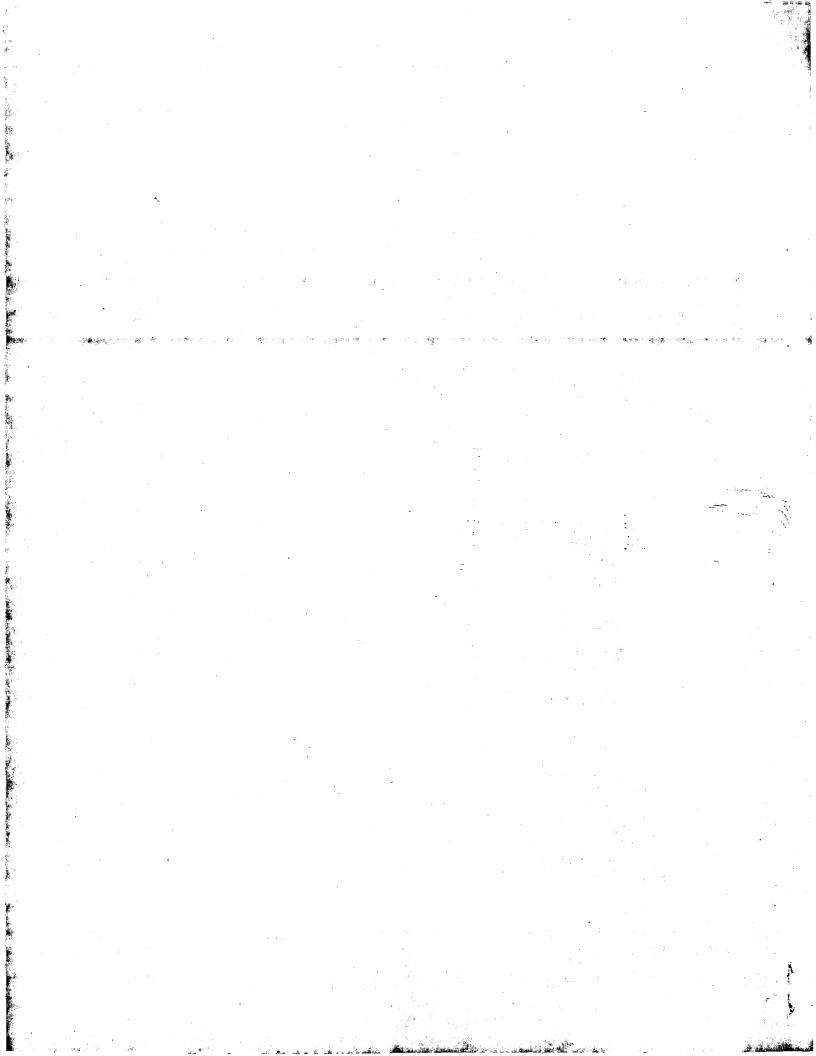
LENGTH: 827

TYPE: PRT

COGRANISM: Homo sapiens

US-10-171-384-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
47.0%; Score 140; DB 9; Length 827;
Best Local Similarity 62.5%; Pred. No. 0.0082;
Matches 25; Conservative 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
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Search completed: May 7, 2003, 17:30:54 Job time: 15.5911 secs



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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Мау Run on:

7, 2003, 16:41:02 ; Search time 9.7446 Seconds (without alignments) 513.008 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-855-754B-21 298 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA

52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: piri:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	· · · · · · · · · · · · · · · · · · ·																													
	Description	68K outer membrane	pertactin - Bordet	outer membrane pro	hypothetical 47.8K	protein-tyrosine-p	cysteine-rich exte	pherophorin-S - Vo	sulfated surface g	UL36 protein - hum	hypothetical proli		hypothetical prote	hypothetical prote	nuclear protein EB	proline-rich prote	proline-rich prote	cysteine-rich exte	chitinase (EC 3.2.	hypothetical prote	hydroxyproline-ric	pistil extensin-li	hypothetical prote	alpha/beta-gliadin	acrosin (EC 3.4.21	extensin - Volvox	T20H2.9 protein -	glyceraldehyde-3-p	hypothetical prote	hypothetical prote
SUMMARIES	ID	A47675	S15204	A32560	JC2301	T14355	A48232	T10798	A33647	ММВЕН 6	A34043	S16748	T48814	AE2295 .	S42442	T17547	S21961	B48232	S51939	T24470	T07907	JQ1696	T18281	E22364	S47538	S22697	A86335	149681	T10340	B96534
	60	7	7	~	~	N	7	7	7	7	~	~	N	7	~	~	~	~	~	~	7	~	7	~	~	~	~	7	~	7
	Query Match Length DB	911	922	910	430	1494	209	599	485	3164	141	449	1952	383	487	544	534	196	439	165	446	426	1474	320	431	464	1137	440	875	494
æ	Query	86.9	85.9	72.8	54.5	50.0	49.7	49.7	49.3	48.8	48.7	48.5	48.5	48.0	47.3	47.0	46.1	45.5	45.3	45.1	45.1	44.8	44.8	44.6	44.5	44.5	44.5	44.0	44.0	43.6
	Score	259	256	217	162.5	149	148	148	147	145.5	145	144.5	144.5	143	141	140	137.5	135.5	135	134.5	134.5	133.5	133.5	133	132.5	132.5	132.5	131	131	130
	Result No.	-	7	က	ಶ	S	9	7	80	σ	10	11	12.	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

circumsporozoite p circumsporozoite p	pneumococcal surfa hypothetical prote Huntington disease	hypothetical prote proline-rich prote	hypothetical prote alpha/beta-gliadin AcOrf-66 protein -	extensin class I (hypothetical prote acrosin (EC 3.4.21	unknown protein [1 hypothetical prote HD protein - mouse
OZZOMB	F95013 F75518 A46068	H83619 T17531	A/1416 T06504 C72858	S14970 E87649 S11674	G86441 S75138 I49729
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129.5	129.5 129.5 128	127.5	127	126 126 126	126 126 126
30	333	36.5	2 8 6 6 6	4 4 4 2 1 2 2	444 544

ALIGNMENTS

	RESULT 1 A47675
	68K outer membrane protein P.68 pertactin – Bordetella bronchiseptica C;Species: Bordetella bronchiseptica
	C;Date: 19*Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A47675
	R;Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J. Gen. Microbiol: 138, 1697-1705, 1992
	A:Title: Cioning, nucleotide sequence and heterologous expression of the protective o A:Reference number: A47675: MIID:92407514: PMID:1527510
	A; Contents: CN7531
	A; Accession: A47675
	A;Status: preliminary
	A: Molecule type: hucleic acid
-	A; Residues: 1-911 <li1></li1>
-	A;Cross-reference3: GB:X54815; GB:S46416; NID:q39396; PIDN:CAA38584.1; PID:q39397
٠	A:Note: sequence extracted from NCBI backbone (NCBIN:11331B, NCBIP:113319)
	5 Best Local Similarity 92.5%; Pred. No. 1.5e-10; Matches 49; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
· · · · · · · · · · · · · · · · · · ·	

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Portactin - Bordetella parapertussis
N.Alternate names: outer membrane protein P70
S.Species: Bordetella parapertussis
C.Species: Bordetella parapertussis
C.Spate: 07,Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999
C.Accession: S15204; S14659
R.Li. L.J. Dougan, G.; Novorny, P.; Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
A.Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo

A; Accession: S15204

A;Molecule type: bNA A;Residues: 1-922'<LIL> A;Cross-rreferences: EMBL:X54547; NID:g39761; PIDN:CAA38419.1; PID:g39762 C;Genetics: A;Gene: prn C;Keywords: membrane protein

Gaps 9 Query Match 85.9%; Score 256; DB 2; Length 922; Best Local Similarity 84.5%; Pred. No. 2.4e-10; Matches 49; Conservative 0; Mismatches 3; Indels

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52 1 Ġakvppaķkpa----POPGPOPPOPPOPPOP---OPOPOPEAPADOPPAGRELSAA

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Gaps

43

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A; Status: preliminary
A; Rotaus: preliminary
A; Residues: 1-209 < wuA-
A; Residues: 1-209 < wuA-
A; Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
A; Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
A; Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A; Reference number: PQ0474; MUID:93005740; PMID:1392607
A; Reference number: PQ0474; MUID:93005740; PMID:1392607
A; Residues: 39-209 <GGL>
A; Residues: 39-209 <GGL>
A; Residues: 39-209 <GGL>
A; Residues: 39-209 <GGL>
C; Covportantal source: stigma, style; strain Petit Havana SRI
C; Superfamily: glutelin stigma, style; strain Petit Havana SRI
C; Superfamily: glutelin extracellular matrix; fertilization; glycoprotein
C; Keywords: cell wall: extracellular matrix; fertilization; glycoprotein
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-209/Product: cysteine-rich extensin-like protein I #status experimental <AMT>
F; 146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cysteine-rich extensin-like protein 1 precursor - common tobacco C; Species: Nicotiana tabacum (common tobacco) C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000 C; Accession: A48232; PQ0475; S24617 R; Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y. Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993 A; Tritle: A tobacco gene family for flower cell wall proteins with a proline-rich doma A; Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECM-glycoproteins: The pherophori
                          EMBL: AF077000; NID: 93598973; PID: 93598974; PIDN: AAC62959.1
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A; Experimental source: strain HK 10; sub_species Nagariensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                 A;Description: may be involved in regulating Ha-ras-dependent cell growt
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                           Length 1494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 209
                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKVPP--APKPAPQPGPQPPQPPQP-PQP-PQPQPQPQPEAP--APQP
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R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM
A;Reference number: Z17154; MUID:97162277; PMID:9009264
A;Accession: T10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 РРАРКРАРОРСРОРОР ---РОРРОРОРОРОРОРОРАРАРОРРА
                                                                                                                                                                                                                                                     Score 149; DB 2; I
Pred. No. 0.0036;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 148; DB 2;
Pred. No. 0.00091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.78;
56.88;
                                                                                                                                                                                                                                                     Query Match 50.0%;
Best Local Similarity 63.3%;
Matches 31; Conservative
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                       A.Cross-references: EMBL:AF07
A.Experimental source: brain
C.Genetics:
A.Gene: PTP-TD14
C.Function:
A; Residues: 1-1494 <CAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
R;Mada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A;Reference number: JC2299; MUID:96051989; PMID:8535973
A;Accession: JC2201
A;Molecule type: DNA
A;Residues: 1-430 <WAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    П
                                                                                                                                                                                                                                               R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number: A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine-phosphatase (EC 3.1.3.48) TD14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-5ep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14355
R;Cao, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, K.R.; Graham, R.M.; Zhou, M.
J. Biol. Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase contains a BROI-like domain and
A;Reference number: 218004; MUID:98361981; PMID:9684860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
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                                                                                                                                                                    Species: Bordetella pertusis
Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
Accession: A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A;Residues: 1-910 <CHA>
A;Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- POPOPOPEAPAPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: it is uncertain whether Met-1 or Met-3 is the initiator C;Kaywords: membrane protein F:1.34/Momain: signal sequence #status predicted <SIG>F:13-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 217; DB 2; Length 91
Pred. No. 8.6e-08;
0; Mismatches 1; Indels
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                                                                                                                                         outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 2; ;
J.00018;
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical 47.8K protein - Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 162.5; 1
Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PPAPKPAPQPGP-----QPPQPPQPPQPPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.8%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: ORF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A32560
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C. Accession: S16748
R. Roberts, M. R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the FMBL Data Library, August 1991
A.Description: Cloining and characterization of a proline-rich gene expressed specific A. Reference number: S16748
A. Accession: S16748
A. Accession: S16748
A. Molecule (rype: mRNA
A. Residues: 1-449 (ROB)
A. Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: 148814
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, April 2000
A;Reference number: 224541
                                        characterized by the repetitio
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C.Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVPPAPKPAPKPAPQPGPQPPQPPQ------PPQPPQPQPQPQPQPEAPAPQPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1952;
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74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Presence in invertebrate genomes of sequences (
A;Reference number: A90159; MUID:90147742; PMID:2105723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 РРАРКРА --- РОРСРОРРОРРОРРОРРОРОРОРОР
                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                         5 PPAPKPAPOPGPQPPQPPQPPQPPQPQPGPAPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 144.5; DB 2;
Pred. No. 0.0028;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 144.5; DB 2;
Pred. No. 0.0087;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                       Score 145; DB 2;
Pred. No. 0.0011;
0; Mismatches 1
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A)Experimental source: cosmid contig 15E6; strain
C;Genetics:
A;Gene: NCSP: 15E6, 220
A;Map position: 2
A;Introns: 281/3
          66-73, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proline-rich protein - rape (fragment)
                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 55.8%;
Matches 24; Conservative
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48.3%;
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Best Local Similarity 54.5%;
Matches 24; Conservative
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Matches 28; Conservative
                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 59-136 <BA2>
A,Cross-references: GB:M32217
                                                                                                             A; Molecule type: DNA
A; Residues: 1-141 <BAK>
A; Cross-references: GB:M32217
A; Accession: B34043
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1952, <SCH>
          Biophys. Res.
                                                                                    A; Accession: A34043
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                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Volvox carteri
C; Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Accession: A33647
R; Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A; Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular
A; Reference number: A33647; MUID:90094551; PMID:2689458
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-fre C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: I30085
R; McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr B. Gen. Virol. 69, 1531-1574, 1988
A; Title: The complete DNA sequence of the long unique region in the genome of herpes sim A; Reference number: A30083; MUID:88274327; PMID:2839594
A; Accession: I30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-3164 <MGS>
A: Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment) (Species: Owenia fusiformis C;Species: Owenia fusiformis C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000 C;Accession: A34043; B34043 R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
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C;Date: 31-Dec-1989 *sequence_revision 31-Dec-1989 *text_change 16-Jun-2000
                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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                                                                            Score 148; DB 2; Length 599;
Pred. No. 0.0021;
2; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 147; DB 2; Length 485;
Pred. No. 0.002;
1; Mismatches 16; Indels
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                                                                                                                                                                                                            Query Match 48.8%; Score 145.5; DB 1; Best Local Similarity 71.1%; Pred. No. 0.011; Matches 32; Conservative 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                    5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРР 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PPAPKPAPQPGPPQPPQPPQPPQPQPQPQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                sulfated surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL36 protein - human herpesvirus 1 (strain 17)
                                                                            Query Match
Best Local Similarity 57.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 49.3%;
Local Similarity 57.5%;
les 23; Conservative
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A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
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Matches
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Length 544;

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-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Molecule type: DNA
A;Residues: 1-544 <GRA>
A;Coss-references: EMBL:U42580; NID:94028896; PIDN:AAC96425.1
A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 140; DB 2;
Pred. No. 0.0064;
5; Mismatches 8
                                                                    R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: 218806
A;Accession: T17547
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illarity 57.8%;
Conservative
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Best Local Similarity
Matches 26; Conserv
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Job time: 10.7445 secs
                                             Accession: T17547
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                                                                                                                                                                                                                                                                                       R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, G
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dambaugh, T.; Hennessy, K.; Chammankit, L.; Kieff, E.
roc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
Title: Uz region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2, Reference number: S42447; MUID:85063846; PMID:6209719
Accession: S42447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: human herpesvirus 4, Epstein-Barr virus
Date: 19-Mar-1997 #text_change 20-Jun-2000
Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
Date: 19-Mar-1997 Bacquence 1 Staten Date: Date:
                                                                                                                                                  A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE2295
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-86,'PPP',89-487 <DAM>
A;Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                         protein all3916 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 0.005;
1; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРР 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 143; DB 2;
Pred. No. 0.0031;
2; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farrell, P.J.

ubmitted to the EMBL Data Library, March 1988; Reference number: S32973
;Accession: S32988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - human herpesvirus 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.3%;
ilarity 50.0%;
Conservative
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Residues: 1-487 <FAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-383 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA Residues: 1-487 <SAM>
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                                                                                                                       Species: Nostoc sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
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                                                                         hypothetical
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T17547 proline-rich protein A57R - Chlorella virus PBCV-1

RESULT 15

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1 GAKVPPAPKPAPQPPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRE 48

us-09-855-754p-21.rag

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec OM protein - protein search, using sw model Мау Run on:

US-09-855-754B-21 298 1 GAKVPPAPKPAPGPGPQPPQ......QPQPEAPAPQPPAGRELSAA Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1988.DAT:*
/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1988.DAT:*
/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq_geneseqp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT./SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT /SIDS2/gcgdata/geneseq/geneseqp-emul/AA2002.DAT/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1997 /SIDS2/gcgdata/geneseg/genesegp-embl/AA199 /gcgdata/geneseq/geneseqp-embl/ A_Geneseq_101002:* : /SIDS2/gcgdata/geneseq/ :: /SIDS2/gcgdata/geneseq/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Pertactin antigen	prn proteins. Bor	Bordetella bronchi	B. bronchiseptica	B. bronchiseptica	Bordetella paraper	Bordetella paraper
ID	AAE16200		AAE16194			AAE16183				
DB	23	23	23	12	13	23	23	23	13	23
% Query Match Length DB ID	52	54	52	911	911	911	26	58	922	922
% Query Match	100.0	96.3	86.9	86.9	6.98	86.9	86.2	85.9	85.9	85.9
Score	298	287	259	259	259	259	257	256	256	256
Result No.	-	7	m	4	S	9	7	80	6	10

		B. bronchiseptica	B. bronchiseptica	ertactin a	bronchi		ordetella pert		8	Peptide BBO5 deriv	683 d	ORFX C	Novel human diagno	human	polype	Human polypeptide	Drosophila melanog	Human polypeptide	Human polypeptide	Human polypeptide	Arabidopsis thalia	~	Novel human diagno	Sugar beet chitina	Arabidopsis thalia	Novel human diagno	Drosophila melanog	Human polypeptide	Novel human diagno	Streptococcus pneu		Streptococcus pneu	S. pneumoniae SP09	treptococcus	н	
0.00	AAETOTA	AAE161	AAE1619	AAR1432	AAE1619	AAE1620	AAE1618	AAE1714	AAE1620	-	AAR1173			ABG0987	AA00441	-	2 ABB70063	-	AA00212	-	-	-	ABG272	AAR28	AAG22	ABG17	ABB67	AAO04		AAW14	AAP93	9 AAW61217	ABP5463	1 AAY81652	ABB7853	
												900		239															Ŋ	m	~	_	_	745 2	و	
		'n.	m.	œ.	ċ.	ci.	~	'n.	in.	m.	'n	49.8	σ'n.	σ,	œ.	œ,	œ,	œ.	<u>.</u>	.ف	'n.	'n.	'n.	'n	'n.	4	4	4	e.	e.		ë.		e,		
	0.00		248.5		238.5	217	217	217	196.5	159	157	148.5	4	4	145		144.5	143		137.5	m	136	136		æ	က	131.5		3	~	~	~	~	129.5	~	
	1:	7.7	13	14	15	16	. 17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

B. bronchiseptica strain II-8 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II. AAE16200 standard; peptide; 52 AA 25-MAY - 2000; 2000US-206969P. 23-MAY-2001; 2001WO-EP06457 26-MAR-2002 (first entry) Bordetella bronchiseptica. W0200190143-A2. 29-NOV-2001. AAE16200; RESULT 1

Guiso-maclouf N, Boursaux-eude C; (INSP) INST PASTEUR.

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

```
The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tells, as well as biological animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
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             S_{X} \times S_{Y} \times S_{Y
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Gaps
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                                                            52;
                                            1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA
     Length
                           Indels
100.0%; Score 298; DB 23;
100.0%; Pred. No. 1.6e-16;
1ve 0; Mismatches 0;
                        52; Conservative
            Best Local Similarity
  Query Match
                        Matches
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¥. AAE16201 standard; peptide; 54 26-MAR-2002 (first entry) AAE16201; **AAE16201**

B. bronchiseptica strain II-9 pertactin outer membrane protein region II. outer membrane protein; vaccine; Bordetella infection; Pertactin; PRN; outer membrane protein; vaccin therapy; antibiotic; antibacterial; region II. 23-MAY-2001; 2001WO-EP06457. Bordetella bronchiseptica, WO200190143-A2. 29-NOV-2001.

Guiso-maclouf N, Boursaux-eude C; (INSP) INST PASTEUR.

25-MAY-2000; 2000US-206969P

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

for

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of present invention relates to Bordetella bronchiseptica

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; PRN; outer membrane protein; vaccine; Bordetella infection; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                     Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                    1 GAKVPPAPKPAPQPGPQPPQPPQPPQP--PQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                            Length 54;
                                                                                                                                                               Score 287; DB 23;
Pred. No. 1.2e-15;
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16194 standard; peptide; 52 AA.
                                                                                                                                                         Query Match 96.3%;
Best Local Similarity 96.3%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-097639/13.
                                                                                                54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN;
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                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16194
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. Gaps ; ; 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA 52 Indels 86.9%; Score 259; DB 23; 92.5%; Pred. No. 1.5e-13; 1ve 0; Mismatches 2; 1 Similarity 92.5%; 49; Conservative Similarity 52 AA; Query Match Best Local s Matches ŏ

22

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Claim 26; Fig 1c; 47pp; English.

membrane protein; piglet; probe; cleavage.

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DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhights in pigs
                                                                                                                                                                                                                                  570.589
/label= Repeat_region
260.262
/label= RGD_tripeptide
701.703
                                                                                                                                                                                                                                                                                           /label= RGD_tripeptide
                                                                                                                                                                                                                          /label= Repeat_region
                                                                                                                                                                            Location/Qualifiers
                       AAR26503 standard; Protein; 911 AA.
                                                                                                                 B. bronchiseptica; P.68; outer
atrophic rhinitis; alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 28pp; English.
                                                                                                                                                                                                 /label= P.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 92.5%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           91GB-0006568
                                                                                                                                                                                                                                                                                                                                                                    92WO-GB00561
                                                                                                                                                                                                                                                                                                                                                                                                                  (WELL ) WELLCOME FOUND LTD
                                                                      (first entry)
                                                                                                                                                     Bordetalla bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard recombinant entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 AA;
                                                                                             prn proteins
                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1991;
                                                                    12-MAR-1993
                                                                                                                                                                                                                                                                                                                    W09217587-A.
                                                                                                                                                                                                                                                                                                                                             15-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles IG;
                                              AAR26503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pertactin antigens. DNA sequence used are represented in AA014319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 259; DB 12; Length 9
Pred. No. 1.3e-12;
0; Mismatches 2; Indels
                                                                                                                         Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                          Location/Qualifiers
266..270
                                AAR14320 standard; Protein; 911 AA.
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599..601
/label= repeat
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/label _ repeat
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1 Similarity 92.5%;
49; Conservative
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                                                                                                                                                                                                                       label-
                                                                                                                                                                                                                                                                                                                                          label=
                                                                                                    Pertactin antigen P.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1991;
                                                                             20-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                               409115571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clare JJ,
                                                       AAR14320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                             eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1989).
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Matches
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3
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The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                      Length 911;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                      Score 259; DB 13;
Pred. No. 1.3e-12;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE16183;
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AAE16183
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                      Claim 26; Fig 1c; 47pp; English.
                                                                                                                     23-MAY-2001; 2001WO-EP06457
                                                                                                                                                        25-MAY-2000; 2000US-206969P
              Bordetella bronchiseptica.
                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                             WPI; 2002-097639/13.
                                               WO200190143-A2.
                                                                                    29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antitions can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                Pertactin, PRN, outer membrane protein, vaccine, Bordetella infection, therapy, antibiotic, antibacterial, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                  Bordetella bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 259; DB 23;
Pred. No. 1.3e-12;
0; Mismatches 2;
                                                                                                                                                      Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.9%;
92.5%;
                                                                                                                                                                                                                                                                                                                                 23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
26-MAR-2002 (first entry)
                                                                                                                     Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD26440
                                                                                                                                                                                                                                                                 WO200190143-A2
                                                                                                                                                                                                                                                                                                  29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16197;
                                                                                                                                                                            Region
                                                                                                                                                                                                               Region
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                            Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, divoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as bloopical and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
The present invention relates to Bordetella bronchiseptica pertactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --POPPOPPOPOPOPOPOPEAPAPOPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%; Score 257; DB 23;
86.0%; Pred. No. 2.3e-13;
.ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKVPPAPKPAPQPGPQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200190143-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
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AAE16197

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us-09-855-754b-21.rag

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                A cosmid library was constructed by transforming E coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40.50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an accillular vaccine against B.parapertussis. Preferred fragments include amino acids Pro5771 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; p.70.
                                             Acellular vaccine for immunisation against whooping cough comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQP--QPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
9
                                                                                                                                                                                                                                                                                                                                                                                       Length 922
                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Score 256; DB 13;
Pred. No. 2.2e-12;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254..304
/note= "Pertactin region I"
554..621
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16185 standard; Protein; 922 AA.
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                                                                                                          Claim 1; Fig. 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella parapertussis.
   WPI; 1992-250033/30.
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                                                                                                                                                                                                                                                                                                                                                        922 AA;
                N-PSDB; AAQ26509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD26442
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                                                                                                                                                                                                                                                                                                                                                        Sequence
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AAE16185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in busifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as antigens and and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "contains 9 direct repeats of Pro-Gln-Pro" 712..714
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..612
te= "contains 9 direct repeats of Pro-Gln-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whooping cough; P70 antigen; P95 precursor protein; vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 256; DB 23;
Pred. No. 2.8e-13;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella parapertussis P95 antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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   Boursaux-eude C;
                                                                                                                     Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR25578 standard; Protein; 922
                                                                                                                                                                                                                                                                                                                                                                                               85.9%;
llarity 84.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35..643
/label= P70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260..262
/note= "mc
266..285
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                              WPI; 2002-097639/13
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
 Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                   58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charles IG;
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR25578;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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Gaps

9

2225×8

Disclosure; Page 34; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in manial such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis

922 AA; Sequence

Gaps. ; 9 Length 922; Indels / Match 85.9%; Score 256; DB 23; 1 Local Similarity 84.5%; Pred. No. 2.2e-12; nes 49; Conservative 0; Mismatches 3; Query Match Best Loca Matches ò g

AAE16195 standard; peptide; 60 RESULT 11 AAE16195

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AAE16195;

26-MAR-2002 (first entry)

B. bronchiseptica strain II-3 pertactin outer membrane protein region

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

ΰ Guiso-maclouf N, Boursaux-eude

WPI; 2002-097639/13.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

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antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                         1 GAKVPPAPKPAPQPGPQP-----PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSA
                                                                                                                                                   10;
                                                                                                            Length 60;
                                                                                                          Score 255; DB 23;
Pred. No. 3.5e-13;
0; Mismatches 2;
                                                                                                            85.6%;
                                                                                                            Query Match 85.6
Best Local Similarity 80.3
Matches 49; Conservative
                                                                         60 AA;
                                                                                                                                                                                                                                                                52 A 52
                                                                                                                                                                                                                                                                                                 60 Å 60
                                                                             Sequence
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AAE16199 standard; peptide; 48 AA. RESULT 12 AAE16199

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AAE16199;

(first entry) 26-MAR-2002

B. bronchiseptica strain II-7 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P

ISNI (dSNI)

Guiso-maclouf N, Boursaux-eude

ວີ

WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin doubte membrane protein) or their fragments. Pertactin (PRN) is used as vacine. Pertactin protein) or their fragments. Pertactin (PRN) is used as undised to detect bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal talls as blological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

48 AA; Sequence

Gaps 4 83.6%; Score 249; DB 23; Length 48; 88.5%; Pred. No. 8.5e-13; ive 0; Mismatches 2; Indels Best_Local Similarity 88.5 Matches 46; Conservative Query Match

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Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                         parapertussis.
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              Pertactin antigen P.70.
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N-PSDB; AAQ14320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1990;
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                                                                         Bordetella
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                                                                                                                                                                                                          B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
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       Length 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guiso-maclouf N, Boursaux-eude C;
                                                                                                                 AAE16196 standard; peptide; 53 AA.
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                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica
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Matches
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pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia microòrganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
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ilarity 84.5%; Pred. No. 1.3e-11;
Conservative 0; Mismatches 3;
Location/Qualifiers
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610..612
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Matches 49; Conserv
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AAR14321 standard; Protein; 922 AA.

AAR14321

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20-JAN-1992 (first entry)

AAR14321;

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                       B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                 AAE16193 standard; peptide; 49 AA.
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AAE16193
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Gaps 3 Score 238.5; DB 23; Length 49; Pred. No. 5.4e-12; 0; Mismatches 2; Indels 5 80.0%; 86.8%; Query Match
Best Local Similarity 86.8°
Matches 46; Conservative

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Search completed: May 7, 2003, 16:47:10 Job time : 28.0187 secs

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Q9alp3 bordeteila
Q9alp3 bordeteila
Q9k5g4 bordeteila
Q9k5g1 bordeteila
Q9alq0 bordeteila
Q9alq0 bordeteila
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Q9as6m9 bordeteila
Q9s6m9 bordeteila
Q9s6m9 bordeteila
Q9s6m1 bordeteila
Q9s7n bordeteila
Q957n bordeteila
Q91198 bordeteila
Q91198 bordeteila
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Q91198 bordeteila
Q9119 bordeteila
Q8110 bordeteila
Q8111 bord sapien
Q9504 poeumocysti
Q9115 bord sapien
Q8177 oryza sativ
Q9504 poeumocysti
Q81196 dictyosteil
Q81196 dictyosteil
Q81196 brassica ol
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Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Berdetella parapertussis, and Bordetella bronchiseptica.";
Infect, Immun. 68.4815.4817 (2000).
EMBL; AJ250091; CAB76445.1;
InterPro; IPR004899; Pertact, Sup.
InterPro; IPR002965; P_rich_extensn.
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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105 AA: 10884 MW; 813F1422271962B2 CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 272; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.2e-17;
Matches 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                 Q9P944
Q9DVW0
P93797
Q9UVD0
                   09ALP7
09K5G4
09ALG0
09ALC0
09ALW5
09SAW6
09SSW0
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MEDLINE=20355389; PubMed=10899896;
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PRINTS; PR01217; PRICHEXTENSN.
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NCBI_TaxID=518;
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SEQUENCE
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bordetella
                                                                                                                                                (without alignments)
403.166 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                               US-09-855-754B-20
272
1 GAKAPPAPKPAPQPGPQPPQ......QRQPEAPAPQPPAGRELSAA
                                                                                                                          7, 2003, 16:38:52 ; Search time 24.5315 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09kjy1
09kjy0
09ahp0
09ahp0
09alp9
09alq4
09k5y1
09k5y3
09k5y3
09k5y3
09k5y3
               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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0985H7
0987Y1
0987Y0
0981H7
0981H9
0981H9
0981H9
0981H9
0981H9
0981H9
0981H9
0981H9
0981H9
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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sp_rodent:*
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Match 1
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                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                              Run on:
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Q9K5H9

SO DE RELEGIE DE LA CONTRE LA CONTRE

RESULT 2

о9к5н9

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"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families camino acid repeats.";
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 115;
                                                                                                                                               Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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EMBL, AR156772; ARF82396.1; -
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL, AF156771; AAF82395.1; -... InterPro; IPR004899; Pertact_sup. InterPro; IPR002965; P_rich_extensn. Pfan; PF03212; Pertactin; 1... PRICHESPRO; IPROFESTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 115 115 11705 MW; ElABD4D347D20652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA; 11693 MW; FA3A76596F7097EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.1%; Score 261.5; DB 2;
98.0%; Pred. No. 4.5e-16;
ive 0; Mismatches 0;
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98.0%; Pred. No. 4.5e-16;
tive 0; Mismatches 0
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                                                                                    (TrEMBLrel. 15, Created)
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                                            PRT;
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Best Local Similarity 98.0
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 98.0
nes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       Keil D.J., Fenwick B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pertactin (Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBL_TaxID=518;
                                                                                                                                                                                                                                   NCBI_TaxID=518;
                                                                                    -OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
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NON_TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KJYO
Q9KJYO;
                                            Q9KJY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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RESULT 4
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                      Q9KJY.
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                                                                                                                                                                                                                                                                                                                                         Boursaux Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertuasis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817.2000).
EMBL; AJ250077; CAB76431.1; ...
InterPro; IPR004899; Pertact_sup.
Pfam, PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250079; CAB76433.1;
-
InterPro. IPR004899: Pertact.sup.
Pfam; PF03212; Pertactin. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.1%; Score 261.5; DB 2; Length 104; llarity 98.0%; Pred. No. 4.2e-16; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Pertactin (P.68) (Fragment).
                        104 AA.
                                                                    Created)
                        PRT;
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MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                                                                                                                                                                      STRAIN-9.73H+;
MEDLINE-20359389; PubMed-10899896;
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                                                                01-OCT-2000 (TrEMBLrel. 15,
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Les 48; Conserv
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Best Loca Matches

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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                   Created)
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                      STRAIN-KM22;
MEDLINE-21117018; PubMed-11179374;
Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
95.6%;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
Pertactin (Fragment).
                Best_Local Similarity 92.3
Matches 48; conservative
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                                                                                                                                                                                                                                                                                  Bordetella.
NCBI_TaxID=518;
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NON_TER
SEQUENCE
    Query Match
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                                                                                                                                                        Q9ALP9
                                                                                                                          RESULT 8
Q9ALP9
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL. AJS20081; CABF6435.1;
InterPro. IPR004899; Pertact. Sup.
InterPro. IPR004899; Pertact. Sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 198;
                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacterla: Proteobacterla: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.1%; Score 261.5; DB 2; Length 98.0%; Pred. No. 7.1e-16; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20575 MW; AC940EC331A725AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA; 11036 MW; 1AC13209D0238107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                        EMBL; AF298300 Pertactin.;
Infect. Immun. 69:1917-1921(2001).
EMBL; AF298890; AR16691.;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact.
InterPro; IPR004899; Pertact.
                                                       PRT;
                                                                                                                                                                                                                                                 MEDLINE=21117018; PubMed=11179374; Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20359389; PubMed=10899896;
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PRINTS; PR01217; PRICHEXTENSN.
NON_TER 107 107
SEQUENCE 107 NA.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03212; Pertactin; 1.
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nes 48; Conservative
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                                                      PRELIMINARY;
                                                                                                                         Pertactin (Fragment).
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                                                                                                                                                                                           NCBI_TaxID=518;
                                                                                                                                                                                                                                        STRAIN-MBORD831
                                                                                                                                                                                Bordetella.
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                                                      09AHP0
09AHP0;
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Q9K5H5;
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                          RESULT 6
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"Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines.";

Submitted (44G-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; [AJ245927; CAB82515.1; -.

InterPro; IPR003992; pertactin.
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Bacteria; Próteobacteria; beta subdivision; Alcaligenaceae;
Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 200;
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Enfect. Immun. 69:1917-1921(2001).
Enfect. Immun. 69:1917-1921(2001).
InterPro: IPR003992; pertactin.
InterPro: IPR004899; Pertact.sup.
InterPro: IPR004899; Pertact.sup.
InterPro: IPR004895; Pertact.sup.
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Best Local Similarity 92.3%; Pred. No. 9.7e-16;
Matches 48; Conservative 0; Mismatches 0;
Score 260; DB 2;
Pred. No. 5.7e-16;
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                                                                                                  0; Mismatches
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Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Broadtella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250087; CAB76441.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                          140 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 192
                                                                                                                                                                                                                          Score 259.5; DB 2; Length 215;
Pred. No. 1.1e-15;
0; Mismatches 0; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bordetella.

NCBI_TaxID=518;
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85.7%; Pred. No. 8.8e-16;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                      22327 MW; 5C21D45CF784B4AE CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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                                 Interpro: IPR003992; pertactin.
Interpro: IPR004899; Pertact_sup.
Interpro: IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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Infect. Immun. 69:1917-1921(2001).
EMBL; AY007263; AAG38439.1; -.
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                                                                                                              PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                              95.4%;
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Best Local Similarity 90.6
Matches 48; Conservative
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Best Local Similarity 85.7
Matches 48; Conservative
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                                                                                                                                                                      215 2
215 AA;
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Q9K5G9
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BOUTSAUX-Edde C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
PPOLYMORDHISM; Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250085; CAB76439.1; -
InterPro; IPR004489; Pertact.
NON_TER 10 109
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                                                                                                                                                                                                                               DB 2; Length 109;
                                                                                                                                                                                                            1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                             Score 260; DB 2; Length 911;
Pred. No. 3.4e-15;
0; Mismatches 0; Indels
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
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                                                   PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTNEAMLY.
SEQUENCE 911 Aa; 94093 MW; DF531A9EB4383A32 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 259.5; DB 2;
Pred. No. 6.4e-16;
0; Mismatches 0;
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 InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
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Best Local Similarity 92.3%;
Matches 48; Conservative C
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les 48; Conservative
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                                            Kell D.J., Fenwick B.;
Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 GAKAPPAPKPAPAPGPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 225
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 122;
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Infect. Immun. 69:1917-1921(2001).
EMBL: AY007265; AAG38441.1;
InterPro: IPR003992; pertactin.
InterPro: IPR004899; Pertact.sup.
InterPro: IPR002965; Pirich_extensn.
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85.7%; Pred. No. 9.5e-16;
1ve 0; Mismatches 0; Indels
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NON_TER 252 252
SEQUENCE 252 AA; 26107 MW; 368C142508D77057 CRC64;
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Last sequence update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
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STRAIN-ATCC19395;
MEDLINE-21117018; Pubmed-11179374;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
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Matches 48; Conservative
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  FROM N.A.
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NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9K5G7
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Q9ALQ2
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DE Pertactin (Pi68) (Fragment).

ON MAILTAXID-518;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-2035;389; PubMed-10899896;

RX MEDLINE-2035;389; PubMed-1089989;

RX MEDLINE-2035;389; PubMed-10899896;

RX MEDLINE-2035;389; PubMed-1089989;

RX MEDLINE-2035;389; PubMed-1089989;

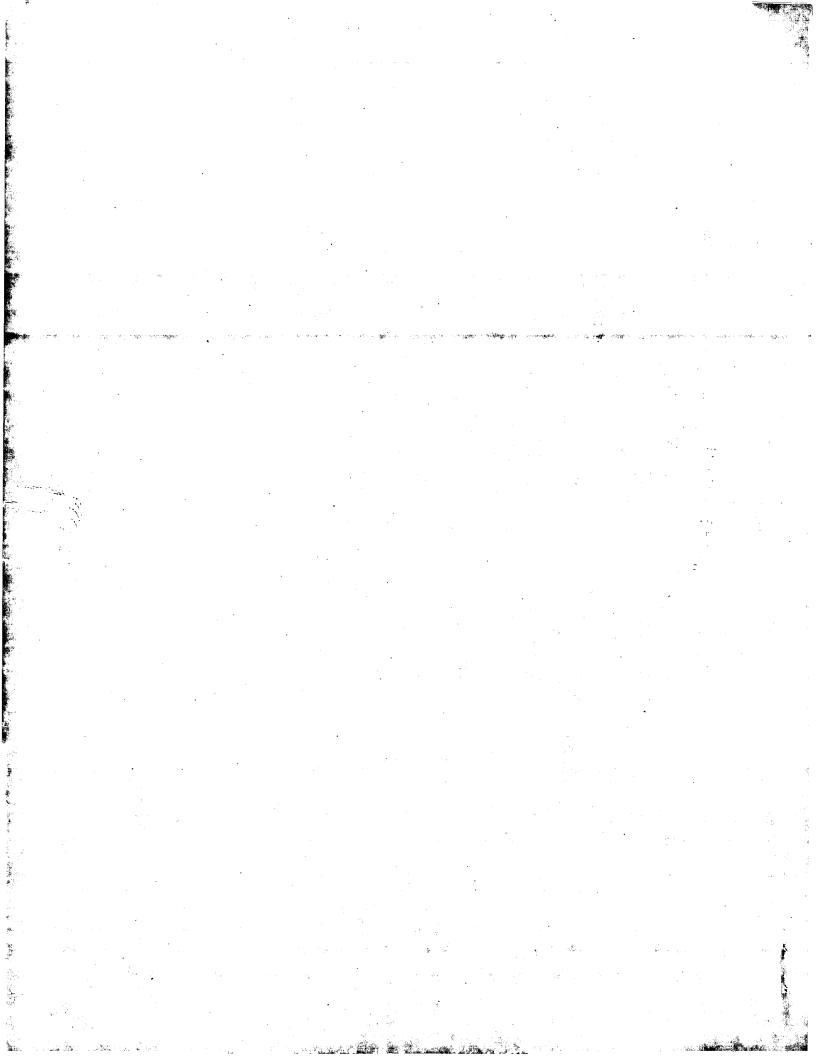
RX MEDLINE-2035;389; PubMed-1089989;

RX MEDLINE-2035;389; PubMed-2039989;

RX MEDLINE-2039989;

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us-09-855-754b-20.rsp

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49 ; Search time 4.66099 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-20 272 1 GAKAPPAPKPAPQPGPQPPQ......QRQPEAPAPQPPAGRELSAA 48 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters: 112892 segs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ption	bordetella	bordetella	bordetella	volvox cart	epstein-bar	owenta fusi	homo sapien	brassica na	homo sapien	rattus norv	mus musculu	autographa	trichoderma	orgyia pseu	nicotiana t	mus musculu	chlamydomon	mns mnscnln	homo sapien	oryctolagus	arabidopsis	homo sapien	mns mnscnjn	emericella	herpes simp	plasmodium	sus scrofa	zea mays (m		homo sapien	homo sapien	caenorhabdí	homo sapien
	Description	Q03035 b	P24328	P14283	P21997	P12978	P21260	060885	P40603	092794	P51111	064467	P41467	099014	083949	003211	P02831	9bdJ60	063943	P42858	P48038	P40602	9umn60	P42859	P78621	P10220	P06914	P08001	P14918	P22670	P58840	P17483	009442	013164
SUMMARIES	ΙΩ	PERT_BORBR	PERT_BORPA	PERT_BORPE	SSGP_VOLCA	EBN2_EBV	YPRO_OWEFU	BRD4_HUMAN	APG_BRANA	MOZ_HUMAN	HD_RAT	G3PT_MOUSE	Y066_NPVAC	KPC1_TRIRE	Y066_NPVOP	EXLP_TOBAC	HXA3_MOUSE	GP1_CHLRE	MEFD_MOUSE	HD_HUMAN	ACRO_RABIT	APG_ARATH	TRX2_HUMAN	HD_MOUSE	SEPA_EMENI	TEGU_HSV11	CSP_PLAYO	ACRO_PIG	EXTN_MAIZE	RFX1_HUMAN	ACRL_HUMAN	HXB4_HUMAN	YP85_CAEEL	MK07_HUMAN
	DB	-	-	ч	-	ч	~	Н	-	-	П	٦	-	-	-	-	-	-	-		-			-	-			-	-	-	-		-	-
	Query Match Length	911	922	910	485	487	141	1362	449	2004	3110	440	808	1139	875	426	443	522	514	3144	431	534	2715	3119	1790	3164	367	415	267	979	232	251	379	815
dip	Query Match	95.6	94.5	82.0	46.7	46.7	45.6	45.2	45.0	44.3	٠.	٠	43.6	43.6	43.4	43.2	43.2	43.2	43.0	42.6	42.3	42.3	41.9	41.5	41.4	41.4	40.3	40.1	39.7	σ,	•	•	39.5	39.3
	Score	260	257	223	127	127	124	123	122.5	120.5	119.5	119	118.5	118.5	118	117.5	117.5	117.5	117	116	115	115	114	113	112.5	112.5	109.5	109	108	108	107.5	107.5	107.5	107
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CAPU_DROME	HXA3_HUMAN	S3A2_MOUSE	CIRF_HUMAN PRP2_MOUSE	TONB_NEIGO	PRP3_MOUSE	S3A2_HUMAN	FM14_MOUSE	FMN1_MOUSE	CSP_PLABE
		٦,		η.	-	-	Н	-	П
1059	443	475	261	283	296	464	1206	1468	339
39.3	30.7	39.0	9.0	38.8	38.8	38.6	38.6	38.6	38.4
107	106.5	106	105.5	105.5	105.5	105	105	105	104.5
34	36	37	36	40	41	42	43	44	45

ALIGNMENTS

PRT; 911 AA.	Created) Last sequence update) Last annitation undate)		a (Alcaligenes bronchisepticus). u: beta subdivision: Alcaligenaceae:			SECUENCE OF 35-44.	v P., Dougan G.,	sequence and heterologous expression of the	procective outer-membrane protein P.68 pertactin from Bordetella bronchiseptica.";		FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN	BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.	SUBGNIT: MONOMER.	E STATE OF	ESIZED ONLI IN THE PRESENCE OF LOW MG(2+)			dure of bloinformatics and the EMBL Outstation - its Institute. There are no restrictions on its	as its content is in no	<pre>1s not removed. Usage by agreement (See http://www.i</pre>	യ	***************************************			Pertact_sup.	pertactin. pertactin_vir.	1, 1.	LN. FRAMLY.	Virulence; Repeat.	70 0	P:34: PERTACTIN (P.68).	POTENTIAL.	OUS EUKARYOTIC	LINES).
STANDARD;	(Rel. 26, Crea (Rel. 26, Last	cursor (Oute	onchiseptica teobacteria	·	, care	N.A., AND	514; PubMed= weather N.F.	leotide sequ	ter-membrane a.";	biol. 138:16	AGGLUTINOGE BY THE R-G-I	ADHESION, P	MONOMER.	MAY CONTRIBE	TONS SINIER	MCDMING TOWNS	OT entry is	Bioinformati	profit inst	and this statement requires a license	ail to licer		CAA01453.1	A47675.	004899; Pert	IPK003991; pert	; Pertactin;	84; PERTACTIN. 84; PRTACTNFAMLY	Signal;	1 34 35 011		713 911		
RESULT 1 PERT_BORBR ID PERT_BORBR	1993	Pertactin precursor (Outer PRN.	Bordetella bronchiseptica Bacteria, Proteobacteria;	Bordetella.	[1]	SECUENCE FROM N.A., AND SECUENCE OF STRAIN-CN7531;	MEDLINE-92407514; Pubmed-1527510; Li J.L., Fairweather N.F., Novotn	"Cloning, nucleotide	protective ou bronchiseptic	G	-!- FUNCTION: MEDIATED		-!- SUBGNIT: MONOMER. -!- SUBCELLINAR LOCAT	1 1			This SWISS-PR	the European	use by non-	entities requ	or send an em		EMBL; A19180; CAA38584.1; EMBL; A19180; CAA01453.1;	PIR; A47675; A47675.	InterPro, IPE	InterPro; IPR	Pfam; PF03212; Pertactin; 1	PRINTS; PRO1482; PERIACTIN. PRINTS; PRO1484; PRIACTNFAM	Outer membrane;	SIGNAL		PROPER 7		
RESULT PERT_B(88	88	N. S	5 5	RA RA	R	RT	RI.	ខម	ខ្ល	88	ខ្ល	36	ខ	ខ្លួ	ខ	ខូខូ	ខ	ខ្ល	3 8	žä	DR	Z C	G. S.	<u>జ</u> జ	žä	ΚM	<u> </u>	F	F F	F	L

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
 CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                         1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                   Length 911;
                                                                                                                                                                                                                                                                               Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                          Pertactin precursor (Outer membrane protein P.70) (P.95).
                                         (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                           Pred. No. 3.1e-10;
                                                                                   Score 260; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.95.
PERTACTIN (P.70).
POTENTIAL.
                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                      922 AA
                                                                                                                                                                                                                         (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 41, Last annotation update
                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIK; SI4609; SI4609.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91251771; PubMed-2041476;
                                                               93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY
                                                                                   95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03212; Pertactin; 1.
                                                                                                         Conservative
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S15204; S15204.
PIR; S14659; S14659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONCENTRATIONS.
                                                               911 AA;
                                                                                             Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
701
266
266
271
276
570
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane;
                                                                                                                                                                                                                                    01-MAR-1992
15-JUN-2002
                                                                                                                                                                                                                          01-MAR-1992
                                                                                                                                                                                                    PERT_BORPA P24328;
                                                                                                                                                                                                                                                                                                    Bordetella.
                                                               SEQUENCE
                                                                                    Query Match
                                                                                                Local
                               REPEAT
REPEAT
           DOMAIN
                                                     DOMAIN
                       REPEAT
                                                                                              Best Loca
Matches
                                                                                                                                                                                          PERT_BORPA
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                                                                                                                                                                                 RESULT
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"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CN2992;
MEDLINE-8926462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular clohing and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1- FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE. SUBUNIT: MONDMER.
SUBGULIT: MONDMER.
SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                  (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                      48
                       LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=92407514; PubMed=1527510;
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                            Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                       Score 257; DB 1; L. Pred. No. 4.8e-10; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 264 AND 332.
MEDLINE=92407514; PubMed=1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96196517; PubMed-8609998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last seq
                                                                                                                                                                               ¥.
                                                                                                                                                                                                                       94.5%;
82.8%;
                                                                                                                                                                               95178
                                                                                                                                                                                                                                               Local Similarity 82.8 tes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                          290
270
275
280
285
603
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                                                                                                                                                                             922 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchiseptica."
                                          266
266
271
276
281
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRN OR OMPE9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERT_BORPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                            Query Match
                                                                REPEAT
REPEAT
                                          DOMAIN
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                                                                                                                                  REPEAT
                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERT_BORPE
                                                                                                                                                                                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETTI H., Mengele R., Wenzi S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of the cellular compartment.";
J. Cell Biol. 109:349-350/1(1989).
-1- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSCUBBLE FIRROWS LAYERS THAT SURROWND INDIVIDIDAL CELLS AT A DISTANCE TO FORM CONTIGUUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE COVALENT CROSS-LINKS ARE FORNED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Volvox.
Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                           CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                   (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 GAKAPPAPKPAPAPGPPQPPQPPQPPQPPQPPQPPAGRELSAA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 223; DB 1; Length 91
Pred. No. 6.3e-08;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                     PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-0cr-1996 (Rel. 34, Last annotation update)
101-6cr-1996 (Rel. 34, Last annotation update)
Volvox carteri.
                                                                                                                                                                                                                                                                                                                                                                                                               (APPROXIMATE).
                                                                                                      PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTNFAMLY.
Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nagariensis / HK10;
MEDLINE-90094551; PubMed-2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3lycoprotein; Sulfation; Hydroxylation
               InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03312; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93452 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%;
ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                        266
266
271
276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P21997;
                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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SSGP_VOLCA
                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
J. Virol. 65:2545-2554(1991).
-I- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90265473; PubMed-2161150;
PELLI L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ranscription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127; DB 1; Length 487;
Pred. No. 0.038;
1; Mismatches 18; Indels
                                                                                                      DB 1; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=10377;
                            195 POLY-PRO.
50436 MW; A52216400A031421 CRC64;
                                                                                              46.7%; Score 127; DB 1; I
54.1%; Pred. No. 0.038;
Live 2; Mismatches 15;
                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 487 AA.
                                                                                                                                                                                                    4 APPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPP
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     PRO-RICH
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                                                                                                                           Harity 54.18;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !- PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3BNA-2 nuclear protein.
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228
260
285 AA;
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                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
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P12978;
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  DOMAIN
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                                                                                                                                                                                                                                                                                                                               RESULT 5
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or send an email to license@lsb-sib.ch).
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D52EFE1CF9960907 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB 1;
Pred. No. 0.14;
2; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 APKPAPQPGPQPPQPPQPPQROPEAPAPQPPAGRELSAA
                                                                                                                                                                                BROMODOMAIN 1.
                                                                                                                                                                                                                                POLY-SER.
POLY-HIS.
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                                                                                                                                                                                                        LYS-RICH
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                                                                                                                                                                   protein
                                                                                                                                        PROSITE; PS00633; BROMODOMAIN_1; 1. PROSITE; PS50014; BROMODOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                       POLY-
POLY-
                                                                                     Interpro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 2.
PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                           POLY
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MEDLINE-94004980; PubMed-8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                152219 MW;
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                                                                                                                                                                    Repeat; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                       45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 52.4%;
nes 22; Conservative
                                     EMBL; AF386649; AAL26987.1;
                                                  EMBL; Y12059; CAA72780.1;
HSSP; Q92831; 1B91.
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                                                                            Genew; HGNC:13575; BRD4
                                                                                                                             ; BROMO;
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1308
1338
721
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                                                                                                                               SMART; SM00297
                                                                                                                                                                      Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APG OR CEX.
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P40603;
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                                                                                                                                                                                                           DOMAIN
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MEDILINE-90147742; PubMed=2105723;
Bakalara N., Collet J., Planells N., Thouveny Y., Fontes M.;
"Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Blochem. Blochem. Blochs. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_FaxID=9606;
                                                                                                                                                                               Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 1; Length 141;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
                  BRD4_HUMAN STANDARD; PRT; 1362 AA. 060885; Q96PD3; 116-OCT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Bromodomain-containing protein 4 (HUNK1 protein).
    PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1- SUBCELLULAR LOCATION: Nuclear (Potential).
1- SIMILARITY: CONTAINS 2 BROMODOMAINS.
                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                        Hypothetical proline-rich protein (Fragment).
                                                                                         141 AA
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0; Mismatches
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NON_TER 1 1 1
DOMAIN 9 58 POLY-
                                                                                                       P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
01-NOV-1995 (Rel. 32, Last ann
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l Similarity 53.8%;
21; Conservative
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French C.A., Fletcher J.A.;
"Human BRD4 protein.";
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                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     141 AA;
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Best Local Similarity
                                                                                                                                                                       Owenla fusiformis.
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                                                                                                                                                                                                           NCBI_TaxID-6347;
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                                                                                           YPRO_OWEFU
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NON_TER
SEQUENCE
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BRD4_HUMAN
                                                                              YPRO_OWEFU
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Gaps

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Length 1362; 18; Indels

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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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Plant J. 3:111-120(1993).
Plant J. 3:111-120(1993).
PLOYELOPHENTAL FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL FINGE: FRAME: STREE: STR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
749 АРАРУРООРРРРРООРРРРРООООООРРРРРРЯМРООАА 790
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OMAIN
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                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   and the EMBL outstation
Swiss Institute of Bioinformatics and the EMBL outstati
Bioinformatics Institute. There are no restrictions on
profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL
TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                  42
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                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-20002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoatomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                              Pred. No. 0.068;
3; Mismatches 12; Indels 17;
                                                                                                                                                                                                                                              3 КАРРАРКРАРОРОРОРОРОРО------РРОРОВОРО---АРАРОРРАВ
                                                                                                                                                                                       Score 122.5; DB 1; Length 449;
                                                                                                                                                                9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                             2004 AA
                                                                                                                                            SIMILARITY.
                                                                                                                    PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001386; Histone_H1/H5.
InterPro: IPR002717; MOZ_SAS.
InterPro: IPR001965; Znf_PHD.
InterPro: IPR001965; Znf_PHD.
InterPro: IPR001965; MOZ_SAS.
InterPol853; MOZ_SAS; I.
SWART; SW00526; H15; I.
                                                                                               IPRO01087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-96376968; PubMed-8782817;
                                                                                                                                            ВX
                                                                                                                                                                48779 MW;
                                                                                                           ; Lipase_GDSL; 1
                                                                         EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                1 Similarity 43.9%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U47742; AAC50662.1; -. Genew; HGNC:13013; ZNF220.
                                                                                                                                                                                      45.0%;
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      (Human).
                        non-profit
                                                                                      PIR; S16748; S16748
InterPro; IPR001087
                                                                                                                                                                 449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                            Pfam; PF00657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 601408;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                            MOZ_HUMAN
Q92794;
                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                           ACT_SITE
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                  MOZ_HUMAN
                                                                                                                                                                                                                                                                                       RESULT
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-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- TISSUE SPECIFICITY: EXPRESSED TO A HIGH DEGREE IN ALL THE REGIONS
OF THE BRAIN OF ADULTS AND IN MEIOTIC CELLS OF THE TESTIS. IN
ADDITION, VERY LOW LEVELS ARE DETECTED IN VARIOUS NON-NEURONAL
TISSUES (HEART, MUSCLE, LIVER, LONG AND KIDNEY).
-1- DEVELOPMENTAL STAGE: IDENTIFIED AT HIGH LEVELS IN NEURONAL TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K., Swaroop M., Kaatz K.W., Collins F.S., Albin R.L.; Widespread expression of the human and rat Huntington's disease gene in brain and nonneural tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hamelster H., Epplen J.T., Rabes O., Hamelster H., Epplen J.T., Rabes O., "Expression of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvejicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 5:259-265(1993).
-1- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT VESICLE FUNCTION.
SMART; SM00249; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_2; 2.
Proto-concogene; Chromosomal translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAPKPAPQPGPQPPQP-PQPPQPPQRQPEAPAPQPP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU.
POLY-SER.
GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120.5;
                                                                                                                                                                                                                                               POLY-GLU.
POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MET-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOZ-CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 4:1173-1182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96133292; PubMed-8528205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94100980; PubMed-8275091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1773-1926 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                       Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                  ZN_FING
                                                                                                                                                                                                                                                                                                                                                    OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HD_RAT
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          3,
OF EMBRYOS AS EARLY AS DAY 14.5, THIS EXPRESSION REMAINS CONSTANT IN ALL FURTHER DEVELOPMENT STAGES (UP TO THE ADULT). ON THE OTHER HAND THE EXPRESSION IN NON-NEURONAL TISSUES IS DOWN-REGULATED FROM
                                            -1- POLYMORPHISM: THE POLY-GIN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPLAINING THE ABSENCE OF A RODENT HD-LIKE DISORDER. POLYMORPHY: CONTAINS 10 HEAT REPEATS.
-1- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Welch J.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-meiotic spermatogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Welch J.E., Schatte B.C., O'Brien D.A., Eddy E.M.;
"Expression of a glyceraldehyde 3-phosphate dehydrogenase gene
specific to mouse specmatogenic cells.";
Biol. Reprod. 46:869-878(1992).
                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                  Score 119.5; DB 1; Length 3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    064467; 060650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific
                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            18 QPPPQPPPPPPPPQPPPQGQPPPPPPLPGPAEEPLHRPKKELSA 65
                                                                                                                                                                                                                                                                                                                                                           33C357E8FC141550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             9 KPAPQPGPQPPQPPQ-PPQRQPEAPAPQP-PA-----GRELSA 47
                                                                                                                                                                                                                                                                  DOMAIN 1.
DOMAIN 2.
DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                              0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA
                                                                                                                                                                                                                                                                  REPEATS D
REPEATS D
REPEATS D
                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                        POLY-PRO.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                   POLY-GLN.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                              EMBL; U18650; AAA90987.1; ALT_SEQ.
                                                                                                                                                                                                                                                                  HEAT
HEAT
HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-Testis;
MEDLINE-92273722; PubMed-1375514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ICR Swiss; TISSUE-Testis;
MEDLINE-95254745; PubMed-7736666;
                                                                                                                                                                                                                   InterPro; TPR000091; Huntingtin.
Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
                                                                                                                                                                                                                                                                                                                                                           3110 AA; 343757 MW;
                                  17.5 DAY OLD EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                 43.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genet. 16:179-189(1995).
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                  2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GAPDH)
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAPDS OR GAPD-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                     Local S...
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G3PT_MOUSE
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                         Repeat
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G3PT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ċ
                                                                                              NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBCILULI: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: TESTIGS-SPECIFIC.
-!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC GERM CELLS. LEVELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING THE SWITCH
                                                                                + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D., "The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 94.0 kpa protein in PoL-LEF3 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                          BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 119; DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 РРАРК------ЕАРАРОРСРОРРОРОРОРОВРОВОВОВ----ЕАРАРОРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
MISSING (IN REF. 2).
L.-> V (IN REF. 2).
05FF0A093D1ABD9C CRC64;
                                             SPERMIOGENESIS AND IN THE SPERMATOZOON.
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  808 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYS/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P56649; 1DSS.
MGD; MG1:95653; Gapda.
InterPro; IPR000173; GaP_dhdrogenase.
Pfam; PF00004; gpdh; 1.
Pfam; PF02800; gpdh, 2.
PRIWTS; PR00078; G3PDHDRGNASE.
PROSITE; PS000071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94303173; PubMed-8030224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M60978; AAA53033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U09964; AAAB0276.1;
                                                                                                                                                                                                                                                                                                                                           DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
100
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                        DURING MATURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y066_NPVAC
P41467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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BINDING
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TOGE NPVOP
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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Y066_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                739
     DR WENT THE FET THE SOLUTION OF THE SOLUTION O
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubicek C.P.;
"Cloning and characterisation of genes (pkc1 and pkcA) encoding
protein kinase C homologues from Trichoderma reesei and Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen. Genet. 250:17-28(1996).
ENZYME REGULATION: STIMULATED ABOUT TWOFOLD BY PHOSPHOLIPIDS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96158841: PubMed-8569684;
MOTAWET R., Lendenfeld T., Mischak H., Muehlbauer M., Gruber F.,
Goodnight J., de Graaff L.H., Visser J., Mushinski J.F.,
Kubicek C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING DOMAINS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fung1; Ascomycota; Perizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
NCBL_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 808;
-1- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                              POLY-PRO. 76A871D2B6633F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 РРАРКРАРОРСРОРРОРРОРРОРО 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        Score 118.5; Di
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      richoderma reesei (Hypocrea jecorina).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000861; REM_repeat.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence
16-027-2001 (Rel. 40, Last sourcatio
Protein kinase C-like (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind
                                                                                                                                                                                                                                                                                                                                    SEQUENCE 808 AA; 93973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 2.
                                                                                                                                                                                                                                                       EMBL; L22858; AAA66696.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                        43.6%;
56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U10016; AAA97432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-QM9414 / Rut C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Q99014;
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                                                                                                                                                                                                                                                                                                              DOMAIN
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BEQUENCE FROM N.A.
MEDLINE-97221300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F!;
"The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ahreng C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95343549; PubMed-7618274;
Marens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3,
gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                           PROSITE; PSG0479; DAG_PE_BIND_DOM_1; 2.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
PROSITE; PS500107; PROTEIN_KINASE_ARP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
PROSITE; PSG0108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          083949; 065364; 010323; 01-100v-1997 (Rel. 35, Created)
01-100v-1997 (Rel. 35, Last sequence update)
01-100v-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71),
Orgyja pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
Virusee, dSDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                      DAG BINDING
DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIrology 210;372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPY AND LDMNPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPPAQMPPQQPPPQQPLPPQPGQYQQQQPAAQKPQPQPPATAQGAAA 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KAPPAPKPAPQPGPQPPQPPQPPQP-PQRQPEA--PAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                           937BB0DAB727B65C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                    PHORBOL-ESTER AND PHORBOL-ESTER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118.5; DB pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.24;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 AA
                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                      POLY-ALA.
POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; PubMed-8609478;
                HR1; 2.
1: Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           126055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                      binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 806-875 FROM N.A.
                                         SMART, SM00109; C1; 2.
SMART, SM00239; C2; 1.
SMART, SM0074; HR1; 2.
SMART, SM00133; S_TK, 1.
SMART, SM00133; S_TK, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             43.6%;
PF00433; pkinase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 55.1
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           1139 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-164623
                              ProDom; PD000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eplication.";
                                                                                                                                                                                                                                       Phorbol-ester
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                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=cv. Petit Havana; TISSUE-Pistil;
MEDLINE-93005740; PubMed=1392607;
Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;
"Developmental expression of tobacco pistil-specific genes encoding novel extensin-like proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Cell 4:1041-1051(1992).
-1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
-1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                       5 PPAPKP-----APQPGPQPPQPPQPP----QPPQRQPEAPAP--QPP 40
                                                                                                                                                                                                                                                  Score 118; DB 1; Length 875; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                     86 91 POLY-PRO.
875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AA
                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000419; Pollen_Ole_e_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                  EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; IFOS.
                                                                                                                                                                                                                                                    43.4%;
illarity 46.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 214019; CAA78397.1;
PIR; JQ1696; JQ1696.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                     Hypothetical protein.
DOMAIN 86 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 29,
                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EXLP_TOBAC Q03211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
                                                                                                                                                                                                                                                                                    25;
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REPEAT
CARBOHYD
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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OM protein - protein search, using sw model

Мау Run on:

7, 2003, 16:41:02; Search time 8.99489 Seconds (without alignments) 513.008 Million cell updates/sec

US-09-855-754B-20 272 1 GARAPPAPKPAPQPGPQPPQ.........QRQPEAPAPQPPAGRELSAA 48 Perfect score: Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUM 110 11	SUMMARIES	Description	68K outer membrane		Q	hypothetical 47,8K	ഗ	sulfated surface q	-	hypothetical prote		hypothetical	proline-rich	hydroxyprolin		cysteine-rich exte	proline-rich prote	proline-rich prote	glyceraldehyde-3-p	Acorf-66 protein			hypothetical			chitinase (EC 3.2.			Ω	•~	•
		DB	7	7	7	7	7	~	7	7	~	7	7	~	~	7	7	7	7	~	Н	~	N	N	~	~	N	~	~	7	
		Length	911	922	910	430	599	485	487	929	1684	141	449	446	1952	209	534	544	440	808	1139	1494	383	875	426	439	206	514	1388	7	
Length DB 922 2 9 922 2 9 922 2 9 922 2 9 922 2 9 923 9 9 9 9	dР	Query	5	4	~	ö	7	ė.	46.7	46.7	46.3	ശ	ഗ	4	44.5	4	4	43.9	43.8	43.6	43.6	43.6	B	n	43.2	43.2	43.0	43.0	7	2	
1 Length 1 Length 2 1		Score	260	257	223	138.5	128	127	127	127	126	124	122.5	121.5	121	120	120	119.5	119	118.5	118.5	18	118	118	117.5	117.5	117	117	116.5	116	
Ouery Match Length 10 95.6 9111 94.5 922 94.5 9111 94.5 922 94.5 922 94.5 922 94.5 922 94.5 922 94.5 922 94.5 922 94.5 922 94.1 1599 94.1 1599 94.1 1599 95.6 1139 95.6 1139 95.6 1139 95.6 1139 95.6 1139 95.6 1139 95.6 1139 95.6 1139 96.7 1139 97.7 440 97.8 470 97.8 470 97.		Result No.	П	7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	

	acrosin (EC 3.4.21	OmpA family protei	extensin homolog T	T20H2.9 protein -	hypothetical prote	protein F2401.6 [1	extensin-like prot	HD protein - mouse	cysteine-rich exte	extensin-like prot	extensin - Volvox	hypothetical prote	UL36 protein - hum	pistil extensin-li	hypothetical prote	hypothetical prote	
	S47538	D87682	T06291	A86335	T31611	A96650	JQ1686	149729	B48232	T10741	S22697	A71416	WMBEH6	PQ0476	н83619	B96534	
	7	~	7	7	~	~	~	7	~	7	~	~	Ч	7	7	~	
	431	449	160	1137	1585	70	151	3119	196	461	464	645	3164	154	270	494	
	42.3	42.3	42.3	42.3	42.1	41.7	41.5	41.5	41.4	41.4	41.4	41.4	41.4	41.2	41.2	9.04	
_	115	115	115	115	114.5	113.5	113	113	112.5	112.5	112.5	112.5	112.5	112	112	110.5	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

	. A47675	
	68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica	eptica
	C; Species: Bordetella bronchiseptica	•
	C;Date: 193Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999	08-Oct-1999
	C; Accession: A47675	
	R;Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.(I.G.
	J. Gen. Microbiol. 138, 1697-1705, 1992	
	A; Title: Cloning, nucleotide sequence and heterologous expression of the protective o	on of the protective o
	A; Reference number: A47675; MUID: 92407514; PMID: 1527510	
	A; Contents: CN7531	
	A; Accession: A47675	
	A;Status: preliminary	
	A; Molecule type: hucleic acid	
	A; Residues: 1-911 <li1></li1>	
	A; Cross-references: GB:X54815; GB:S46416; NID:q39396; PIDN:CAA38584.1; PID:q39397	8584.1: PID:039397
	A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)	BIP:113319)
:	Query Match 95.6%; Score 260; DB 2; Length 911;	
	Best Local Similarity 92.3%; Pred. No. 7.2e-11;	
	Matches 48; Conservative 0; Mismatches 0; Indels	4; Gaps 1;
	QY 1 GAKAPPAŅKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48	48
	DD 559 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQPPAPAPQPPAGRELSAA 610	610

pertactin - Bordetella parapertussis
N.Alternate names: outer membrane protein P70
C.Species: Bordetella parapertussis
C.Species: Bordetella parapertussis: C.Species: Bordetella S15204; S14659
R.H.L.J.; Dougan, G.; Novotny, P.; Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
A.Fite: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A.Ficesrance number: S15204; MUID:91251771; PMID:2041476
A.Rosiques: 1-922 CLIL>
A.Rosiques: 1-922 CLIL>
A.Rosiques: 1-922 CLIL>
A.Gross-references: EMBL:X54547; NID:939761; PIDN:CAA38419.1; PID:939762
C.Genetics:
A.Gene: prn
C.Keyword8: membrane protein

Gaps Query Match 94.5%; Score 257; DB 2; Length 922; Best Local Similarity 82.8%; Pred. No. 1.2e-10; Matches | 48; Conservative 0; Mismatches 0; Indels 10;

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---PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48 1 GAKAPPAPKPAPQPG----

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Gaps

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Length 599; 15; Indels

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A;Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ucclear protein EBNA2 - human herpesvirus 4
C; Species; human herpesvirus 4, Epstein-Barr virus
C; Species; human herpesvirus 4, Epstein-Barr virus
C; Sate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Accession: 542442; 532988; 542447
R; Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Rieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A; Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: A; Reference number: 542440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Volvox carteri
C.Species: Volvox carteri
C.Species: Volvox carteri
C.Species: 10-8pr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C.Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C.Species: A3647
R.Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-351, 1989
A.Fitle: The extracellular matrix of Volvox carteri: molecular structure of A; Reference number: A33647; MUID:90094551; PMID:2689458
A; Reference number: A33647; MUID:90094551; PMID:2689458
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-485 CERT>
A; Cross references: GB:X51616; NID:921999; PIDN:CAA35953.1; PID:g1405821
C; Keywords: glycoprotein
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A; Residues: 1-487 <SAM>
R; Residues: 1-487 <SAM>
B; Residues: 1-487 <SAM>
A; Residues: 1-487 <SAM>
A; Reference number: S32973
A; Accession: S3298
A; Accession: S3298
A; Molecule type: DNA
A; Residues: 1-487 <FAR>
A; Residues: 1-487 <FAR>
A; Residues: 1-487 <FAR>
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
A; Cross-references: EMBL: V01555; NID: 9590719
A; Reference number: S42447; MUID: 85063846; PMID: 6209719
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A;Realdues: 1-88, 'PPP', '99-487 <DAM>
A;Cross-references: EMBL:RO3333; NID:9330443; PIDN:AAA45903.1; PID:9330444
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                            Score 128; DB 2;
Pred. No. 0.032;
1; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 APPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPP 40
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Pred. No. 0.032;
                                                                                                                                                                                                                                                                                                                                            sulfated surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                         5 РРАРКРАРОРСРОРОРОРОРОРОВАРАРОРР 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.7%;
52.5%;
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Best Local Similarity 54.1%;
Matches 20; Conservative
                                                                                                                                                                                  47.1%;
55.6%;
                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 20; Conservative
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Best Local Similarity
A; Residues: 1-599 <GOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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C;Species: Oc.Jan.1995 #sequence_revision 06-Jan.1995 #text_change 28-May-1999
C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
Nakamura, Y.
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A;Reference number: JC2299; MUID:96051989; PMID:8535973
                                                                                                                                                                                                                                                                                     P.; Morriss
                                                                                                                                                                                      C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
C;Accession: A32560
R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number: A32560; MUD:89264462; PMID:2542937
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R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin A;Reference number: 217154; MUID:97162277; PMID:9009264
A;Accession: T10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JC2301
A; Molecule type: DNA
A; Residues: 1-430 < MAD>
A; Cross-references: GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06706.1; PID:d1007278;
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A Molecule type: DNA
A Residues: 1-910 < CHA>
A; Residues: 1-910 < CHA>
A; Residues: 1-910 < CHA>
A; Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
A; Note: it is uncertain whether Met-1 or Pet-3 is the initiator
C; Keywords: membrane protein
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
   GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 223; DB 2; Length 91
Pred. No. 2.1e-08;
0; Mismatches 0; Indels
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                                                                                                                                                         outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 138.5; DB 2;
Pred. No. 0.005;
1; Mismatches 6;
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PPAPKPAPQPGP-----QPPQPPQPPQPPQ--RQPEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical 47.8K protein - Pneumocystis carinii N; Alternate names: ORF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.9%;
Best Local Similarity 47.5%;
Matches 29; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.0%;
ilarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 42; Conserv
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            564
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Epstein-Barr nuclear antigen

Length 487;

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Gaps

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Length 485;

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Gaps

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C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C; Accession: S16748
R; Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. R; Description: Cloning and characterization of a proline-rich gene expressed specific A; Reference number: S16748
A; Robiccule type: mRNA
A; Residues: 1.449 CROB>
A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                     characterized by the repetitio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Species: Chlamydomonas reinhardtii
C. Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
C. Accession: 70907
R. Rodriguez-Martinez, H.; Haring, M.A.; Von Gromof, E.; Beck, C.F.
submitted to the EMBL Data Library, July 1997
A. Accession: 70907
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Accession: 10406 - RODD
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Gross-references: EMBL.A.F015883; NID:9238472; PIDN:AAB69862.1; PID:92384728
A. Experimental source: gametes
C. Genetics:
C. Genetics:
A. Gene: GAS28
F; 11-29/Domain: signal sequence #status predicted <SIG>F; 30-446/Product: hydroxyproline-rich glycoprotein GAS28 #status predicted <WHT>
                    proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxyproline-rich glycoprotein GAS28 precursor - Chlamydomonas reinhardtii
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Pred. No. 0.07;
4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 124; DB 2;
Pred. No. 0.019;
0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PPAPKPAE,QPGPQPPQPPQPPQPPQRQPEAPAPQPPAGR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 122.5; Di
Pred. No. 0.06;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proline-rich protein - rape (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 44.7%;
Best Local Similarity 51.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.9
Matches 25; Conservative
     hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
S16748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                            hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: C96623
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUID:21016719; PMID:11130712
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-929 <STO>
A; Conney 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Homo sapiens (man)
;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127; DB 2; Length 929;
Pred. No. 0.053;
4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T02632
R;Bemis, G.; Rohlfing, T.; Morris, M.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of Homo sapiens PAC clone DJ1186C01.
A;Reference number: 214682
A;Accession: T02632
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMB
A;Residues: 1-1684 <BEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AKAPPAPK-PAPQPGPQPPQ-----PPQPPQRQPEAPAPQPPAGRE 44
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 7
A;Note: intron positions not resolved (incomplete sequence)
A;Note: WUGSC:H_DJ1186C01.1
                                                                                  PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 APAAPGPAPSPAPVPAPPPPPPPPATPVTPAPVPP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein DJ1186C01.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 АРРАРКРАРОРСРОРОРОРОРОРОВОВАРАРОРР 40
Mismatches
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.7%;
illarity 51.0%;
Conservative
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Best Local Similarity
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A; Map position: 1
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Matches

ö g 5

42 67

Genetics

RESULT 10 A34043

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AMAT?

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Gaps

7;

Indels

ð

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proline-rich protein APG - Arabidopsis thaliana (G.Species: Arabidopsis thaliana (mouse-ear cress) (G.Species: Arabidopsis thaliana (mouse-ear cress) (G.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 (G.Accession: S21961 (G.D.) Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991 (A.Description: Cloning and characterization of a proline-rich gene expressed specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PPAPKPAPQPGPQP----PQPPQPPQ-----PPQRQPEAPAPQP-PA 41
                                                                                                                                                                                                                                                                                             A; Accession: S21961
A; Molecule type: DNA
A; Residues: 1-534 <ROB>
A; Cresidues: 1-534 <ROB>
C; Genetics: EMBL: X60377; NID:922598; PID:922599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 7, 2003, 16:55:38
Job time : 17.9949 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 256/1; 299/3; 387/3; 470/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.2%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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Reference number: PQ0474; MUID:93005740; PMID:1392607
Accession: PQ0475
                                                                                                                                                                                                                                                                                             C; Accession: T48814
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Nicotiana tabacum (common tobacco)
Cibate: 25-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
Cibate: 25-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
Cibate: 25-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
Cibate: 26-May-19-May-19-May-19-May-1994 #text_change 01-Dec-2000
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: glutelin
Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <WAT>
F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                      C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 121; DB 2; Length 1952;
Pred. No. 0.24;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         steine-rich extensin-like protein 1 precursor - common tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.1%; Score 120; DB 2; Length 209; Best Local Similarity 51.2%; Pred. No. 0.049; Matches 22; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 39-209 <GOL>
A; Residues: 39-209 <GOL>
A; Cross-references: EMBL:214020; NID:g19918; PID:g19919
A; Experimental source: stigma, style; strain Petit Havana SR1
C; Superfamily: glutelin
                                                                                                                                                                                                   hypothetical protein 15E6.220 [imported] - Neurospora crassa
32 SPPSPSPPPPPSPPPPPPPPPPPPPPPPPPPQPDAPARKRPPPPA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 РРА-РКРАРОРСРОРРОРРОРРОРОВЕАРАРОРР 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 59.5:
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 224541
A; Accession: T48814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
Molecule type: mRNA
Residues: 1-209 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: NCSP:15E6.220
A; Map position: 2
A; Introns: 281/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
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5 PPAPKPAPQPGPQP-----PQPPQPPQP-PQRQPEAPAPQPPA 41

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Gaps

10;

Score 120; DB 2; Length 534; Pred. No. 0.1; 2; Mismatches 10; Indels

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:53:34 ; Search time 14.3918 Seconds (without alignments) 306.927 Million cell updates/sec Мау Run on:

US-09-855-754B-20 272 Perfect score:

1 GAKAPPAPKPAPQPGPQPPQ......QRQPEAPQPPAGRELSAA 48 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

349150 seqs, 92025710 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:

/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:

/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*/ptcdata/2/pubpaa/US09_NEW_PUB.pep:* 6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 20, Appl	sequence 14, Appl	15,	4	18,	19	9	21,	22	Sequence 17, Appl	16,	23,	'n			<u>.</u>	Sequence 43, Appl	a,	
Desc	Sec	Sec	Sec	Sec	Sec	Sed	Sec	Seo	Sec	Sed	Sec	Sed	Sed	Sed	Sed	Se	S	Sed	Se
DI	US-09-855-754-20	US-09-855-754-14	US-09-855-754-15	US-09-855-754-4	US-09-855-754-18	US-09-855-754-19	US-09-855-754-6	US-09-855-754-21	US-09-855-754-22	·US-09-855-754-17	US-09-855-754-16	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-09-976-740-43	2 US-10-023-529-43	2 US-10-023-523-43	9 US-09-976-740-47	
BB	6	6	6	6	0	6	6	6	σ	6	6	6	9	σ	σ			-	
Query Match Length DB	48	49	52	911	26	28	922	52	54	52	59	42	910	33	538	538	538	550	550
Query Match	100.0	96.1	92.6	95.6	94.9	94.5	94.5	91.5	91.2	89.7	88.4	82.0	82.0	74.4	43.2	43.2	43.2	42.6	42.6
Score	272	261.5	260	260	258	257	257	249	248	244	240.5	223	223	202.5	117.5	117.5	117.5	116	116
Result No.	·	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19

Sequence 47, Appl Sequence 7, Appl Sequence 9, Appl Sequence 2, Appl Sequence 4, Appl Sequence 1, Appl Sequence 1, Appl Sequence 4, Appl Sequence 6, Appl Sequence 10, Appl Sequence 125, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 6, Appl Sequence 11, Appl Sequence 6, Appl Sequence 11, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl	Sequence 50, Appl Sequence 21, Appl Sequence 32, Appl Sequence 16, Appl Sequence 62, Appl Sequence 2, Appl Sequence 2, Appl Sequence 34988, A Sequence 967, Appl Sequence 967, Appl Sequence 63, Appl
12 US-10-023-523-47 10 US-09-904-987-7 9 US-10-077-584-9 10 US-09-823-240-2 9 US-10-171-384-1 9 US-10-171-384-1 10 US-09-925-300-1444 9 US-10-038-010-4 9 US-10-073-240-10 9 US-10-073-240-10 9 US-09-238-513B-61 9 US-09-298-523B-61 9 US-09-298-523B-61 9 US-09-298-523B-61 9 US-09-298-523B-61	9 US-10-001-873-50 9 US-10-043-487-282 10 US-09-910-087-21 12 US-10-042-417-32 10 US-09-765-572-160 9 US-09-298-523B-62 10 US-09-864-761-34988 10 US-09-864-761-36844 10 US-09-764-864-967 9 US-09-298-523B-63
1550 683 802 171 171 171 827 531 863 863 691 691 691	1134 416 509 197 641 701 707 171 171 171
44444446666666666666666666666666666666	88.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8
1116 1116 1117 1118 1118 1118 1119 1119 1119 1119	104.5 103.5 103.5 103.5 103.5 102.5 102.5
2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000044444 00000000000000000000000000

ALIGNMENTS

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APPLICAMY: GUISO-WACLORF, NICOLARDA APPRADENTIALS OF THE REPEATED TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA PARPERTUSSIS, TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REFERENCE; GASSO-GOOOO
CURRENT APPLICATION NUMBER: US/09/655,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATERTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 272; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
Sequence 20, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
                                                                                                APPLICANT: BOUNSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-855-754-14
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APPLICANT: BOURAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF, INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED Sequence 14, Aprilcation US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
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US-09-855-754-19
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LENGTH: 56
                                                                                                                                                                                                           TYPE: PRT
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APPLICANT: BOURSAUX-EUDE, CARCLINE
APPLICANT: GUISC-MACLOUF, NICOLE
APPLICANT: GUISC-MACLOUF, NICOLE
APPLICANT: GUISC-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRANCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: IMMUNGRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHIESPILCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-00000
CURRENT APPLICATION NUMBER: 128/09/855,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITTLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 49;
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Pred. No. 2.2e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 261.5; DB 9;
Pred. No. 1.6e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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Publication No. US20020192237A1
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Best Local Similarity 92.3%;
Matches 48; Conservative (
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1 Similarity 98.0%;
48; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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US-09-855-754-15
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US-09-855-754-4
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LENGTH: 52
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APPLICANT: BOURSANTION:
APPLICANT: BOURSANTSON:
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: REGIONS OF PERTACTION IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
FILE REPERRENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUISO-WACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR PPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
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Pred. No. 2.3e-11;
0; Mismatches 0;
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85.7%; Pred. No. 3.2e-12;
iive 0; Mismatches 0
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US-09-855-754-18
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; Sequence 18, Application US/09855754
; Publication No. US20020192237A1
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Best Local Similarity 92.3%;
Matches 48; Conservative
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Best Local Similarity 85.79
Matches 48; Conservative
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SOFTWARE: PatentIn Ver
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Gaps

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APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN FILLE OF INVENTION: BORDETELLA COMPOSITIONS
FILLE REPERENCE: 03495-0206-0000
CURRENT PAPLICATION NUMBER: US/09/855,754
CURRENT PAPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSETWARE: PATENTIN VET. 2.1
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: PRESENTES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/955,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPPQPPQPPQP-----PQRQPEAPAPQPPAGRELSAA
                                                      Length 52;
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                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPPQPPQPPQP----PQRQPEAPAPQPPAGRELSAA
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88.7%; Pred. No. 2.8e-11;
Live 0; Mismatches 0;
                                                   Score 249; DB 9;
Pred. No. 1.3e-11;
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Pred. No. 1.5e-11;
                                                                                                  0; Mismatches
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ORGANISM: Bordetella bronchiseptica
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US-09-855-754-22
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Sequence 22, Application US/09855754

Publication No. US20020192237A1

GENERAL INFORMATION:
                                                 91.5%;
88.5%;
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Best Local Similarity 85.2%;
Matches 46; Conservative
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                                            Query Match
Best Local Similarity 88.5
Matches | 46; Conservative
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Matches 47; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.
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  US-09-855-754-21
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LENGTH: 54
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LENGTH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERIACTIN IN BORDETELLA PERIUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000 CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                        Length 58;
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Pred. No. 3.8e-11;
0; Mismatches 0; Indels
                                                                                                                                                                   Score 257; DB 9; 7
Pred. No. 3.8e-12; 0; Mismatches 0;
                                                                                             ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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US-09-855-754-6
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; Sequence 6, Application US/0985754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
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nilarity 82.8%;
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Best Local Similarity 82.8%;
Matches 48; Conservative
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SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.
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SOFTWARE: Patentin Ver.
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les 48; Conserv
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US-09-855-754-21
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LENGTH: 922
                  SEQ ID NO 19
LENGTH: 58
TYPE: PRT
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LENGTH: 52
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CURRENT APPLICATION NUMBER: 05/09/065,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOIL 2.1
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
COURRENT PILLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
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                         DB 9; Length 59;
GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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Pred. No. 6.8e-10;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bordetella bronchiseptica US-09-855-754-16
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                        US-09-855-754-16; Sequence 16, Application US/09855754; Publication No. US20020192237A1
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Best Local Similarity 87.5%;
Matches 42; Conservative (
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                               TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PATTLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND FITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND FITLE OF INVENTION: MUNDROBENC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT PELICATION NUMBER: 60/206,969

PRIOR FILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-05-25
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Pred. No. 8.8e-09;
); Mismatches 0;
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81.2%; Pred. No. 1.7e-08;
tive 0; Mismatches 0
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82.0%; Score 223;
Best Local Similarity 87.5%; Pred. No. 8.
Matches 42; Conservative 0; Mismatche
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
us/09855754
                                                                                                                GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella pertussis
US-09-855-754-5
Sequence 5, Application US/0985 Publication No. US20020192237A1
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SOFTWARE: Patentin Ver. 2.1
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Matches 39; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 910
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Search completed: May 7, 2003, 17:30:54 Job time: 15.3918 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	May 7, 2003, 16:38:52; Search time 29.6422 Seconds (Without alignments) 403.166 Million cell updates/sec	US-09-855-7548-19 335 1 GAKAPPAPKPAPQPGPGPQRQPEAPAPQPPAGRELSAA 58	BLOSUM62 Gapop 10.0 , Gapext 0.5	671580 seqs, 206047115 residues	Total number of hits satisfying chosen parameters: 671580	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
	OM protein - pi	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seq Maximum DB seq	Post-processing

7: sp_mhc:*
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4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:*

SPTREMBL_21:* 1: sp_archea:* 2: sp_bacteria:*

Database :

sp_fung1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Q9k5q7 bordetella	09k5h3 bordetella	09k5q9 bordetella	_	_		Q9alp9 bordetella	Q914e2 bordetella	09k5h1 bordetella			Q9k5h9 bordetella	Q9k5h7 bordetella		09kiv0 bordetella	O9ahpO bordetella	
SUMMARIES			ID	Q9K5G7	Ф9к5н3	Q9K5G9	Ф9КЛХ9	Q9ALQ2	Q9K5H5	Q9ALP9	Q9L4E2	Q9K5H1	Q9ALQ4	Q9K5G1	Q9K5H9	Q9K5H7	Q9KJY1	Q9KJY0	09анро	
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		Query	Length	111	115	111	122	252	107	200	911	109	215	107	104	105	115	115	198	
•	opi	Query	Match	100.0	93.7	90.4	90.4	90.4	84.8	84.8	84.8	84.3	84.3	79.1	78.7	78.7	78.7	78.7	78.7	
			Score	335	314	303	303	303	284	284	284	282.5	282.5	265	263.5	263.5	263.5	263.5	263.5	
		Result	Q	П	8	ю	4	S	9	7	89	6	10	11	12	13	14	15	16	

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1 GAKAPPAPKPAPOPGPQPGPQPPQPPQPPQPPQPPQPQPQPGPAPAPQPPAGRELSAA 58

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Query Match
100.0%; Score 335; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.3e-21;
Matches 58; Conservative 0; Mismatches 0; Indels (

09k5g5 bordetella 09k194 bordetella 09k194 bordetella 09k107 bordetella 09k107 bordetella 09k107 bordetella 09k106 bordetella 09k108 bordetella 09k108 bordetella 09k108 bordetella 09k109 bordetella 09k109 bordetella 08k101 bordetella 08k10 bordetella 09k10 bordetella 09k014 pneumocysti 09k015 bordetella 09k014 breumocysti 09k10 breumocysti 09k00 pneumocysti 09k00 pneumocysti 08k00 pneumocysti 08k00 pneumocysti 08k00 pneumocysti	ALIGNMENTS RT; 111 AA. ated) t sequence update) t annotation update) t annotation update) t annotation; Alcaligenaceae; subdivision; Alcaligenaceae; 96; ns of Pertactin in Bordetella ssis, and Bordetella bronchiseptica."; 0). ensn.
09K5G5 09K5G5 09KLP3 09ALP3 09ALP3 09ALP5 09SSM9 09SSM9 09SSN0 09SSN0 09SSN1 09SSN1 09SSN1 09SSN1 09SSN1 09ULL5 09ULL5 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW1 09SW2 0	ALIGNMENTS PRT; 111 AA. Created Last sequence update) Last annotation updat Last annotation updat Calcaligenes bronchisep beta subdivision; Alcal Begions of Pertactin in pertussis, and Bordetel Ct_sup. Last NRSN. NRSN.
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National Section 1979, National Section 1970, National Section 1970,
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                        Pertactin (Fragment).

Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.4%; Score 303; DB 2; Length 12 94.8%; Pred. No. 1.5e-18; tive 0; Mismatches 1; Indels
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122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
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Infect. Immun. 69:1977-1921(2001).
InterPro; PR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Prich_extensn.
Pfam; PF03212; Pertactin; I.
PRIWTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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01-OCT-2000 (TrEMBLrel. 15, Last seq
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Best Local Similarity 94.8
Matches 55; Conservative
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MEDIATRE-20135389; PubMed-10899896;
MEDIATRE-20135389; PubMed-10899896;
BOUTSBUX-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella perapertussis, partuasis, bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250087; CAB76441.1;
                                                                                                                                                                                                                                                                                                                                                                   MEDITRE-20159389; PubMed-10899896;
Boursaux Fude C., Guiso N.;
Boursaux Ende C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJJ50083; CAB76431.1: -
InterPro; IPR002965; P. Fitch_extensn.
Pfam; PF0212; Pertactin.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 314; DB 2; Length 115;
Pred. No. 1.8e-19;
0; Mismatches 0; Indels
                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                               01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Interpro; IPR002965; P_rich_extensn.
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PRINTS; PR01217; PRICHEXTENSN.
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1 Similarity 96.7%;
58; Conservative
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                                                              PRELIMINARY;
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Best Local Similarity
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                                                                                     09к5н3;
                                                              Q9K5H3
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Q9K5G9
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NCBI_TaxID-518;
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4817.2000).
EMBL: AJ250081; CAB76435.1;
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                                                      1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRDPAPAPAGRELSAA
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                   Length 252;
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Pred. No. 5.1e-17;
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                                     Indels
368C142508D77057 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Last annotation update)
                 Score 303; DB 2; L/
Pred. No. 2.7e-18; .
0; Mismatches 1;
                                                                                                                         107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Created)
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InterPro; IPR002965; P_rich_extensn.
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MEDLINE-21117018; PubMed-11179374;
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infect. Immun. 69:1917-1911(2001).
EMBL: AY007213, AAG38447.1.
InterPro; IPR003992; pertactin.
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26107 MW;
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89.7%;
                  Query Match 90.4%;
Best Local Similarity 94.8%;
Matches 55; Conservative
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                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                        107 AA;
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252 AA;
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01-JUN-2002
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Gaps
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EMBL, AJ245927; CAB82515.1; -.
InterPro: PR003992; pertactin.
InterPro: IPR003991; pertactin.
InterPro: IPR003991; pertactin.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                  Length 200;
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20826 MW; 9F3AC6E4128942E6 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                84.8%; Score 284; DB 2; L
89.7%; Pred. No. 8.3e-17;
tive 0; Mismatches 0;
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Pred. No. 2.8e-16;
0; Mismatches 0;
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InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam. PF03212; Pertactin; 1.
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PRINTS; PR01484; PRTACTNFAMLY.
                                                                               PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 52; Conserv
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Best Local Similarity
Matches 52; Conserv
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SEQUENCE FROM N.A.
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Bordetella
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SEQUENCE
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SEQUENCE
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Q9K5H7
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Q9K5H9
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         Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
portussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ550085; CAB76439.1;
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
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                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPQPPQPPQPPQPPQPPQPPQPPQRQPAPAPQPPAGRELSAA 58
                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPPAPAPQPPAGRELSAA
                                                                                                                                                         5;
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                                                                                                                                    DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Novel Genetic and Phenotypic Heterogeneity in Bordetella Bornochiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL, AY007263; AAG38439.1; ...
InterPro: IPR003992; pertactin.
InterPro: IPR004899; Pertact Sup.
                                                                                                                                ch 84.3%; Score 282.5; DB 2; Length : I Similarity 89.7%; Pred. No. 6.8e-17; 52; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22327 MW; 5C21D45CF784B4AE CRC64;
                                                                                                           109 AA; 11192 MW; 85EBEF7483665DD3 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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MEDLINE=21117018; PubMed=11179374;
MEDLINE-20359389; PubMed-10899896;
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PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                   109
                                                                                                                                                                                                                                                                                                                 Pertactin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AA;
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NCBI_TaxID=518;
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Matches 52
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Q9K5G1
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Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL; AJ250077; CAB76431.1;
InterPro; IPR004899; Pertact_sup.
MEDLINE-20359389; PubMed-10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL; AJ250095; CAB76449.1;
Enterpro; IPR004899; Pertact_sup.
InterPro; IPR002965; P.rich_extensn.
PF03212; Pertactin; 1.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                   79.1%; Score 265; DB 2; Length 10
84.5%; Pred. No. 1.9e-15;
ive 0; Mismatches 5; Indels
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104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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107 AA; 11073 MW; AOA339BFF0EABBC6 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Matches 49; Conservative
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4815.4817(2000).
EMBL; AJ250079; CAB76433.1; -.
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"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
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           (Alcaligenes bronchisepticus).
beta subdivision; Alcaligenaceae;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
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105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
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Last annotation update)
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84.5%; Pred. No. 2.6e-15;
Live 0; Mismatches 0;
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Pred. No. 2.4e-15;
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                                                                                        MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                            InterPro; IPR004899; Pertact_sup. Pfam; PF03212; Pertactin; 1.
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Best Local Similarity 84.5%;
Matches 49; Conservative
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         Bordetella bronchiseptica
Bacteria; Proteobacteria;
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                                                                SEQUENCE FROM N.A.
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                                          NCBI_TaxID=518;
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Q9KJY0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 115;
                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL AFL56772: AAF82396.1;
InterPro: IRF004899; Pertact_sup.
PF03212; Pertactin; 1.
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115 AA; 11705 MW; Elabd4D347D20652 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Job time: 30.6422 secs
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nes 49; Conserv
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                                                                                          Bordetella.
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Sugar beet chitina
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Human ORFX ORF2085
Novel human diagno
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Human polypeptide
Synthetic Bordetel
Human polypeptide
                   B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
Pertactin antigen
B. bronchiseptica
Bordetella pertuss
Bordetella pertuss
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   Bordetella parapen
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AAY33500
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              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB seq Maximum DB seq

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (RNN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying carresponding proteins, glycoproteins or their mixtures when used in affinity arcmancopraphic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of
                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
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Claim 26; Fig 1c; 47pp; English
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiques can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    B. bronchiseptica strain II-2 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\rm II}\,.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRDEAPAPQPPAGRELSAA
                                                                                  Length
                                                                                                                                                    GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                    Score 261.5; DB 23; Length
Pred. No. 3.4e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.6%; Score 260; DB 23;
ilarity 92.3%; Pred. No. 4.7e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                          AAE16194 standard; peptide; 52
                                                                                   96.1%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica.
                                                                                                                     48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-097639/13.
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Matches 48; Conserv
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guiso-maclouf N,
                                                   49 AA;
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                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                       Sequence
                                                                                     Query Match
Best Local
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                                                                                                                     Matches
                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                             AAE16194
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Gaps

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20-JAN-1992

AAR14320;

RESULT 4 **PAR14320**

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The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic.

    B. bronchiseptica; P.68; outer membrane protein; piglet; probe;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 260; DB 13;
Pred. No. 4e-13;
0; Mismatches 0;
                                                                                                                                                          cleavage
                                                                                                                                                                                                                                                                                                               /label- RGD_tripeptide 701..703
                                                                                                                                                                                                                                                                                                                                     701..703
/label= RGD_tripeptide
                                                                                                                                                                                                                                                     266..279
/label- Repeat_region
                                                                                                                                                                                                                                                                                                  Repeat_region
                                                                                                                                                                                                                Location/Qualifiers
                         AAR26503 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16183 standard; Protein; 911 AA.
                                                                                                                                                         atrophic rhinitis; alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 28pp; English
                                                                                                                                                                                                                             35..632
/label= P.68
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Best Local Similarity 92.3%;
Matches 48; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-GB00561.
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                                                                                                                                                                                                                                                                                               /label= Ro
                                                                                                                                                                                  Bordetalla bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                   570..589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-366258/44.
N-PSDB; AAQ34566.
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                                                                                                              prn proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                W09217587-A.
                                                                                 12-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                             15-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles IG;
                                                       AAR26503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16183;
                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                        Region
RESULT 5
AAR26503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 ancoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%; Score 260; DB 12; Length 911;
illarity 92.3%; Pred. No. 4e-13;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                   Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                       Location/Qualifiers
266.270
/label= repeat
271.275
/label= repeat
                                      AAR14320 standard; Protein; 911 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WELL ) WELLCOME FOUNDATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                    87..589
/label- repeat
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label- repeat
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/label- repeat
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                                                                                                                                                                                                                                                                                                      574..576
/label= re
                                                                                             (first entry)
                                                                                                                                                                               Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                             570..572
/label- re
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/label- re
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                                                                                                                         Pertactin antigen P.68.
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N-PSDB; AAQ14319.
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nes 48; Conserv
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28-MAR-1991; 02-APR-1990;

Clare JJ,

Sequence Query Match

Best Loca Matches

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WO9115571-A 17-0CT-1991

Peptide

Peptide Peptide Peptide Pept1de

Peptide Peptide Peptide Peptide ä

Gaps

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Indels

Length 911;

48

WO200190143-A2 29-NOV-2001

Region Region

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(outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 259.5; DB 2
Pred. No. 5.2e-14;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                              Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16197 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.48;
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                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
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                        Bordetella bronchiseptica.
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Best Local Similarity 90.6
Matches 48; Conservative
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                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AA;
                                                                                                                                                                                                                                                                                                              Guiso-maclouf N,
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                                                                     WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodgical fluids, such as human or other animal cells, as well as bloodgical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
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                                                 Bordetella bronchiseptica pertactin outer membrane protein, p.68.
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Pred. No. 4e-13;
0; Mismatches 0; Indels
                                                                                                                                                                                                               Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                       therapy; antibiotic; antibacterial; p.68.
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Best Local Similarity 92.3%;
Matches 48; Conservative
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26-MAR-2002 (first entry)
                                                                                                                                                                    Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
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AAE16196;

AAE16196 RESULT

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Sequence

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DB 23; Length 0; Indels

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     8888888888888
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                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

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                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPA-----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.9%; Score 258; DB 23; Length 56; 85.7%; Pred. No. 7.1e-14; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boursaux-eude C;
  Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                     Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16198 standard; peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guiso-maclouf N,
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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Matches
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purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify intibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb
                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35..643
/label= P70
260..262
/note= "motif associated with cell-cell adhesion"
266..285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575..612
/note= "contains 9 direct repeats of Pro-Gln-Pro"
712..714
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acellular vaccine for immunisation against whooping cough -
comprises protein uncontaminated by B. para:pertussis components
and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                              --POPPOPPOPPOROPEAPAPOPPAGRELSAA
                                                                                                                                                                                                               Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "contains 5 direct, tandem repeats"
                                                                                                                                                                                                             Score 257; DB 23;
Pred. No. 8.7e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
35..643
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                                                                                                                                                                                                                                                                                                                                                                                           AAR25578 standard; Protein; 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 20pp; English.
                                                                                                                                                                                                               94.5%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
                                                                                                                                                                                                                              Best Local Similarity 82.8
Matches 48; Conservative
                                                                                                                                                                                                                                                                             GAKAPPAPKPAPQPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-250033/30.
                                                                                                                                                                                53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ26509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles IG;
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR25578;
                                                                                                                                                                                                                Query Match
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Protein
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clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found tentain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612. 88888888888

922 AA; Sequence

Gaps Indels 10; Length 922; Score 257; DB 13; Pred. No. 6.9e-13; 0; Mismatches 0; 94.5%; 82.8%; 48; Conservative Best Local Similarity Query Match Matches

ij

48 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA g ö

RESULT 11 AAE16185

AAE16185 standard; Protein; 922 AA.

AAE16185;

(first entry) 26-MAR-2002 Bordetella parapertussis pertactin outer membrane protein, p.70.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.

Bordetella parapertussis.

254..304 /note= "Pertactin region I" 564..621 Location/Qualifiers Region Reg ton

/note= "Pertactin region II"

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

N-PSDB; AAD26442

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Disclosure; Page 34; 47pp; English

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPA-------PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                              48
                                                                                                                                                                                                   1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                             10;
                                                                                                          Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 60;
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Pred. No. 1.1e-13;
0; Mismatches 0;
                                                                                                          Score 257; DB 23;
Pred. No. 6.9e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boursaux-eude C;
                                                                                                                                                                                                                                                                                                         AAE16195 standard; peptide; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.1%;
Best Local Similarity 80.0%;
Matches 48; Conservative
                                                                                                        Ouery Match 94.5%;
Best Local Similarity 82.8%;
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-097639/13.
                                                                          922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                           AAE16195;
                                                                            Sequence
                                                                                                                                                                                                                                                                        RESULT 12
AAE16195
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    bronchiseptica strain II-8 pertactin outer membrane protein region II.

    B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                          Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.5%; Score 249; DB 23; Length 52; llarity 88.5%; Pred. No. 3.4e-13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                    AAE16200 standard; peptide; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16201 standard; peptide; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                 (first entry)
                                                                                                                                                                                                                      Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA;
                                                                                                                                                                                                                                                   40200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                  AAE16200;
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AAE16201
                         RESULT 13
                                         AAE16200
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Perfactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.2%; Score 248; DB 23; Length 54; 85.2%; Pred. No. 4.2e-13; 1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- repeat
276..280
/label- repeat
281..285
/label- repeat
575..577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR14321 standard; Protein; 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266..270
/label= repeat
271..275
/label= repeat
                                                                                                                                                                                                                                         23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                  25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JAN-1992 (first entry)
                                                        Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 85.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin antigen P.70.
                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-097639/13.
                                                                                                                    W0200190143-A2.
                                                                                                                                                                             29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR14321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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for

ij

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.8%; Score 247; DB 12; Length 922;
82.8%; Pred. No. 4.2e-12;
tive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 he 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1C; 38pp; English.
                                                     /label= repeat
586.588
/label= repeat
589..591
/label= repeat
                                                                                                                                                     592..594
/label= repeat
/395..597
/label= repeat
598..600
/label= repeat
/label= repeat
/label= repeat
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  79..581
label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-GB00487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      90GB-0007416.
                                      583..585
/label= re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-325214/44.
N-PSDB; AAQ14320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1990;
                                                                                                                                                                                                                                                                                                                                       W09115571-A.
                                                                                                                                                                                                                                                                                                                                                                            17-OCT-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                            Peptide
Peptide
                                        Peptide
                                                                               Peptide
                                                                                                                    Peptide
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0; Indels 10;

Best Local Similarity 82.8 Matches 48; Conservative

à

Search completed: May 7, 2003, 16:47:09 Job time: 25.9404 secs

	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	
OM protein - pr	OM protein - protein search, using sw model	
Run on:	May 7, 2003, 16:41:51; Search time 7.93186 Seconds (without alignments) 178.054 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-855-754B-20 272 1 GAKAPPAPKPAPQPGPQPPQQRQPEAPAPQPPAGRELSAA 48	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	

262574 Total number of hits satisfying chosen parameters: 262574 segs, 29422922 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/Packfiles1.pep:* /cgn2_6/ptodata/1/1aa/5A_COMB.pep:* /cgn2_6/ptodata/1/1aa/5B_COMB.pep:* Issued_Patents_AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ŭ	4, Appl1	6, Appli	2, Appli	11, Appl	11, Appl	8, Appli	16, Appl	16, Appl			30, Appl		6, Appli	6, Appli	42, Appl	21, Appl	15, Appl	5202236	520236	8, Appli	2, Appli	66, Appl	149, App		4, Appli	4, Appli	21, Appl
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Patent No.	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence						
ID	US-08-460-269C-4	US-08-460-269C-6	US-08-460-269C-2	US-08-237-716-11	US-08-750-624-11	US-08-460-269C-8	US-08-246-982A-16	US-08-453-265-16	US-09-041-886-28	US-09-041-886-29	US-09-041-886-30	US-09-041-886-31	US-08-246-982A-6	US-08-453-265-6	US-08-457-273B-42	US-08-556-419-21	US-09-041-886-15	5202236-3	5202236-37	US-08-457-273B-8	US-08-155-888-2	US-09-179-558-66	US-09-314-268-149	US-09-314-268-134	US-09-026-587-4	US-09-227-420-4	US-08-860-635A-21
DB	4	4	4	Н	4	4	Н	Н	4	4	4	4	-		~	m	4	9	9	7	m	4	4	4	~	~	4
% Query Match Length	911	922	910	33	24	23	3119	3119	513	530	552	589	3144	3144	3144	3144	3144	334	331	3118	478	311	75	106	380	380	509
% Query Match	95.6	94.5	82.0	48.9	46.7	45.6	42.8	42.8	42.6	42.6	42.6	42.6	42.6	42.6	42.6	42.6	42.6	42.3	41.9	41.5	40.3	39.5	38.8	38.4	38.4	38.4	38.2
Score	260	257	223	133	127	124	116.5	116.5	116	116	116	116	116	116	116	116	116	115	114	113	109.5	106.5	105.5	104.5	104.5	104.5	104
Result No.	п	8	e	*	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 21, Appl Sequence 143, App	Sequence 143, App	Sequence 160, App Sequence 2, Appl1 Sequence 2, Appl1	200	00	999	Sequence 4, Appli Sequence 3, Appli	Sequence 65, Appl
US-09-281-476-21 US-08-818-112-143 US-08-818-111-138	US-09-056-556-143 US-09-072-596-138	US-U8-961-083-160 US-07-945-283-2 US-07-882-292-2	US-08-331-644-2 PCT-US93-04102-2	US-09-095-443-2 US-08-929-417-2	US-08-749-391-2 US-09-390-200-2 US-08-642-255-32	US-09-142-551A-4 US-09-142-551A-3	US-07-609-716-65
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509 174 174	174	1958 480	480 480	1274	4 8 8 5 4 8 5 5 4 8 5 5 6 6 5	370 396	408
38.1	386.1	38.1 37.7 37.5	37.5	36.9	9 9 9	36.6	36.6
103.5	103.5	102.5	102	100.5	100 200 5 5 6 7	. 66 60 60 60 60 60 60 60 60 60 60 60 60 6	99.5
28 29 30	3333	3 3 4 3 4 5	36 37	338	0 4 4 0 1 0	4 4	45

ALIGNMENTS

APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN CORRESPONDENCE ADDRESS:
ADDRESSEE: Milen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995 FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION: ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-08-460-269C-4 TELEPHONE: (703) 243-6333 Sequence 4, Application US/08460269C Patent No. 6197548 SEQUENCE CHARACTERISTICS: LENGTH: 911 amino acids TYPP: amino acid COMPUTER READABLE FORM: TELEFAX: (703) 2 INFORMATION FOR SEQ ID NO: NUMBER OF SEQUENCES: INFORMATION: GENERAL

4 Score 260; DB 4; Length 911; Pred. No. 6.9e-16; 0; Mismatches 0; Indels Query Match 95.6%; Best Local Similarity 92.3%; Matches 48; Conservative (

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Gaps

1 GAKAPPAPKPA----POPGPOPPOPPOPPOPPOROPEAPAPOPPAGRELSAA 48 ŏ q

Gaps

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Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   Score 223; DB 4;
Pred. No. 1.2e-12;
0; Mismatches 0
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                              NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LIPSCOMB, Martin J
APPLICANT: CIRKLES, Ian G
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UNV-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-UNY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08237716 Patent No. 5589384
                                                                                                                                                                          TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,955
                                                                                                                                                                                                                                                                                                                                                                                                     82.0%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-237-716-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
TILLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                 ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STRETT: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 257; DB 4;
Pred. No. 1.3e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO; 6:
US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                         ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                              Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 82.8 Matches 48; Conservative
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-460-269C-2
                             JS-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
         RESULT 2
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Region

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CITY: Washington STATE: D.C.
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         RESULT 6
US-08-460-269C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127; DB 4; Length 24;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
                                                                                                                                                                                                                                Score 133; DB 1;
Pred. No. 4.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Sim & McBurney
6th Floor, 330 University Avenue
           /label- LTB sequence
                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                             6 РАРКРАРОРСРОРРОРРОРРОРОВАРАРОР 39
                                                                                                                                                                                                                                                                                                                                                5 PGPEIAPQPGPPQPPQP-----QPEAPAPEP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                  /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PQPGPQPPQPPQP-----QPEAPAPQPP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQPGPQPPQPPQPPQRQPEAPAPQPP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/750,624
26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Randil, All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/CDCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%;
ilarity 79.3%;
Conservative
                                                                                                                                                                                                                                Query Match 48.9%;
Best Local Similarity 70.6%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
                                                                                                                  NAME/KEY: Region
LCCATION: 10.31
CTHER INFORMATION: OTHER INFORMATION: US-08-237-716-11
OTHER INFORMATION:
                                                               LOCATION: 4.7
OTHER INFORMATION:
                                           NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Gaps
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APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Duyao, Mabel P.
APPLICANT: Hunding F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                            APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROFEIN IN
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 124; DB 4;
Pred. No. 2.1e-05;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-460-269C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 APQPGPQPPQPPQPPQRQPEAPAPQP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APQPGPQPPQP-----QPEAPAPQP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08246982A Patent No. 5686288 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
Sequence 8, Aprlication US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 2000;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.68;
79.38;
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 79.3
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                               SEOUENCES:
                                                                                                                                                                                                                                                     CITY: ARLINGTON
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Gaps

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Best Local Similarity 49.0%; Pred. No. 0.0076;
Matches 25; Conservative 2; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                     6 РАРКРАРОРСРОРРОРРОРРОРОЯ В В РОВРОРРА - - 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 116;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 29, Application US/09041886
; Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.6%;
Best Local Similarity 46.4%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 513 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-041-886-29
                                                                                                                                                                                                                                                 US-09-041-886-28
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                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5; DB 1; Length 3119; 0.0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Amboose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
APPLICANT: Gusella, James F.
APPLICANT: Gusella, James F.
APPLICANT: Ambound Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPA-----GRELSA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTONNEY/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                         FILING DATE: MAY 20, 1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKEY NUMBER: 0609.3880002
TELECOMMULICATION INFORMATION:
TELECHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.8%; Score 116.5;
49.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISTRATION UNBABER: 36,203
REFERENCE, DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPRAX: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                              (202) 371-2600
(202) 371-2540
OR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.03
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-246-982A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                 TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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Indels 14;
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Bredesen, Sharroz
APPLICANT: Broaden, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                               LUNESSEE: Campbell & Flores LLP
STREEF: 4370 La Johla Village Drive, Suite 700
STATE: California
COUNTRY: United States
ZIP: 92122
Mprime -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                              sequence 28, Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Depen
TITLE OF INVENTION: Polypeptides and Methods of
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
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Length 3119;

DB 1;

42.8%; Score 116.5;

Query Match

5

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Gaps
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                                                                                                                                                            6 PAPKPAROPGPOPPOPPOP--POROPEAPAPOPPAG------RELSA 47
                                                                                                                                                                                    41 РРРРРРРРИЗТРОДИРОДИРОДАФРИТИРОВРОВРРРРИЗТИВЕРГИКРИКЕТСЯ 96
                                                                                                                Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agtent No. 5686,200
Statent No. 5686,200
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Ousels Nabel P.
APPLICANT: Gusels James F.
                                                              Score 116; DB 4; Length 552;
Pred. No. 0.0018;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 116; DB 4; Length 589;
Pred. No. 0.0019;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Proapoptotic Peptides of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG--
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                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/09041886
Patent. No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.4%;
Matches 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31
                                                                   Query Match
Best Local Similarity 46.4%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 43/0 ....
CITY: San Diego
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-041-886-31
; MOLECULE TYPE: peptide US-09-041-886-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13 | US-08-246-982A-6
                                                                                                                                                                                                                                                                                                  US-09-041-886-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                        RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PAPKPAPQPGPQPPQPPQPPQP--PQRQPEAPAPQPPAG------RELSA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 116; DB 4; Length 530;
Pred. No. 0.0017;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharioz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                           ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHX: (619) 535-9001
TELEPHX: (619) 535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RESISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-09-041-886-30
Sequence 30, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.4%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4370 La Jolla Vi
CITY: San Diego
STATE: California
COUNTR: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 530 amino acids
amino acid
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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14; Gaps
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                        Length 3144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURTRAINT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 116; DB 2;
Pred. No. 0.0085;
                                                                                                                                                                    Score 116; DB 1;
Pred. No. 0.0085;
1; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 РАРКРАРОРБРОРРОРРОРРОР--РОКОРЕАРАРОРРАС
                                                                                                                                                                                                                                                    6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG-
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                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Lin, Biaoyang
APPLICANT: Lin, Biaoyang
TILLE OF INVENTION: Mouse Model for Huntil
TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42, Application US/08457273B Patent No. 5849995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Raleigh
STATE: No. 5849995th Carolina
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
ATTORNEY-AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Virginia Bennett
PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%;
ilarity 46.4%;
Conservative
                                                                                                                                                                      Query Match
42.6%;
Best Local Similarity 46.4%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3144 amino acids
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-854-1401
:NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-265-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS: sin
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Best Local Similarity
Matches 26; Conserv
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                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-457-273B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
APPLICANT: Gusella, James F.
ATILLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 3144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PAPKPAPQPGPQPPQPPQPPQP--PQRQPEAPAPQPPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                    Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08453265 Patent No. 5693757
                                     1100 New York Avenue
                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERNCE/DOCKET NUMBER: 06
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.4<sup>†</sup>
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-246-982A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                         CITY: Washington STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

g ò

Search completed: May 7, 2003, 16:57:24 Job time: 10.0228 secs

NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
FELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

STREET:

ä

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49 ; Search time 5.63203 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-855-754B-19 335 1 GARAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 58

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

SUMMARIES

		Description	P24328 bordetella	Q03035 bordetella		P21997 volvox cart		_	P12978 epstein-bar			orgyla	herpes	arabidc	Q64467 mus musculu	sпш						_					P25050 herpesvirus	~	P05143 mus musculu	Q99014 trichoderma	P51111 rattus norv	O08816 rattus norv	bos	_	Q09442 caenorhabdi
SUMMAKIES	;	a	PERT_BORPA	PERT_BORBR	PERT_BORPE	SSGP_VOLCA	APG_BRANA	YPRO_OWEFU	EBN2_EBV	ACRO_RABIT	GP1_CHLRE	X066_NPVOP	TEGU_HSV11	APG_ARATH	G3PT_MOUSE	FM14_MOUSE	FMN1_MOUSE	MOZ_HUMAN	SEPA_EMENI	RFX1_HUMAN	EXLP_TOBAC	CAPU_DROME	ACRO_PIG	COLL_HSVSC	S3A2_HUMAN	S3A2_MOUSE	COLL_HSVS7	PRP2_MOUSE	PRP3_MOUSE	KPC1_TRIRE	HD_RAT	WASL_RAT	WASL_BOVIN	WASL_HUMAN	YP85_CAEEL
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		Match Length	922	911	910	485	449	141	487	431	555	875	3164	534	440	1206	1468	2004	1790	979	426	1059	415	102	464	475	105	261	296	1139	3110	501	202	202	379
di	Query	Match	100.0	84.8	62.4	49.6	49.4	48.1	45.5	44.9	44.2	44.2	٠.	42.2	ς.	ij	41.9	ij	41.2	40.7	40.4	40.4	ö	ö	σ.	φ.	39.3	39.3		σ	6	œ	ω.	38.8	
	Ċ	score	335	284	209	166	165.5	161	152.5	150.5	148	148	146.5	141.5	141	140.5	140.5	139	138	136.5	135.5	135.5	134.5	134	133	132	131.5	131.5	131.5	3	130.5	130	130	130	129.5
	Result	2	1	7	e	4	S	v	7	œ	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29		31	35	33

mus musculu homo sapien	mus musculu mus musculu trypanosoma	rattus norv pseudomonas mus musculu	mus musculu triticum ae homo sapien
P70315 060885 D04726	P02831 070324 P09791	P10164 Q05613 Q63943	P42859 P04723 P42858
WASP_MOUSE BRD4_HUMAN GDA6 WHEAT	HXA3_MOUSE MOT8_MOUSE PARB_TRYBB	PRP2_RAT TONB_PSEPU MEFD_MOUSE	HD_MOUSE GDA3_WHEAT HD_HUMAN
520 1362 296	565 129	172 243 514	3119 282 3144
888	38.5 1.1.6 1.1.8	6.7.5.6 8.8.8.6	37.6
128.5 128.5	127.5 127.5 126.5	126.5 126.5 126.5	126 126 126
35 35 35	388	0444	4 4 4 2 4 6

ALIGNMENTS

	ALIGNMENIS	
RESU	RESULT 1	
PERI	T.	
AC.	P24328;	
TO C	01-MAR-1992 (Rel. 21, Creat	
120	15-JUN-2002 (Rel. 41,	
DE	Pertactin precursor (Outer	
NS C		
So		
38	nc bacteria; Fruteobacteria; Deta Subdivision; Alcaligenaceae; C Bordefella	•
š		
RN		
RP		
. R		
XX.		
\$ £	A bi b.J., bougam G., Novocmy F., Charles I.G.; UT "P.70 pertactin, an outer-membrane protein from Bordetella	
RT	parapertussis: cloning, nucleotide sequence and	ssion in
RT	Escherichia coli.";	
RL	Mol.	
ខ	-1- FUNCTION:	PROCESS
<u>ဗ</u>		NI
38	C BACTEKTAL ADHESION, AND THUS PLAY A KOLE IN VIRULENCE.	
38	- ÷	
88	-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE	COUGH.
8		(2+)
ຍ	CONCENTRATIONS.	
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38	C This SWISS-PROT entry is copyright. It is produced through a collaboration	collaboration
36		Outstation -
3 8		TOUR OU TER
88	c modified and this statement is not removed. Usage by and for commercial	or commercial
ပ		.ch/announce/
ខ	c or send an email to license@lsb-sib.ch).	
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, a	EMBL: A26124:	
DR	EMBL	
DR	PIR; S152	
Y C	Tatompac, Throodepo.	
D VX	InterPro	
DR	InterPro; IPF003991;	
DR	Pfam; PF03212; Pertac	
S i	PRINTS; PR01482;	
N D		
FT	SIGNAL 1 34	
FT	CHAIN 35 922	
FT	CHAIN 35 647	
FT	PROPEP 648 922	
F.I.		z

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                             ö
                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: Outer membrane.
-i- DISEASE: MAY CONTIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                                                       621
                                                                                            (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
             LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Gen. Microbiol. 138:1697-1705(1992).
-!- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protective outer-membrane protein P.68 pertactin from Bordetella
bronchiseptica.";
                                                                                                                                                                                                                                         CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                             Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2007 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                         Indels
                                                                                                                                                        100.0%; Score 335; DB 1;
100.0%; Pred. No. 9.6e-14;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERTACTIN (P.68).
                                                                                                                                                                                                                                                                                                                                      911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; A1975, PT A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
Throw TPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92407514; PubMed-1527510;
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PRINTS; PR01484; PRTACTNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003991; pertacti
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54815; CAA38584.1; -. EMBL; A19180; CAA01453.1; -.
                                                                                                                          92178
                                                                                                                                                                          Local Similarity 100.
nes 58; Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                               280
                                                                                                                            322 AA;
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                                                                                                                                                                                                                                                                                                                                 PERT_BORBR
Q03035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella.
                                                                                                                              SEQUENCE
                                                                                                                                                           Query Match
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Matches
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Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;
Nature 381:90-92(1996).
-1- FUNCTION: AGGLUTINOGEN THAT BINDS TO EURARYOTIC CELLS; A PROCESS MEDIATED BY THE R.G. D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAX A ROLE IN VIRULENCE.
-1- SUBUNIT: MONOMER.
-1- BISEASE: MAY CONTRIBUTE TO THE DISSASE STATE OF WHOOPING COUGH.
-1- DISEASE: MAY CONTRIBUTE TO THE DISSASE STATE OF LOW MG(2+)
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane
protein P.69 from Bordetella pertusais.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                         28
                                   SITE (POTENTIAL).
REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G., "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
 ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                   9
                                                                                                                                                                               Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                            01-7NN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                             Score 284; DB 1; Length 91
Pred. No. 9.2e-11;
0; Mismatches 0; Indels
                                                                                                      280 3 (APPROXIMATE).
501 7 X 3 AA REPEATS OF P-Q-P.
93995 MW; 3078DF6ECZD987A1 CRC64;
                             ELL ATTACHMENT
X 5 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                              910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Microbiol, 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                  LINES)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                           84.8%;
89.7%;
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                                                                                                                                                                                                                   52; Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                 703
275
270
275
280
                                                                                                                           601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis.
                                                                                                                                        911 AA;
                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=520;
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                                                                                                                                                                                                                                                                                                                                                                          PERT_BORPE
P14283;
                                                                                                                                            SEQUENCE
                                                                                                                                                                               Query Match
                                                                                                                                                                                                    Best Local
                                                                                       REPEAT
                                                                                                        REPEAT
                                                                                                                           DOMAIN
                                                                       REPEAT
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                                                                                                                                                                                                                   Matches
SELETETE
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EMBL; J04560; AAA22980.1; ALT_SEQ.

PRO-RICH.

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CEX.
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P40603;
                DOMAIN
SEQUENCE
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ACT_SITE
SEQUENCE
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                                                   Query Match
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   DOMAIN
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APG_BRANA
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Bril H., Mengele R., Wenzl S., Engel J., Sumper M.;

Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;

Ertl H., Mengellar matrix of Volvox carteri: molecular structure of the extracellular compartment.*

J. Cell Biol. 109:3499-3501(1989).

-1- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE FOR FORM CONTIGUOUS CELLULAR COMPATRENTER. SSG 185 IS THE MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-1- FTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                               X 5 AA TANDEM REPEATS OF G-G-A-V-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                             CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                  1; Indels 16;
                                                                                                                                                                                                                                          (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                          Length 910;
                                                                                                                                                                                                                                                                                        Score 209; DB 1;
Pred. No. 2.3e-06;
0; Mismatches 1;
                                                                                                                     PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                              (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA
                                                                                  Outer membrane; Signal; Virulence; Repeat.
SIGNAL 1 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A33647; A33647.
Glycoprotein; Sulfation; Hydroxylation.
                                                                                                                                   POTENTIAL
          InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                          PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                 93452 MW;
                                                                                                                                                                                                                                                                                        ch 62.4%;
1 Similarity 70.7%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X51616; CAA35953.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                 276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                        REPEAT
DOMAIN
SEQUENCE
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PROPEP
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REPEAT
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sperimatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KAPPAPKPAPQPGPQPGPQPPQPPQP------PQPPQPPQPPQRQPEAPAPQPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURATIĆN.
-!- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
1-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 449;
                                                                                     Length 485;
                                                                                                                           Indels
                                                                                                                                                                                               5 PPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPP 50
                                         50436 MW; A52216400A031421 CRC64;
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9EFB6A3AB28EEA15 CRC64;
                                                                                 49.6%; Score 166; DB 1; L. 56.5%; Pred. No. 0.00048; Live 2; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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llarity 47.5%; Pred. No. 0.00049;
Conservative 4; Mismatches 17
                                                                                                                                                                                                                                                                                                                    449 AA
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PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                        POLY-PRO
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48779 MW;
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
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4/28
4/9 AA;
228
260
485 AA;
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Best Local Similarity
Matches 29; Conserv
                                                                                                     Best Local Similarity
Matches 26; Conserv
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Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 48.2
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                    - PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                              487 AA;
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Haffull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen J.I., Wang F., Kieff E.; "Spetch 2 mutations define essential domains for transformation and transactivation."; "Urtol. 65.2546.2554(1991).
-i- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        MEDLINE-9014772. PubMed=2105723;

Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;

Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";

Blochem. Blophys. Res. Commun. 166:66-73(1990).

PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins."; Virology 176:563-574(1990).
                                                                                                                                                                     Bukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Ovenildae; Ovenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 161; DB 1; Length 141; 55.1%; Pred. No. 0.00039; ive 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPPQRQPEAPAPQPPAGR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BYRF1
Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AA; 15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-T-H MOTIF (POTENTIAL).
                                    YPRO_OWEFU STANDARD; PRT; 141 AA. P21266; P21261; Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-WO-1995 (Rel. 32, Last annotation update) Wypothetical proline-rich protein (Fragment) owenia fusiformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90266473; Pubmed-2161150;
Petti L., Sample C., Kieff E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10377;
                                                                                                                                                                                                                         NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EBN2_EBV
P12978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
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DOMAIN
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Matches
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                                                            ACCOUNT BY A REPLACE OF THE REPLACE 
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between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA. >> LYS-XAA. SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-New Zealand white; TISSUE-Testis;

STRAIN-Sew Zealand white; TISSUE-Testis;

STRAIN-Sew Zealand white; TISSUE-Testis;

MEDLINE-9458861; PubMed-8086468;

Richardson R.T., O'Rand M.

Richardson R.T., O'Rand M.

"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";

Bicohim. Biophys. Act 1219:215-218(1994).

IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Activator; Nuclear protein; DNA-binding; Phosphorylation; Repeat: PONALN PPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQR-----QPEAPAPQPPAGREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 X 2 AA TANDEM REPEATS OF DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 152.5; DB Pred. No. 0.003; 4; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 AA
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V01555; CAA24877.1; ALT_INIT.
TRANSFAC; T01618; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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33, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%;
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Repeat;
                                                                                                                                                                                                 Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-164623;
                                                                                                                                                            Glycoprotein:
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YOG6_NPVOP
                                                                                                                                                                                                 DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
        à
                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding cell wall hydroxyproline rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
Pfam; PF00089; trypsin; 1.
PRINTS; PR0722; CHYMOTRYPSIN.
BARRT; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_LER; 1.
Hydrolase; Serine protease; Glycorotein; Zymogen; Sperm; Signal.
                                                                                                                             ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Bukaryota; Viidiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonaceae; Chlamydomonas
NCBL_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILNB-2115902; Pubmed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GP1_CHLRE STANDARD, PRT; 555 AA.

O9FPO6, 003927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91017504; PubMed-1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKAPPAPKPAPQPGPQP-GPQPP----QPPQPPQPPQPPQPPQRDEAPAPQPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                21; Indels
                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          1C015A4E0BC0C668 CRC64;
                                                                                                                                                                                                                                                                                               CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0036;
0; Mismatches 2
                                                                                                                                                                       SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: Associates with GP2 and GP3.
-1- PTM: N-glycosylated and O-glycosylated.
                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                      44.9%; Score 150.5; 52.7%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                        46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                            140
238
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein 1).
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ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                    DISULFID
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                                                                                                                                         CHAIN
PROPEP
DOMAIN
                                                                                                   SIGNAL
                                                                                                                               CHAIN
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Matches
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear nollyhadrogis virus genome".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 806-875 FROM N.A. MEDLINE-95343549; MEDLINE-95343540; Pubmed-7618274; Ahrens C.H., Carlson C., Rohrmann G.F.; Identification, sequence, and transcriptional analysis of lef-3, gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 VEGETATIVE CELL WALL PROTEIN GP1.
49 x 5 AA APPROXIMATE PPSPX REPEATS.
PDLY-PRO.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
6A584A99465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-2721300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.2%; Score 148; DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 APPAPKPAPQPGPQPPQPPQPPQPPQP---PQPPQPPQRQPEAPAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 210 372-382(1995).
-1- SIMILARIȚY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q83949, Q65364; O10323; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 98.6 kDa protein (ORF71).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.00
2; Mismatches
                                                                                                                                                           EMBL; M58496; AA69706.1; ALT_EEQ. GlycoSulteDB; Q9FPQ6; ...
InterPro; IPRO02965; P_itch_extensn. InterPro; IPRO03882; Pistil_extensin. PRINTS; PRO1217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; Pubmed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54219 MW;
                                                                                                                                EMBL; AF309494; AAG45420.1; -
                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.08;
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Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-88274327; PubMed-2839594; MGGeoch D.J., Dallan A., Frame M.C., MGGROCH D.J., Dalrymple M.A., Davison A.J., Dollan A., Frame M.C., Taylor P.; Taylor P.; Taylor P.; Taylor D., Perry L.J., Soctt J.E., Taylor P.; Taylor P.; The complete DNA sequence of the long unique region in the genome of
                                                                                                                                                                             Gaps
                                                                                                                                         Gaps
                                                                                                                                                              5 PPAPKPA-----PQPGPQPGPQPPQPP-----QPPQPPQPPQRQPEAPAPQ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.7%; Score 146.5; DB 1; Length 3164; 67.9%; Pred. No. 0.026; 1ve 2; Mismatches 8; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 X 2 AA TANDEM REPEATS OF P-Q.
                                                                                                               Score 148; DB 1; Length 875; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC5D31FF4F9FE3F4 CRC64;

        DOMAIN
        86
        91
        POLY-PRO.

        SEQUENCE
        875 Aa;
        98603 MW;
        F03DB1B430D33C42 CRC64;

                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL)6).
                                                                                                                                                                                                                                                                                           PRT; 3164 AA.
                                                                                                                           Pred. No. 0.008
3; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3164 AA; 335857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X14112; CAA32311.1; -. PIR; I30085; WMBEH6.
                    EMBL, U75930; AAC59070.1; -. EMBL, U39145; AAB04047.1; -. EMBL, D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                               Query Match

Best Local Similarity 47.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2980
                                                                  Hypothetical protein.
DOMAIN 86 9
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                         TEGU_HSV11
                                                                                                                                                                                                                                  146 P 146
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densiby—Jackson L., Kuo A., Leder P.,

"A variant limb deformity transcript expressed in the embryonic mouse
"Ind defines a novel formin.";

"Ind defines a no
                        between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PPAPK----PAPQPGPQPGPQPPQPPQPPQPPQRQP----EAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
MISSING (IN REF. 2).
L -> V (IN REF. 2).
05FF0A093DIABD9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              005859;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAX, 2000 (Rel. 39, Last annotation update)
Formin 1 isoform IV (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 141; DB 1
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           CYS/PRO-RICH.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                          MGD; MGI:95653, Gapds.
InterPro: IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo;
MEDLINE-92112033; PubMed=1339380;
                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; NAD
                                                                                                                                                                                                                                                                               Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47657 MW;
                                                                                                                                                         EMBL; M60978; AAA53033.1; -.
EMBL; U09964; AAA80276.1; -.
HSSP; P56649; IDSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.1%;
54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
43
440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                                         Glycolysis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FM14_MOUSE
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- FOUNCION: MAY PLAY AN IMPORTANT ROLE IN REGULATING THE SWITCH
BETWEEN DIFFERENT PATHWAYS FOR ENBERY PRODUCTION DURING
SPERMIOGENESIS AND IN THE SPERMATOZOON.
- CATALYTIT OF TYVETAL Gehyde 3-phosphate + phosphate +
NADL+) = 3-phospho-D-glyceroyl phosphate + NADH.
-- PATHWAY: Second phase of 91ycolysis; first step.
-- SUBDINIT: HOMOTETRAKER (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-- DEWELOPHRITAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC
GERM CELLS. LEVELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
                                                                                                               ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  3 KAPPAPKPAPQPGPQPGPQ-----PPQPPQP-PQPPQPPQPPQPPQRPPAP----- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ICR SW189, TISSUE-Testis;
MEDLINE-95254745; PubMed-7736666;
Welch J.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-melotic spermatogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Mokaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CD-1; TISSUE-Testis;
MEDLINE-92273722; PubMed-1375514;
Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.;
Expression of a glyceraldehydd 3-phosphate dehydrogenase gene specific to mouse specimatogenic cells.";
Biol. Reprod. 46:869-878(1992).
                                                                                                                                                                                                                                                                          Score 141.5; DB 1; Length 534;
Pred. No. 0.014;
5; Mismatches 15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         064467; 060650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                                                                                                           S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                   POTENTIAL
                                     Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                              141 E
325 E
58007 MW;
                                                                                                                                                                                                                                                                          42.2%;
llarity 43.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1.12) (GAPDH).
                                                                                                                                                                                                                                       534 AA;
                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||
158 PPKPPA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 1.2.1.12) (
GAPDS OR GAPD-S
                                                                                                                                                                                                                                                                                                                                                                                                                                 46 APQPPA 51
                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G3PT_MOUSE
                                                                                                                                    ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                   CONFLICT
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                                                                                Signal.
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DAN THE TELETICS
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PIM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.

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SUBFAMILY.
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SEQUENCE
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Kidney, and Testis;
MEDLINE-90363291; PubMed-2392150;
MOYGHIK R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.;
"'Formins': proteins deduced from the alternative transcripts of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 APPAPKPAPQPGPQP---GPQPPQPPQPPQP------PQPPQPPQRQPEAPAPQPP 50
-1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-1- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97224459; PubMed-9119367;
Wang C.C., Chan D.C., Leder P.;
"The mouse formin (Fmn) gene: genomic structure, novel exons, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                  EMBL; X62379; CAA44244.1; -.
PIR; S24407; S24407.
MGD; MG: 1010115; Fmn.
InterPro; IPR003104; FH2.
InterPro; IPR003104; FH2.
Pfam; PF02181; FH2; 1.
PRINTS; PR00828; FORMIN.
SMARY; SMO0498; FH2; 1.
Nuclear protein; Developmental protein; Alternative splicing; Phosphorylation; Colled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 140.5; DB 1; Length 1206; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER.
W; 4DFB38CB52BD8EE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
FH1 (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL). POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last annotation update)
Formin 1 isoforms I/II/III (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 29, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic mapping.";
Genomics 39:303-311(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Limb deformity gene.";
Nature 346:850-853(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMN1_MOUSE
Q05860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 PG 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                 11. Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

12. FUNCTION: IS IMPORTANT FOR THE MORPHOGENESIS OF LIMB AND KIDNEY
AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR MAY BE
INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

12. SUBCELLULAR LOCATION: Nuclear
13. ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (SHOWN HERE), IB,
11. III AND IV (AC 00589); ARE PRODUCED BY ALTERNATIVE SPLICING.
20. DIFFERENT SIZE TRANSCRIPES EXIST WITHIN ANY ONE TISSUES AND
21. DIFFERENT SIZE TRANSCRIPES EXIST WITHIN ANY ONE TISSUE.
21. LIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN
22. ILIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN
23. CIAND: IT IS PRESENT TRROUGHOUT THE BENERY
24. COMPARTMENT, PREDOMYNAULY IN THE DEVELOPING LIMB BUD, THE PROTEIN
25. COMPARTMENT, PREDOMYNAULY IN THE POSTERROR REGION. DURING
26. COMPARTMENT, PREDOMYNAULY IN THE POSTERROR REGION. DURING
27. THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
28. THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
29. THE EPITHELIAL COMPARTMENT ON SERINE AND POSSIBLY THREONINE RESIDUES.
20. THE EPITHELIAL COMPARTMENT ON SERINE AND POSSIBLY THREONINE RESIDUES.
20. THE EPITHELIAL COMPARTMENT ON SERINE AND POSSIBLY THREONINE RESIDUES.
20. STHALARITY: CONTAINS I FORMIN HOMOLOGY 2 (FH2) DOMAIN.
20. STHALARITY: BELONGS TO THE FORMIN HOMOLOGY 2 (FH2) DOMAIN.
20. STHALARITY: BELONGS TO THE FORMIN HOMOLOGY 2 (FH2) DOMAIN.
20. THE PARTICLE COMPANTIVE THE FORMIN HOMOLOGY 2 (FH2) DOMAIN.
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20. THE PARTICLE COMPANTIVE THE FORMIN THE FORMIN THE FORMIN THE FORMIN T
                                          Vogt T.F., Jackson-Grusby L., Rush J., Leder P.; "Formins: phosphoprotein isoforms encoded by the mouse limb deformity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; Developmental protein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 140.5; DB 1; Length
Pred. No. 0.033;
1; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EF2FB1E9CA9DAF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM IB).
MISSING (IN ISOFORM II).
IA -> SV (IN ISOFORM III).
MISSING (IN ISOFORM III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL)
FH1 (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO. POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-SER.
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MEDLINE=93296176; PubMed=8516300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S11515; S11515.
MGD; MGI:101815; Fmn.
InterPro; IPR003104; FH2.
InterPro; IPR001265; Formin.
Pfam; PF02181; FH2; 1.
PRINTS; PR00828; FORMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X53599; CAA37668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.28;
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Best Local Similarity 45.2
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1468
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51 AG 52 | | 970 PG 971

qq

Search completed: May 7, 2003, 16:48:11 Job time : 6.63203 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:41:02 ; Search time 10.8688 Seconds (without alignments) 513.008 Million cell updates/sec Run on:

US-09-855-754B-19

335 1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	pertactin - Bordet	He	outer membrane pro	hypothetical 47,8K	sulfated surface q	proline-rich prote	pherophorin-S - Vo	hypothetical proli		a	cysteine-rich exte	acrosin (EC 3.4.21	chitinase (EC 3.2.	hypothetical prote		hypothetical prote		proline-rich prote	hypothetical prote	드	hypothetical prote	proline-rich prote	. extensin homolog T	T20H2.9 protein -	glyceraldehyde-3-p	hypothetical prote	formin isoform IV	formin - mouse	hypothetical prote
SUMMARIES	DI	S15204	A47675	A32560	JC2301	A33647	S16748	T10798	A34043	AE2295	S42442	A48232	847538	S51939	T48814	B48232	T10340	ММВЕН 6	T17547	н83619	T07907	B96534	S21961	T06291	A86335	149681	C96623	S24407	S11515	F75518
	DB	7	7	7	7	~	~	7	~	7	7	7	~	7	7	7	~	-	~	7	~	~	~	~	~	~	~	~	7	N
	Query Match Length	922	911	910	430	485	449	599	141	383	487	209	431	439	1952	196	875	3164	544	270	446	494	534	760	1137	440	929	1206	1468	839
ď	Query Match	100.0	84.8	62.4	50.3	49.6	49.4	49.3	48.1	46.6	45.5	45.4	44.9	44.8	44.8	44.3	44.2	43.7	43.6	43.1	43.1	43.0	43.0	42.2	42.2	42.1	42.1	41.9	41.9	41.8
	Score	335	284	209	168.5	166	165.5	165	191	156	152.5	152	150.5	150	150	148.5	148	146.5	146	144.5	144.5	144	144	141.5	141.5	141	141	140.5	140.5	140
	Result No.	-	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

protein-tyrosine-p	pistil extensin-li	extensin - Volvox	regulatory factor	pistil extensin-li	unknown protein [1	microfilarial shea	acrosin (EC 3.4.21	hypothetical prote	hypothetical prote	ORF2 protein - sai	immediate-early pr	alpha/beta-qliadin	spliceosome-associ	proline-rich prote	proline-rich prote
55	16	97		969	41	99	.70	16	. 11	.10	IIF	164	55	649	990
T1435	P00476	S22697	A35913	JQ1696	G8644	84696	A3417(A71416	T316	B34770	EDBEIF	E2236	A47655	C29149	B39066
7	~	~	~	~	~	~	-	~	7	~	-	7	~	7	~
1494	154	464	979	426	1201	228	415	645	1585	102	1460	320	464	227	278
41.2	41.0	40.9	40.7	40.4	40.3	40.1	40.1	40.1	40.1	40.0	40.0	39.7	39.7	39.6	39.4
138	137.5	137	136.5	135.5	135	134.5	134.5	134.5	134.5	134	134	133	133	132.5	132
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	42

ALIGNMENTS

RESULT 1 S15204	
pertactin + Bordetella parapertussis	
N;Alternate names: outer membrane protein P70	
C;Species: Bordetella parapertussis	
C;Date: 07:Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-oct-1999	
C; Accession: S15204; S14659	
R;Li, L.J.; Dougah, G.; Novotny, P.; Charles, I.G.	
Mol. Microbiol. 5, 409-417, 1991	
A:Title: P:70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo	9
A; Reference number: S15204; MOID:91251771; PMID:2041476	
A; Accession: S15204	
A; Molecule type: DNA	
A; Residues: 1-922 <lil></lil>	
A; Cross-references: EMBL: X54547; NID: q39761; PIDN: CAA38419.1; PID: q39762	
C;Genetics:	
A;Gene: prn	
C;Keywords; membrane protein	
Query Match 100.0%; Score 335; DB 2; Length 922;	
Desc. Local Similarity 100.0%; Fred. No. 7.96-15; Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY I GAKAPPARKAAPOGPOGPOGPOPOPOPOPOPOPOGPOGPOGPOFF 58	
DD 564 GAKAPPANKPANPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOPANPOPANPOPAN 621	

RESULT 2

68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica C; Species: Bordetella bronchiseptica C; Species: Bordetella bronchiseptica C; Date: 19-pecies: Bordetella bronchiseptica C; Date: 19-pecies: Bordetella bronchiseptica C; Date: 19-pecies: 19-pec

A) Accession: A47675 A) Status: preliminary A; Molecule fype: incled acid A; Residues: 1-911 <LII> A; Cross-references: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397 A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

; 9 Query Match

84.8%; Score 284; DB 2; Length 911;
Best Local Similarity 89.7%; Pred. No. 1.3e-11;
Matches | 52; Conservative 0; Mismatches 0; Indels

ï

Gaps

1 GAKAPPAÈKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPBAPAPQPPAGRELSAA 58

δ

Length 485;

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Score 166; DB 2;
Pred. No. 0.00024;
2; Mismatches 18;
                                                5;
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Best Local Similarity 55.3%;
Matches 26; Conservative
  49.6%;
llarity 56.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 49.4%;
Best Local Similarity 47.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pherophorin-S - Volvox carteri
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
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    Query Match
Best Local S:
Matches 26
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                                                                                                                                                                                                               RESULT 6
S16748
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C. Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Accession: A33647
R; Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
A; Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
A; Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular
A; Reference number: A33647; MUID:90094551; PMID:2689458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nilternate names: ORF-3
C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
Nam Res. J, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
                                                                                                              Outer membrane protein P.69 precursor - Bordetella pertussis
C;Species: Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: O'Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Sci. US.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number: A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: D31909; GB: D17441; NID: 9559718; PIDN: BAA06706.1; PID: d1007278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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A;Reaidues: 1-485 <ERT>
A;Cross references: GBX51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----APAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 15910 <CHA>
A; Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
       GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: membrane protein
F;l-34/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPPGPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 209; DB 2; Le
Pred. No. 7.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Some 168.5; DB 2; Similarity 52.5%; Pred. No. 0.00015; 11; Conservative 2; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sulfated surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 47.8K protein - Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.4%;
70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 70.7 tes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-430 <WAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                 A; Accession: A32560
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proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S16748
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991
A;Bescription: Cloning and characterization of a proline-rich gene expressed specific A;Reference number: S16748
A;Accession: S16748
A;Recession: S16748
A;Recession: S16748
A;Recession: S16748
A;Recession: S16748
A;Residues: 1-449 < RNA
A;Residues: 1-449 < RNA
A;Residues: Data Control of a proline-rich gene expressed specific A;Residues: Data Control of A;Residues: Data
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C; Date: 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T10798
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
A; Title: Differential targetting of closely related ECM-glycoproteins: The pherophori A; Reference number: Z17154; MUID: 97162277; PMID: 9009264
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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Pred. No. 0.00025;
4; Mismatches 17; Indels 11
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                                                                                                                                                                  5 PPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPP
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Pred. No. 0.00033;
1; Mismatches 20;
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1; Mismatches
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A;Residues: 1-431 <RIC>
A;Cross-references: EMBb:U05204; NID:9451841; PIDN:AAA61630.1; PID:9451842
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C;Keywords: glycoprotein; hydrolase; serine proteinase
F;40-283/Domain: trypsin homology <TRY>
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A:Molecule type: mRNA
A:Residues: 1-209 < WUA>
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Matches 27; Conserv
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Matches 27; Conserv
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C; Nostoc 20.
C; Nosto
A;Title: Presence in invertebrate genomes of sequences characterized by the repetition of Steference number: A90159; MUID:90147742; PMID:2105723
A;Refedence number: A34043
A;Molecule type: DNA
A;Residues: 1-141 cBAR>
A;Residues: 1-141 cBAR>
A;Cross-references: GB:M32217
A;Accession: B34043
A;Accession: B34043
A;Residues: 59-136 cBA2>
A;Cross-references: GB:M32217
A;Cross-references: GB:M32217
A;Cross-references: GB:M32217
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R;Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2.
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Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a
A;Feference number: S42440; MUID:86259739; PMID:3460083
A;Accession: S42442
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A;Experimental source: strain PCC 7120
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
C;Accession: S42442; S32988; S42447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 161; DB 2; Length 14
Pred. No. 0.0002;
0; Mismatches 22; Indels
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Pred. No. 0.00087;
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A; Residues: 1487 <SAM>
R; Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A; Reference number: $32973
A; Accession: $32988
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54.38;
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Best Local Similarity 55.1%;
Matches 27; Conservative
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hes 25; Conservative
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A; Residues: 1-487 <FAR>
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A; Molecule type: DNA
A; Residues: 1-383 <KUR>
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A)Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cysteine-rich extensin-like protein 1 precursor - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000 C;Accession: A48232; po0475; S24617 F;Wu, H:;Zou, J:;May, B:;Gu, Q:;Cheung, A:Y. Proc. Natl Acad: Sci. U.S.A. 90, 6829-6833, 1993 A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A;Reference number: A48232; MUID:93342083; PMID:8341705
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A:Title: Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproa A:Reference number: 847538; WUID:94368861; PMID:8086468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acrosin (EC 3.4.21.10) precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 26 Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
                                                          A; Molecule | type: DNA
A; Mesidues: 1-88, 'PPP', '99-487 < DAM>
A; Cross references: EMBL: KO3333; NID: 9330443; PIDN: AAA45903.1; PID: 9330444
C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Keywords; cell wall; extracellular matrix; fertilization; glycoprotein fr.149/momain: signal sequence #status predicted <SIG>. 150-209/Product: cysteine-rich extensin-like protein 1 #status experimer F:146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                            PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQR-----QPEAPAPQPPAGREL 55
                                                                                                                                                                                                                                                                                    ..
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4
                                                                                                                                                                                                                      Length 487
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Pred. No. 0.00099;
I; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPKPAPOPGPOPGPOPPOP---POPPOPPOP-POROPEAPAPOPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:919919
Petit Havana SR1
A;Reference number: S42447; MUID:85063846; PMID:6209719
A;Accession: S42447
                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                Score 152.5; DB Pred. No. 0.0018; 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A: Molecule type: mRNA
A: Residues: 39-209 <GOL>
A: Cross-creences: EMBL: 214020; NID: 919918; IS. Experimental source: stigma, style; strain C; Superfamily: glutelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                45.5%;
llarity 48.2%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.4%;
54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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C;Species: Micotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: B48232; PQ0474; S.24666
C;Accession: B48232; May, B.; Gu, O.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Developmental expression of tobacco pistil-specific genes encoding novel ext A;Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: glutelin
C; Keywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosadues: 1-196 <WUNA
A;Rosatues: 1-196 <WUNA
A;Crosarreferences: GB:L13440; NID:g310924; PIDN:AAA34060.1; PID:g310925
A;Crosarreferences: GB:L13440; NID:g310924; PIDN:AAA34060.1; PID:g310925
B;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 РАРКРАРОРСРОРСРОРРОРОР---РОФРОРРОРОR----ОРЕАРАРОРРА 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 'MAG',1-105 <GOL>
A;Cros-references: EMBL:214014
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.3%; Score 148.5; DB:
50.9%; Pred. No. 0.0016;
iive 5; Mismatches 14
                                                                           cysteine-rich extensin-like protein 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 7, 2003, 16:55:29
Job time: 12.8688 secs
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Best Local Similarity 50.99
                                                                                                                                                                                                                                                                                                 A; Accession: B48232
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A;Reference number: 224541
                                                                                                                                                                                                                                                                                                                                      C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Date: 28-Oct.1996 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Caccession: S51939; S72315; 845025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A. Plant Mol. Biol. 27, 211-216, 1995
A;Title: A prolline-rich chitinase from Beta vulgaris.
A;Reference number: S51939; MUID:95170004; PMID:7865792
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:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Gross-references: EMBL:X79301; NID:9488730; PID:9488731
A:Note: the authors translated the codon TGC for residue 416 as Gly
A;Accession: S72315
                   Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KAPPAPKPAPQPGPQPGPQPPQPPQP-PQPPQPPQPPQREA-PAPQPPAGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150; DB 2; Length 439;
Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1952 <SCH>
A; Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A; Experimental source: cosmid contig 15E6; strain 74
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 15E6.220 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 РРАРКРАРОРСРОРСРОРРОРРОРРОРРОРРОРРОРРОРРОРОВАРАРОРРА 51
Score 150.5; DB 2;
Pred. No. 0.0021;
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Pred. No. 0.0073;
3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: plant chitinase homology
C;Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted
F;26439/Product: chitinase #status predicted <AMR
F;183-423/Domain: plant chitinase homology <PCH>
                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 44.8%;
1 Similarity 50.0%;
27; Conservative
              44.9%;
nilarity 52.7%;
Conservative
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Best Local Similarity 51.1%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 191-397 <BER2>
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Best Local Similarity
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  chitinase (EC 3.2.1.14)
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A; Residues: 1-439 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
Introns: 248/1; 300/2
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                                                                   Matches
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Gaps

7;

Length 196; Indels

DB 2;

Sequence 47, Appl Sequence 2, Appl Sequence 20, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 7, Appl Sequence 1002, Ap Sequence 1002, Ap Sequence 1002, Ap Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 11345, A Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl

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TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PERAPERUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGHISEPHTCA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOT: 2.1
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAN.
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 US-10-023-523-47

0 US-09-812-240-2

0 US-09-812-240-2

0 US-09-912-111-70

US-10-043-487-282

US-10-043-487-282

US-10-020-215-2

US-10-020-215-2

US-09-950-987-7

US-09-955-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

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US-09-925-299-1002

US-10-101-813-10

US-10-01-873-10

US-10-01-873-12

US-10-042-417-32

US-10-042-417-32

US-10-042-417-32

US-10-042-417-32

US-10-086-464-4

US-10-086-464-2

US-10-086-464-2

US-10-086-464-3

US-10-077-584-9

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US-10-077-584-9
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Best Local Similarity 100.0%; Pred. No. 2.9e-16;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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: LENGTH: 58

: TYPE: PRT

: ORGANISM: Bordetella bronchiseptica

US-09-855-754-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUNESAUX EULDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-855-754-19
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306.927 Million cell updates/sec
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Sequence 47,
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1 GARAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
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US-09-855-754-16
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US-09-855-754-4
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AMMINGGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%; Score 335; DB 9;
1 Similarity 100.0%; Pred. No. 2.7e-15;
58; Conservative 0; Mismatches 0;
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Pred. No. 3.6e-14;
0; Mismatches 1
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US-09-855-754-18
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella parapertussis US-09-855-754-6
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Publication No. US20020192237A1
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 55; Conserv
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LENGTH: 922
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JUDICATION NO. USZULZUJAJANI

TUDICANT: GURCAUATION

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BORDEFELLA PRAPERTUSSIS,

TITLE OF INVENTION: BORDEFELLA PRAPERTUSSIS, AND BORDEFELLA

TITLE OF INVENTION: BONDEFELLA PRAPERTUSSIS, AND IN

TITLE OF INVENTION: IMMUNCAENIC COMPOSITIONS

FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: 05/09/855,754

CURRENT APPLICATION NUMBER: 60/206,969

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2000-05-25

NUMBER OF SEC ID NOS: 24

SOFTWARE: PATCHING VOY: 2.1
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERRUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION INVENER: US/O9/455,754
CURRENT APPLICATION NUMBER: US/O9/455,754
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                         Score 298.5; DB 9;
Pred. No. 7.3e-14;
0; Mismatches 0;
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89.7%; Pred. No. 5.9e-13;
iive 0; Mismatches 0
CURRENT APPLICATION NUMBER: US/09/855,754
                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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US-09-855-754-15
                                                                                                                                                                                                                                                                        Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-855-754-15; Sequence 15, Application US/09855754; Publication No. US20020192237A1
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Best Local Similarity 95.0%;
Matches 57; Conservative
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Matches 52; Conservative
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Query Match
Best Local Similarity 84.5
Matches 49; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 20
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US-09-855-754-20
       US-09-855-754-22
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LENGIH: 49
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Publication No. US20020192237A1

GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: PROINTEPTICES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: 05/206,969

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VET. 2.1

LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                     Length 911;
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                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                             Score 284; DB 9;
Pred. No. 6e-12;
0; Mismatches 0,
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                                                                                                     TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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ORGANISM: Bordetella bronchiseptica
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                                                                                                                                                                                                                                             Query Match 84.8%;
Best Local Similarity 89.7%;
Matches 52; Conservative
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Best Local Similarity 87.9%;
Matches 51; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 22
LENGTH: 54
SOFTWARE: Patentin Ver.
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                                 SEQ ID NO 4
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRARBETUSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PRARBETUSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PRARBETUSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/9855,754
CURRENT FILING DATE: 2001-09-10
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                                                        Gaps
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILLING DATE: 2001-09-10
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Best Local Similarity 82.8%; Pred. No. 3.3e-11;
Matches 48; Conservative 0; Mismatches 0;
Score 265; DB 9;
Pred. No. 1.1e-11;
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754-20
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79.18;
84.58;
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RESULT 14
US-09-855-754-24
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LENGIH: 910
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LENGTH: 39
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Best Local S
Matches 41
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS,
                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRPQRPQRPAPQPPAGRELSAA
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Pred. No. 4.1e-08;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 256; DB Pred. No. 4e-11 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
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US-09-855-754-21
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                         Sequence 21, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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1 Similarity 70.7%;
41; Conservative
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l Similarity 84.5%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-(NUMBER OF SEQ ID NOS: 24 SOFTWARE: PatentIn Ver. )
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Best Local Similarity
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US-09-855-754-23
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABETUSSIS, AND BORDETELLA PREPERTUSSIS, AND ENVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                       REPEATED
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                                                                                                          APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERRUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGRIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGLISSPICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-0026-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT PELLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
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Pred. No. 4.9e-07;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09855754 Publication No. US20020192337A1 GENERAL INFORMATION: APPLICANT: BOURSAUX EUDE, CAROLINE
                                                                                CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella pertussis
US-09-855-754-5
Sequence 5, Application US/09859 Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 62.4%;
1 Similarity 70.7%;
41; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                             APPLICANT: BOURSAUX-EUDE,
                                                         GENERAL INFORMATION
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GENERAL INFORMATION:

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us-09-855-754b-19.rapb
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Sindon W.
APPLICANT: Law, Sindon W.
APPLICANT: Law, Sindon W.
APPLICANT: ALION AND ALLAD A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: APPLEADED.
FILE REPERENCE: 1079-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT APPLICATION NUMBER: US/06/61,289
PRIOR FILING DATE: 2000-07-14
PRIOR PELLING DATE: 1997-11-26
PRIOR PELLING DATE: 1997-11-27
PRIOR PELLING DATE: 1997-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEAL DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEAL DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEG ID NOS: 53
NUMBE
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Search completed: May 7, 2003, 17:30:53 Job time : 18.3901 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein -

Мау Run on:

7, 2003, 16:41:51 ; Search time 9.58433 Seconds (without alignments) 178.054 Million cell updates/sec

US-09-855-754B-19 Title:

335 1 GAKAPPAPKPAPQPGPGP......QRQPEAPAPQPPAGRELSAA 58 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 segs, 29422922 residues Searched: Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:

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/cgn2_6/ptodata/1/iaa/PcrVB_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 6, Appli	4	~ ~	Patent No. 5202236		Н	16,	134,	2, 4	11	8	28,	29,	30,	31,	9	Sequence 6, Appli	42	21	15,	12,	12,	2, A	143		143,	138,
	O.	US-08-460-269C-6	US-08-460-269C-4	US-08-460-269C-2	5202236-37	5202236-3	US-08-246-982A-16	US-08-453-265-16	US-09-314-268-134	US-09-095-443-2	US-08-237-716-11	US-08-457-273B-8	US-09-041-886-28	US-09-041-886-29	US-09-041-886-30	US-09-041-886-31	US-08-246-982A-6	US-08-453-265-6	US-08-457-273B-42	US-08-556-419-21	US-09-041-886-15	US-08-534-342-12	US-08-675-140-12	US-08-155-888-2	US-08-818-112-143	US-08-818-111-138	US-09-056-556-143	US-09-072-596-138
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æ (Match	100.0	84.8	62.4	44.8	43.0	40.1	40.1	38.4	38.1	37.9	37.8	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.5	37.5	37.5	37.2	37.2	37.2	37.2
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	Sequence 100, App Sequence 2, Appli	Sequence 2, Appli	Sequence 32, Appl	Sequence 65, Appl	Sequence 65, Appl	Sequence 65, Appl	Sequence 66, Appl	7	,	Sequence 1, Appli	4	7	ω,	Sequence 66, Appl	Sequence 33, Appl	Sequence 66, Appl
US-08-750-624-11	US-08-301-083-100 US-08-749-391-2	US-09-390-200-2	US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65	US-09-179-558-66	US-08-929-417-2	US-09-080-897-4	US-08-899-595-1	US-09-323-735-4	US-09-109-841-2	US-08-460-269C-8	US-07-609-716-66	US-08-642-255-33	US-08-475-411A-66
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24	485	485	330	408	408	408	311	351	1255	1255	1255	490	23	357	357	357
37.0	36.6	36.6	36.4	36.4	36.4	36.4	35.8	35.8	35.5	35.5	35.5	35.1	34.9	34.9	34.9	34.9
124	122.5	122.5	122	122	122	122	120	120	119	119	119	117.5	1117	117	117	1117
788, 788,	3.6	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 922;
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SEARING SYSTEM: PC-DOS/MS-DOS
SOFWHARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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100.0%; Pred. No. 1.4e-21
ilve 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 03-Jun-1995
ATTORNEY,AGENT INFORMATION:
NAME: LEDOVIEz, RICHARIM
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPCLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                           Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 58; Conservative
                         US-08-460-269C-6
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RESULT 1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      **APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 APPAPAFAPAFAPAPAPAPPNPNPSPFSPPSPPSPPSPPSP 50
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Pred. No. 2.8e-06;
0; Mismatches 21.
                                                                                                                                                                                                                                                                                                                                                                                      Score 209; DB 4;
Pred. No. 6.7e-11;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
                                                                                                    REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR ESO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
                                                                                                                                                                                                                                         TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
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APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,445
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                             NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.4%;
Best Local Similarity 70.7%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 39
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Patent No. 5202236
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5202236-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08460269C

Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHARL A.

TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                               Sequence 4, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 284; DB 4;
Pred. No. 2.9e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 911 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 243
TELEPAX: (703) 243-6
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.8%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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RESULT 3

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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GENERAL INFORMATION:
APPLICANT: DOORDAR, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIRUSES
FILE REFERENCE: 3789/80902
CURRENT APPLICATION NUMBER: US/09/314,268
CURRENT FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Juyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof CORRESPONDENCE. 25
CORRESPONDENCE. 25
ADDRESSEE: C+----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KPAPQPGPQPPQPPQPPQPPQPPQPPQPPQPPQPEAPAPQP--PAGRELSA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 30-MAY-1995
GLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 134.5; DB 1;
Pred. No. 0.00041;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 128.5; DB 4
Pred. No. 6.9e-05;
3; Mismatches 17
                                                                                                                                                                             Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ludvig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/COCKET NUMBER: 0609.3880003
FELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Human papillomavirus type 21
US-09-314-268-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 134, Application US/09314268 Patent No. 63463,77
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 371-2600
TELEFRX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.9%;
Matches '28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.7%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEC ID NOS: 179
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                      STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-314-268-134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Pat
SEQ ID NO 134
LENGTH: 106
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                                                                                                                                                                                                                     4 APPAPKPAPQPG-----PQPGPQ------PQPGPQPPQPPQPPQPPQPPAPAP 47
                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 6; Length 334;
9.1e-06;
                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP--PAGRELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATH:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: MAY 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134.5; DB 1;
Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                              Score 144;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08246982A Patent No. 5686288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08453265
Patent No. 5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNET/AGENT INFORMATION:
NAME: GOLGACELI, JOSGE, A.
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHORE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.9%;
Matches 28; Conservative
                                                                                                              43.08;
                                                                                                                                     44.48;
        ; FILING DATE: 13-SEP-1984; SEQ ID NO:3: LENGTH: 334
                                                                                                        Query Match
Best Local Similarity 44.49
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: M
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washi
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-246-982A-16
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US-08-453-265-16
                                                                                                                                                                                                                                                                       48 QPP 50
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                                                                  5202236-3
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E: Nixon & Vanderhye, P.C.
1100 No. 5589384th Glebe Road, 8th Floor
APPLICANT: CHARLES, Ian G
APPLICANT: FATRWEATHER, Noil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREESSE: Nixon SPREEN
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: , CTHER INFORMATION: , CTHER INFORMATION: E
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Region LOCATION: 4..7 OTHER INFORMATION:
                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: PatentT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                          STATE: Virginia
COUNTRY: USA
                                                                                                                                          STREET: 1100 NO CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-457-273B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
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     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 127.5; DB 4; Length 1274; Pred. No. 0.00074; 1; Mismatches 12; Indels 35;
                                                                                                                                                                              Sequence 2, Application US/09095443
; Patent No. 6342593
; GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Plowman, Gregory
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: WALDHIEG, KICHARI J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 23,327
REFERENCE/DOCKET NUMBER: 23,327
TELEPHONE: (213) 489-1600
TELEPAX: (213) 489-1600
TELEPAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE .. COMPUTER: IBM COMPATIBLE .. DOS 5.0 SOFTWARE: FASICED for Windows 2.0 CURRENT APPLICATION DATA: BPLICATION NUMBER: US/09/095,443 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 QAPGLLPPQSPYPYAPQPGVLGQPP 649
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callifornia
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 Q-----QPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.1%;
Best Local Similarity 43.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-09-095-443-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                            98 PPPPNGHD 105
                                                          47 POPPAGRE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-237-716-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
                                                                                                                                                    RESULT 9
US-09-095-443-2
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Gaps
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pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 37.9%; Score 127; DB 1; L Best Local Similarity 57.5%; Pred. No. 3.3e-05; Matches 23; Conservative 2; Mismatches 3;
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 PAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PGPEIAPQPGPQPPQPPQP------QPEAPAPEP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- LTB sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= hinge region
                                  FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION 1815
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08457273B Patent No. 5849995 GENERAL INFORMATION:
                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 117
REFERENCE/DOCKET NUMBER: 117
TELECOMMUNICATION: TELEPHONE: 703-816-4000
TELEFRAX: 703-816-4100
                                                                                                                                                                                                                                               32,955
                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-810-410-11: SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayden, Michael
Lin, Biaoyang
Nasir, Jamal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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Sequence 11, Application US/08237716 Patent No. 5589384

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14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     13 QPGPQPGPQPPQPPQPPQPPQPPQP--PQRQPEAPAPQPPAG------RELSA 57
                                                                                                                                                                                                                                                                     Score 126; DB 4; Length 513;
Pred. No. 0.00044;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides; Dependent
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 ОРСРОРСРОРРОРРОРРОРРОРРОР--РОКОРЕАРАРОРРАС-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 126; DB 4;
Pred. No. 0.00046;

    Mismatches

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NAME: Campbell, Cathryn A.
REGISTARION UMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (519) 535-9001
TELEPHONE: (519) 535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
           P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/041,886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                             TELECOMMUNICATION INFORMATION TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                   Query Match 37.6%;
Best Local Similarity 47.5%;
Matches 28; Conservative
           REFERENCE/DOCKET NUMBER:
                                                TELEPHONE: (619) 535-900
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                         : 513 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 530 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.5
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 513 amino act
                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La
CITY: San Diego
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-041-886-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3118;
    Mouse Model for Huntington's Disease and
Related DNA Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 KPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP--PAGRELSA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 126.5; DB 2; Length
Pred. No. 0.002;
3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477-85A
                                                                                                Arthurs PO bon CITY: Raleigh STATE: No. 5849995th Carolina
TITLE OF INVENTION: Mouse Model
TITLE OF INVENTION: Related DNA
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: VITGIALA Bennett
STREET: PO BOX 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.9%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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E: California
TRY: United States
92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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16; Indels 14; Gaps
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                                   GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Brabizadeh, Sharioz
APPLICANT: Rabizadeh, Sharioz
TITLE OF INVENTION: Prospototic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                               OF ELANTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: JALLE
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ОРGРОРGРОРРОРРОРРОРРОРРОР--РОКОРЕАРАРОРРАС-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 4;
Pred. No. 0.00047;
1; Mismatches 16
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Sequence 30, Application US/09041886 Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELERAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 37.6%;
Best Local Similarity 47.5%;
Matches 28; Conservative
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STREET: 43/0 C.
CITY: San Diego
STATE: Callfornia
...mpv: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 552 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
COUNTRY: United States
2IP: 92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-041-886-30
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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| CLASSIFICATION: | ATTORNEY/AGENT INFORMATION: | ATTORNEY/AGENT INFORMATION: | ANAME: Campbell, Cathryn A. | RECISTRATION NUMBER: 31,815 | RECISTRATION NUMBER: 31,815 | REFERENCE/DOCKET NUMBER: P-LJ 2626 | TELEPHOME: (619) 535-9001 | TELEPHOME: (619) 535-9001 | TELEPAT: (619)
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